

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 15, 2005, 01:44:12 ; Search time 13388 Seconds
(without alignments)
11375.466 Million cell updates/sec

Title: US-10-015-391A-276
Perfect score: 3143
Sequence: 1 gggctgaggcactgagagac.....aaatataaggcttaaaaaaa 3143

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	3143	100.0	3143	6	AX697208	AX697208 Sequence
2	3143	100.0	3143	9	AY358531	AY358531 Homo sapi
3	3068.4	97.6	3257	9	BC020974	BC020974 Homo sapi

	4	3041.4	96.8	3252	9	AB029394	AB029394 Homo sapi
	5	3040.8	96.7	3104	6	AR564550	AR564550 Sequence
	6	3035.8	96.6	3191	6	BD249136	BD249136 27 human
	7	2682.2	85.3	2981	6	AX746794	AX746794 Sequence
	8	2682.2	85.3	2981	9	AK091127	AK091127 Homo sapi
	9	2476.4	78.8	2768	6	AX512887	AX512887 Sequence
	10	2284.4	72.7	2286	6	CQ716130	CQ716130 Sequence
	11	2283	72.6	2283	6	AR564551	AR564551 Sequence
c	12	2281	72.6	2281	6	AX528271	AX528271 Sequence
	13	2228.4	70.9	2271	6	AX528269	AX528269 Sequence
	14	1834.8	58.4	1838	6	BD157628	BD157628 Primer fo
	15	1834.8	58.4	1838	6	AX879068	AX879068 Sequence
	16	1834.8	58.4	1838	9	AK022349	AK022349 Homo sapi
	17	1760	56.0	3159	10	BC025800	BC025800 Mus muscu
	18	1727.6	55.0	3046	6	AR564562	AR564562 Sequence
	19	1727.6	55.0	3046	6	AR564565	AR564565 Sequence
	20	1727.6	55.0	3046	10	MMRNASEMB	X85991 M.musculus
	21	1719.4	54.7	3123	10	BC081943	BC081943 Rattus no
	22	1340	42.6	164168	9	AL135927	AL135927 Human DNA
c	23	1340	42.6	164179	9	AC007227	AC007227 Homo sapi
	24	696.6	22.2	775	6	BD146867	BD146867 Primer fo
	25	696.6	22.2	775	6	AX866805	AX866805 Sequence
c	26	498	15.8	567	6	BD152367	BD152367 Primer fo
c	27	498	15.8	567	6	AX872305	AX872305 Sequence
	28	494	15.7	1223	6	AX704742	AX704742 Sequence
	29	486.6	15.5	166620	10	AC102388	AC102388 Mus muscu
	30	486.6	15.5	233316	2	AC145168	AC145168 Mus muscu
	31	470	15.0	988	6	AX430331	AX430331 Sequence
	32	439.6	14.0	230635	2	AC128319	AC128319 Rattus no
	33	439.6	14.0	246036	2	AC097816	AC097816 Rattus no
	34	439.6	14.0	289877	2	AC119762	AC119762 Rattus no
	35	327.8	10.4	400	6	CQ666347	CQ666347 Sequence
	36	327	10.4	2405	6	BD157650	BD157650 Primer fo
	37	327	10.4	2405	6	AX879101	AX879101 Sequence
	38	327	10.4	2405	9	AK022416	AK022416 Homo sapi
	39	280.4	8.9	106784	2	AC136250	AC136250 Rattus no
	40	263.6	8.4	2498	6	CQ774966	CQ774966 Sequence
	41	263.6	8.4	3766	6	BD171175	BD171175 Novel gen
	42	263.6	8.4	3766	6	BD183514	BD183514 Novel gen
	43	263.6	8.4	3766	9	AB051532	AB051532 Homo sapi
	44	263.6	8.4	3776	6	CQ774964	CQ774964 Sequence
	45	263.6	8.4	3781	6	AX376386	AX376386 Sequence
	46	263.6	8.4	3781	6	AX697184	AX697184 Sequence
	47	263.6	8.4	3781	9	AY358392	AY358392 Homo sapi
	48	263.6	8.4	3807	9	AY445887	AY445887 Homo sapi
	49	251.6	8.0	3528	9	AK026108	AK026108 Homo sapi
	50	247	7.9	2808	6	CQ774962	CQ774962 Sequence
	51	247	7.9	3765	10	AK173249	AK173249 Mus muscu
	52	246.6	7.8	2390	6	AX418422	AX418422 Sequence
	53	246.6	7.8	2471	6	CQ722969	CQ722969 Sequence
	54	238.2	7.6	2715	5	BC077964	BC077964 Xenopus l
	55	237.8	7.6	3293	6	AX174731	AX174731 Sequence
	56	236.6	7.5	2155	6	AX060303	AX060303 Sequence
	57	236.6	7.5	2156	6	AX060313	AX060313 Sequence
	58	236.6	7.5	2284	6	AX060305	AX060305 Sequence
	59	236.6	7.5	2646	6	AX704763	AX704763 Sequence
	60	236.6	7.5	3537	9	AY358842	AY358842 Homo sapi

	61	236.6	7.5	3579	6	CQ868733	CQ868733 Sequence
	62	235	7.5	3503	10	S79463	S79463 M-Sema F=a
	63	235	7.5	4228	6	CQ868724	CQ868724 Sequence
	64	233.6	7.4	3776	6	BD171174	BD171174 Novel gen
	65	233.6	7.4	3776	6	BD183504	BD183504 Novel gen
	66	233.6	7.4	3776	9	AB051526	AB051526 Homo sapi
	67	233.6	7.4	3782	6	CQ868727	CQ868727 Sequence
	68	233.2	7.4	3868	6	AX528275	AX528275 Sequence
	69	230	7.3	2433	6	CQ777653	CQ777653 Sequence
	70	230	7.3	2433	6	AR266586	AR266586 Sequence
	71	230	7.3	2433	10	MMRNASMC	X85992 M.musculus
	72	225.4	7.2	2558	6	AX528277	AX528277 Sequence
	73	225.4	7.2	3112	6	AX528279	AX528279 Sequence
	74	225.4	7.2	3752	9	HSM806571	BX537671 Homo sapi
	75	221	7.0	3874	10	AK173247	AK173247 Mus muscu
c	76	216.2	6.9	224	6	AX330634	AX330634 Sequence
c	77	216.2	6.9	224	6	AX330817	AX330817 Sequence
	78	200.8	6.4	2967	9	IR1955967	AL390081 Homo sapi
	79	189.6	6.0	8095	6	AX535046	AX535046 Sequence
	80	189.6	6.0	8144	6	AX644354	AX644354 Sequence
	81	153.4	4.9	2589	6	AX695553	AX695553 Sequence
	82	153.4	4.9	4157	6	AR343060	AR343060 Sequence
	83	153.4	4.9	4157	6	AX695552	AX695552 Sequence
	84	153.4	4.9	4157	6	BD010283	BD010283 Drug. 1/2
	85	153.4	4.9	4157	6	BD092987	BD092987 Screening
	86	153.4	4.9	4157	9	HSU60800	U60800 Human semap
	87	153.4	4.9	4284	9	HSM808364	BX648216 Homo sapi
	88	153.4	4.9	4675	9	BC054500	BC054500 Homo sapi
c	89	153.2	4.9	106784	2	AC136250	AC136250 Rattus no
	90	152.6	4.9	1712	6	AX780890	AX780890 Sequence
	91	152.6	4.9	1712	9	AK026133	AK026133 Homo sapi
	92	148.2	4.7	4304	5	BC078116	BC078116 Xenopus l
	93	147	4.7	1024	6	AX675553	AX675553 Sequence
	94	143.6	4.6	2586	6	AX695550	AX695550 Sequence
	95	143.6	4.6	2769	6	E16310	E16310 Murine mRNA
	96	143.6	4.6	2769	6	AX695549	AX695549 Sequence
	97	143.6	4.6	2769	6	BD010282	BD010282 Drug. 1/2
	98	143.6	4.6	2769	6	BD092986	BD092986 Screening
	99	143.6	4.6	2769	10	MMU69535	U69535 Mus musculu
	100	143.6	4.6	4407	10	BC049780	BC049780 Mus muscu
	101	141	4.5	967	6	AX079880	AX079880 Sequence
	102	139.4	4.4	2907	9	BC017476	BC017476 Homo sapi
	103	139.4	4.4	3523	6	CQ868731	CQ868731 Sequence
	104	139	4.4	2813	6	AX405622	AX405622 Sequence
	105	131.4	4.2	3635	10	AF036585	AF036585 Mus muscu
	106	129.6	4.1	2232	6	CQ717182	CQ717182 Sequence
	107	126	4.0	1801	6	AX195917	AX195917 Sequence
	108	126	4.0	1801	9	AF216389	AF216389 Homo sapi
	109	126	4.0	2058	6	CQ721152	CQ721152 Sequence
	110	126	4.0	2311	6	AX195927	AX195927 Sequence
	111	126	4.0	2311	9	AF293363	AF293363 Homo sapi
	112	126	4.0	3524	6	AR342566	AR342566 Sequence
	113	126	4.0	3524	9	AB022433	AB022433 Homo sapi
	114	126	4.0	3721	6	AR528723	AR528723 Sequence
	115	126	4.0	3721	6	AX454682	AX454682 Sequence
	116	126	4.0	3721	6	AX464410	AX464410 Sequence
	117	126	4.0	3721	6	AX491160	AX491160 Sequence

118	126	4.0	3721	9	AY358939	AY358939 Homo sapi
119	125.4	4.0	3692	6	AR342565	AR342565 Sequence
120	125.4	4.0	3847	10	AB000776	AB000776 Rattus no
121	121.8	3.9	2641	9	BC010701	BC010701 Homo sapi
122	121.8	3.9	2811	6	CQ716147	CQ716147 Sequence
123	121.8	3.9	3791	9	AK091481	AK091481 Homo sapi
124	121.8	3.9	4456	6	AX492978	AX492978 Sequence
125	121.8	3.9	4559	9	AB040878	AB040878 Homo sapi
126	121.8	3.9	4725	6	AX574568	AX574568 Sequence
127	121.8	3.9	4725	9	AY358124	AY358124 Homo sapi
128	121.8	3.9	6408	6	AX528273	AX528273 Sequence
129	121.4	3.9	2820	6	AR559565	AR559565 Sequence
130	121.4	3.9	2820	6	AX305067	AX305067 Sequence
131	121.4	3.9	2865	6	AR559564	AR559564 Sequence
132	121.4	3.9	2865	6	AX305065	AX305065 Sequence
133	121.4	3.9	3105	6	AR559560	AR559560 Sequence
134	121.4	3.9	3105	6	AX305057	AX305057 Sequence
135	121.4	3.9	3150	6	AR559558	AR559558 Sequence
136	121.4	3.9	3150	6	AX305053	AX305053 Sequence
137	121.4	3.9	3237	6	AR559561	AR559561 Sequence
138	121.4	3.9	3237	6	AX305059	AX305059 Sequence
139	121.4	3.9	3282	6	AR559559	AR559559 Sequence
140	121.4	3.9	3282	6	AX305055	AX305055 Sequence
141	121.4	3.9	3411	6	AR559563	AR559563 Sequence
142	121.4	3.9	3411	6	AX305063	AX305063 Sequence
143	121.4	3.9	3456	6	AR559562	AR559562 Sequence
144	121.4	3.9	3456	6	AX305061	AX305061 Sequence
145	121.4	3.9	4074	6	AR559566	AR559566 Sequence
146	121.4	3.9	4074	6	AX305069	AX305069 Sequence
147	120.2	3.8	4144	6	BD270048	BD270048 Secreted
148	120.2	3.8	4494	9	BC077726	BC077726 Homo sapi
149	116.8	3.7	4350	5	BC061707	BC061707 Danio rer
150	115.8	3.7	3018	10	AF288666	AF288666 Mus muscu
151	114.4	3.6	2675	6	CQ869696	CQ869696 Sequence
152	114.4	3.6	2770	10	AF030430	AF030430 Mus muscu
153	114.4	3.6	4139	10	BC062979	BC062979 Mus muscu
154	114.4	3.6	4702	10	BC059238	BC059238 Mus muscu
155	113.8	3.6	4008	10	AB002563	AB002563 Rattus no
156	113	3.6	4310	10	AF134918	AF134918 Mus muscu
157	113	3.6	4326	10	BC049183	BC049183 Mus muscu
158	112.8	3.6	2271	5	AB072930	AB072930 Gallus ga
159	112.2	3.6	2650	5	BC078280	BC078280 Danio rer
160	112.2	3.6	2993	5	AF073289	AF073289 Danio rer
161	111	3.5	2948	9	BC038411	BC038411 Homo sapi
162	111	3.5	2971	6	AX136143	AX136143 Sequence
163	111	3.5	2971	6	BD123524	BD123524 Secretory
164	111	3.5	2971	9	AK075384	AK075384 Homo sapi
165	111	3.5	4293	9	HSM801526	AL136552 Homo sapi
c 166	110	3.5	344	6	AX400975	AX400975 Sequence
c 167	107.8	3.4	557	6	BD152451	BD152451 Primer fo
c 168	107.8	3.4	557	6	AX872389	AX872389 Sequence
169	107.6	3.4	2408	9	BC017658	BC017658 Homo sapi
170	106.8	3.4	2606	6	CQ868729	CQ868729 Sequence
171	106.2	3.4	606	5	AF461179	AF461179 Xenopus l
c 172	106	3.4	106	11	G19685	G19685 human STS A
173	106	3.4	2843	10	AB013729	AB013729 Mus muscu
174	106	3.4	3555	10	AF363973	AF363973 Mus muscu

175	105.4	3.4	2094	6	AR559570	AR559570 Sequence
176	105.4	3.4	2094	6	AX305076	AX305076 Sequence
177	105.4	3.4	2517	6	AR559572	AR559572 Sequence
178	105.4	3.4	2517	6	AX305080	AX305080 Sequence
179	105.4	3.4	2598	6	AR559574	AR559574 Sequence
180	105.4	3.4	2598	6	AX305084	AX305084 Sequence
181	105.4	3.4	2951	6	AR559583	AR559583 Sequence
182	105.4	3.4	2951	6	AX305102	AX305102 Sequence
183	105.4	3.4	4726	9	BC051030	BC051030 Homo sapi
184	104.4	3.3	3192	10	AB014074	AB014074 Rattus no
185	104.4	3.3	3288	10	AB000817	AB000817 Rattus no
186	102.8	3.3	2337	6	AX155172	AX155172 Sequence
187	102.6	3.3	2354	10	AF038652	AF038652 Mus muscu
188	102.6	3.3	3062	10	AK129459	AK129459 Mus muscu
189	102.6	3.3	4002	10	AB021291	AB021291 Mus muscu
190	102.4	3.3	2109	6	AR559569	AR559569 Sequence
191	102.4	3.3	2109	6	AX305074	AX305074 Sequence
192	102.4	3.3	2532	6	AR559571	AR559571 Sequence
193	102.4	3.3	2532	6	AX305078	AX305078 Sequence
194	102.4	3.3	2575	6	AR541792	AR541792 Sequence
195	102.4	3.3	2613	6	AR559573	AR559573 Sequence
196	102.4	3.3	2613	6	AX305082	AX305082 Sequence
197	102.4	3.3	4094	9	AB046839	AB046839 Homo sapi
198	102	3.2	1890	6	BD274951	BD274951 POLYNUCLE
199	102	3.2	1890	6	AR474080	AR474080 Sequence
200	102	3.2	2278	6	AR448304	AR448304 Sequence
201	102	3.2	2585	6	CQ720350	CQ720350 Sequence
202	102	3.2	2981	6	CQ720351	CQ720351 Sequence
203	102	3.2	3093	6	AX026741	AX026741 Sequence
204	102	3.2	3333	6	BD274939	BD274939 POLYNUCLE
205	102	3.2	3333	6	AR474068	AR474068 Sequence
206	102	3.2	3498	6	BD274938	BD274938 POLYNUCLE
207	102	3.2	3498	6	AR474067	AR474067 Sequence
208	102	3.2	3550	6	BD190797	BD190797 Secreted
209	102	3.2	3550	6	AX099520	AX099520 Sequence
210	102	3.2	3862	6	AX026746	AX026746 Sequence
211	102	3.2	3862	9	AF279656	AF279656 Homo sapi
212	102	3.2	4250	6	AX926617	AX926617 Sequence
213	102	3.2	4250	6	AX926666	AX926666 Sequence
214	102	3.2	4250	9	AB037789	AB037789 Homo sapi
215	102	3.2	4280	6	AR542082	AR542082 Sequence
216	102	3.2	4612	6	CQ869699	CQ869699 Sequence
217	102	3.2	6060	6	BD160721	BD160721 Primer fo
218	102	3.2	6060	6	AX884099	AX884099 Sequence
219	102	3.2	6060	9	AK027867	AK027867 Homo sapi
220	100.2	3.2	3730	9	AF339152	AF339152 Homo sapi
221	100.2	3.2	3826	9	AF339154	AF339154 Homo sapi
222	100.2	3.2	5261	9	AB058772	AB058772 Homo sapi
223	99.8	3.2	2997	10	AB091533	AB091533 Mus muscu
224	99.8	3.2	3093	10	AB091534	AB091534 Mus muscu
225	99.8	3.2	3165	10	AB091535	AB091535 Mus muscu
226	99.8	3.2	3222	10	AB091536	AB091536 Mus muscu
227	99.8	3.2	3792	10	HSSEMG	X97818 M.musculus
228	99.8	3.2	4658	10	BC052397	BC052397 Mus muscu
229	99.8	3.2	5596	10	BC060680	BC060680 Mus muscu
230	99.8	3.2	6161	10	AK122515	AK122515 Mus muscu
231	99.8	3.2	6330	10	AB091532	AB091532 Mus muscu

232	99	3.1	2893	6	BD177663	BD177663 SBSEMN1 p
233	99	3.1	2893	6	E35443	E35443 SBSEMN1 pol
234	99	3.1	2893	6	AX003081	AX003081 Sequence
235	99	3.1	2894	6	BD177664	BD177664 SBSEMN1 p
236	99	3.1	2894	6	E35444	E35444 SBSEMN1 pol
237	99	3.1	2894	6	AX003083	AX003083 Sequence
238	98.6	3.1	1797	6	AR559578	AR559578 Sequence
239	98.6	3.1	1797	6	AX305092	AX305092 Sequence
240	98.6	3.1	2220	6	AR559580	AR559580 Sequence
241	98.6	3.1	2220	6	AX305096	AX305096 Sequence
242	98.6	3.1	2301	6	AR559582	AR559582 Sequence
243	98.6	3.1	2301	6	AX305100	AX305100 Sequence
244	98.6	3.1	2790	6	AR322399	AR322399 Sequence
245	98.6	3.1	3407	9	AB022434	AB022434 Homo sapi
246	98.6	3.1	3432	6	AR322398	AR322398 Sequence
247	95.6	3.0	1812	6	AR559577	AR559577 Sequence
248	95.6	3.0	1812	6	AX305090	AX305090 Sequence
249	95.6	3.0	2235	6	AR559579	AR559579 Sequence
250	95.6	3.0	2235	6	AX305094	AX305094 Sequence
251	95.6	3.0	2316	6	AR559581	AR559581 Sequence
252	95.6	3.0	2316	6	AX305098	AX305098 Sequence
253	95	3.0	4830	5	BC059288	BC059288 Xenopus l
254	93.2	3.0	4259	10	BC065137	BC065137 Mus muscu
255	93.2	3.0	4540	10	AK129018	AK129018 Mus muscu
256	92	2.9	1173	6	CQ860139	CQ860139 Sequence
257	91.8	2.9	2557	9	BC062984	BC062984 Homo sapi
258	91.6	2.9	3949	10	MMSEMF	X97817 M.musculus
259	91.2	2.9	4982	6	AX780545	AX780545 Sequence
260	90.2	2.9	2505	9	AK000376	AK000376 Homo sapi
261	89.8	2.9	2787	6	AR322397	AR322397 Sequence
262	89.8	2.9	3195	6	AR322396	AR322396 Sequence
263	89.4	2.8	978	6	CQ731229	CQ731229 Sequence
264	88.8	2.8	2800	9	BC024220	BC024220 Homo sapi
265	88.8	2.8	2816	9	BC013975	BC013975 Homo sapi
266	88	2.8	557	6	CQ832364	CQ832364 Sequence
267	86.4	2.7	4460	10	BC054532	BC054532 Mus muscu
268	86.2	2.7	1419	6	AX364922	AX364922 Sequence
269	84.6	2.7	807	5	CR391534	CR391534 Gallus ga
270	84.6	2.7	2300	9	AB083186	AB083186 Homo sapi
271	84.2	2.7	4286	6	AR447980	AR447980 Sequence
272	83	2.6	2919	6	CQ716390	CQ716390 Sequence
273	83	2.6	2919	6	AX743094	AX743094 Sequence
274	83	2.6	2919	9	HSU28369	U28369 Homo sapien
275	81.6	2.6	2765	9	BC009113	BC009113 Homo sapi
276	81.4	2.6	2319	10	MUSCOSE	L41541 Mus musculu
277	81.4	2.6	2672	9	AB021292	AB021292 Homo sapi
278	81.4	2.6	4013	10	BC057588	BC057588 Mus muscu
279	81.4	2.6	5952	10	MUSC1	D85028 Mus musculu
280	81.2	2.6	3148	5	AF086761	AF086761 Danio rer
c 281	80.4	2.6	601	11	BV179579	BV179579 sqnml0593
282	80.2	2.6	3780	6	CQ592026	CQ592026 Sequence
283	79.8	2.5	2813	9	AF217991	AF217991 Homo sapi
284	79.8	2.5	2913	10	MMRNAEMD	X85993 M.musculus
285	79.6	2.5	2349	6	AX253547	AX253547 Sequence
286	79.6	2.5	2628	6	AX253545	AX253545 Sequence
287	79.6	2.5	3568	6	AX253549	AX253549 Sequence
288	79.6	2.5	4469	9	AK024425	AK024425 Homo sapi

	289	79.6	2.5	4700	9	AB029496	AB029496 Homo sapi
	290	79.6	2.5	4859	6	BD242858	BD242858 Secreted
	291	79.4	2.5	2256	6	CQ721836	CQ721836 Sequence
	292	78.6	2.5	3560	6	AR040601	AR040601 Sequence
	293	78.6	2.5	3560	6	I47057	I47057 Sequence 59
	294	78.6	2.5	8024	3	DRODSEM	L26082 Drosophila
	295	78.2	2.5	1923	6	AR411150	AR411150 Sequence
	296	78.2	2.5	2319	10	RNSIIICN1	X95286 R.norvegicu
	297	78.2	2.5	3261	6	AR411149	AR411149 Sequence
	298	78.2	2.5	3694	6	AR411148	AR411148 Sequence
	299	78	2.5	1491	6	AR559568	AR559568 Sequence
	300	78	2.5	1491	6	AX305072	AX305072 Sequence
	301	77.8	2.5	151951	2	AC084300	AC084300 Homo sapi
c	302	77.8	2.5	153459	2	AC011116	AC011116 Homo sapi
	303	77.8	2.5	154667	9	AC078794	AC078794 Homo sapi
	304	77.8	2.5	303396	2	AC092975	AC092975 Homo sapi
	305	76.6	2.4	862	6	BD145714	BD145714 Primer fo
	306	76.6	2.4	862	6	AX865652	AX865652 Sequence
	307	76.6	2.4	1588	6	BD157304	BD157304 Primer fo
	308	76.6	2.4	1588	6	AX878565	AX878565 Sequence
	309	76.6	2.4	1588	9	AK021660	AK021660 Homo sapi
	310	76.6	2.4	1896	6	AX685965	AX685965 Sequence
	311	76.6	2.4	2191	6	AX685969	AX685969 Sequence
	312	76.6	2.4	2290	9	AF389426	AF389426 Homo sapi
	313	76.6	2.4	2359	6	AX685973	AX685973 Sequence
	314	76.6	2.4	3196	6	AX685971.	AX685971 Sequence
	315	76.6	2.4	3205	6	AX685967	AX685967 Sequence
	316	76.6	2.4	3364	6	AX685975	AX685975 Sequence
	317	76.6	2.4	4234	6	AX492975	AX492975 Sequence
	318	76.6	2.4	5886	9	AF389427	AF389427 Homo sapi
	319	76.6	2.4	5924	9	AB040912	AB040912 Homo sapi
	320	76.6	2.4	5925	9	AF389430	AF389430 Homo sapi
	321	76.6	2.4	5943	9	AF389428	AF389428 Homo sapi
	322	76.6	2.4	6111	9	AF389429	AF389429 Homo sapi
	323	76.2	2.4	2340	6	CQ730744	CQ730744 Sequence
	324	76.2	2.4	2340	6	AX155170	AX155170 Sequence
	325	75.6	2.4	154456	2	AC126320	AC126320 Mus muscu
	326	75.2	2.4	1998	10	MUSSEMAIII	L40484 Mus musculu
	327	74	2.4	2337	5	AF083382	AF083382 Danio rer
c	328	74	2.4	250257	2	AC097828	AC097828 Rattus no
	329	72.4	2.3	2132	9	AF258577	AF258577 Homo sapi
	330	71.6	2.3	1330	5	CR352446	CR352446 Gallus ga
	331	71.6	2.3	1937	5	BC045964	BC045964 Danio rer
	332	71.4	2.3	7127	6	CQ726090	CQ726090 Sequence
	333	71.4	2.3	8056	9	HSU52840	U52840 Homo sapien
	334	71.2	2.3	1194	6	AR559576	AR559576 Sequence
	335	71.2	2.3	1194	6	AX305088	AX305088 Sequence
	336	70.4	2.2	2265	10	AF080091	AF080091 Mus muscu
	337	70.4	2.2	3943	10	BC057048	BC057048 Mus muscu
	338	69.8	2.2	2616	3	DRODSEMA	L26083 Drosophila
	339	69.8	2.2	2628	3	AY095026	AY095026 Drosophil
	340	69.8	2.2	2661	6	CQ600060	CQ600060 Sequence
	341	69.8	2.2	2670	6	AR040602	AR040602 Sequence
	342	69.8	2.2	2670	6	I47058	I47058 Sequence 61
	343	69.8	2.2	2746	6	CQ581481	CQ581481 Sequence
	344	69.8	2.2	3443	3	AY128437	AY128437 Drosophil
	345	69.8	2.2	3546	3	BT011447	BT011447 Drosophil

c 346	69.8	2.2	18445	6	CQ581480	CQ581480 Sequence
c 347	69.8	2.2	18459	6	CQ600059	CQ600059 Sequence
c 348	69.8	2.2	59880	3	AC005647	AC005647 Drosophil
c 349	69.8	2.2	143450	2	AC017124	AC017124 Drosophil
c 350	69.8	2.2	185425	3	AC099027	AC099027 Drosophil
351	69.8	2.2	271179	3	AE003806	AE003806 Drosophil
352	69.2	2.2	718	5	AY744920	AY744920 Petromyzo
353	68.8	2.2	2499	10	BC010976	BC010976 Mus muscu
354	66.6	2.1	916	10	AF036162	AF036162 Mus muscu
355	66.4	2.1	179362	2	CR762413	CR762413 Danio rer
356	66.2	2.1	233499	10	AC110236	AC110236 Mus muscu
c 357	66.2	2.1	278713	2	AC113289	AC113289 Mus muscu
358	65.8	2.1	1851	6	CQ580833	CQ580833 Sequence
359	65.8	2.1	185236	2	AC113686	AC113686 Rattus no
360	65.8	2.1	267077	2	AC106340	AC106340 Rattus no
361	65.2	2.1	648	6	AR559567	AR559567 Sequence
362	65.2	2.1	648	6	AX305070	AX305070 Sequence
363	65.2	2.1	4117	10	AK173219	AK173219 Mus muscu
364	65	2.1	2715	5	GGU28240	U28240 Gallus gall
365	64.8	2.1	192039	5	BX322793	BX322793 Zebrafish
c 366	64.6	2.1	222420	5	BX005234	BX005234 Zebrafish
367	64.2	2.0	4122	3	AF007158	AF007158 Drosophil
368	64.2	2.0	4254	6	CQ586155	CQ586155 Sequence
369	64.2	2.0	4270	3	AF181625	AF181625 Drosophil
370	64.2	2.0	12646	6	CQ586154	CQ586154 Sequence
c 371	64.2	2.0	177816	2	AC017643	AC017643 Drosophil
c 372	64.2	2.0	194897	3	AC007697	AC007697 Drosophil
c 373	64.2	2.0	246095	3	AE003802	AE003802 Drosophil
374	63.8	2.0	2509	6	CQ716140	CQ716140 Sequence
375	63.8	2.0	2530	6	CQ812254	CQ812254 Sequence
376	63.8	2.0	2530	6	AX743092	AX743092 Sequence
377	63.8	2.0	2530	6	BD084822	BD084822 Diagnosis
378	63.8	2.0	2530	9	HUMHSEM	L26081 Homo sapien
379	63.8	2.0	2530	11	G31703	G31703 sWSS1973 Er
380	63.8	2.0	2601	6	AR040598	AR040598 Sequence
381	63.8	2.0	2601	6	I47054	I47054 Sequence 53
382	63.8	2.0	2709	6	AX207154	AX207154 Sequence
383	63.6	2.0	2851	3	SCAFAS4X	L00709 Schistocerc
384	63	2.0	804	5	AB167389	AB167389 Oryzias l
385	63	2.0	999	5	BX931974	BX931974 Gallus ga
386	62.8	2.0	3435	10	AF363972	AF363972 Mus muscu
387	62.6	2.0	2843	5	BC070859	BC070859 Xenopus l
388	62.6	2.0	7218	6	I66494	I66494 Sequence 14
389	62	2.0	2854	6	AR040600	AR040600 Sequence
390	62	2.0	2854	6	I47056	I47056 Sequence 57
391	61.6	2.0	3416	5	BC076684	BC076684 Xenopus t
392	61.2	1.9	662	6	BD150362	BD150362 Primer fo
393	61.2	1.9	662	6	AX870300	AX870300 Sequence
394	61	1.9	3172	10	AF363971	AF363971 Rattus no
395	60.8	1.9	2000	6	AX655393	AX655393 Sequence
396	60.2	1.9	2325	5	AY030051	AY030051 Xenopus l
397	60	1.9	60	6	CQ546209	CQ546209 Sequence
c 398	59.8	1.9	7832	6	CQ580832	CQ580832 Sequence
c 399	59.8	1.9	79660	3	AC004249	AC004249 Drosophil
c 400	59.8	1.9	179332	2	CR354550	CR354550 Danio rer
c 401	59.8	1.9	230310	2	AC120079	AC120079 Rattus no
402	59.8	1.9	258223	3	AE003807	AE003807 Drosophil

c 403	59.4	1.9	180238	2	AC073688	AC073688 Mus muscu
c 404	59.4	1.9	222610	10	AC026385	AC026385 Mus muscu
405	59	1.9	2383	10	AF080090	AF080090 Mus muscu
c 406	59	1.9	125020	9	AF429315	AF429315 Homo sapi
407	58.8	1.9	3263	5	GGU02528	U02528 Gallus gall
408	58.4	1.9	351	6	AR559575	AR559575 Sequence
409	58.4	1.9	351	6	AX305086	AX305086 Sequence
410	58.4	1.9	2872	10	MMRNASEMA	X85990 M.musculus
c 411	58.2	1.9	107568	2	AC144398	AC144398 Rattus no
412	58	1.8	39780	6	AX695548	AX695548 Sequence
c 413	58	1.8	181823	10	AC126547	AC126547 Mus muscu
414	57.6	1.8	3552	6	CQ861392	CQ861392 Sequence
415	57.6	1.8	3552	9	HSU38276	U38276 Human semap
416	57.4	1.8	2816	5	BC057717	BC057717 Xenopus l
c 417	57.4	1.8	193329	2	CR749746	CR749746 Danio rer
c 418	57.4	1.8	213792	2	BX927177	BX927177 Danio rer
419	57	1.8	125020	9	AF429315	AF429315 Homo sapi
420	56.8	1.8	2195	9	BC044602	BC044602 Homo sapi
421	56.6	1.8	48244	6	AX695551	AX695551 Sequence
c 422	56.6	1.8	52064	9	AL929575	AL929575 Human DNA
c 423	56.6	1.8	110000	2	BX572642_4	Continuation (5 of
424	55.8	1.8	211297	5	AL935286	AL935286 Zebrafish
c 425	55.8	1.8	232735	2	AC115240	AC115240 Rattus no
426	55.8	1.8	273754	2	AC120615	AC120615 Rattus no
427	55.6	1.8	273	6	AX312904	AX312904 Sequence
428	55.6	1.8	10385	6	CQ868726	CQ868726 Sequence
c 429	55.6	1.8	199721	9	AC092636	AC092636 Homo sapi
430	55.4	1.8	886	5	GGU28242	U28242 Gallus gall
431	55.2	1.8	3706	9	AF339153	AF339153 Homo sapi
c 432	55.2	1.8	181162	5	AC144487	AC144487 Gasterost
c 433	55	1.7	102042	2	AC150097	AC150097 Gallus ga
c 434	55	1.7	116621	2	AC150102	AC150102 Gallus ga
435	55	1.7	166376	2	AC150119	AC150119 Gallus ga
c 436	55	1.7	186553	2	AC150177	AC150177 Gallus ga
c 437	55	1.7	252109	2	AC150037	AC150037 Gallus ga
438	55	1.7	254439	2	AC150047	AC150047 Gallus ga
c 439	54.4	1.7	2000	6	AX655393	AX655393 Sequence
c 440	54.2	1.7	1654	6	AR496855	AR496855 Sequence
c 441	54.2	1.7	1654	6	AR512137	AR512137 Sequence
442	54.2	1.7	50517	2	BX957261_3	Continuation (4 of
443	54.2	1.7	106104	5	BX950190	BX950190 Zebrafish
444	54.2	1.7	110000	2	BX957261_2	Continuation (3 of
445	54.2	1.7	163513	2	CR450694	CR450694 Danio rer
446	54.2	1.7	184499	5	BX005201	BX005201 Zebrafish
447	53.2	1.7	1224	6	AR495332	AR495332 Sequence
448	53.2	1.7	1224	6	AR510614	AR510614 Sequence
c 449	53	1.7	195962	2	AC058820	AC058820 Homo sapi
c 450	53	1.7	202381	9	AC091167	AC091167 Homo sapi
451	52.6	1.7	2328	6	CQ768868	CQ768868 Sequence
452	52.6	1.7	2328	10	MMSEMH	Z80941 M.musculus
453	52.6	1.7	2898	10	AF034744	AF034744 Mus muscu
454	52.6	1.7	2935	10	BC057956	BC057956 Mus muscu
455	52.6	1.7	3737	10	AK129116	AK129116 Mus muscu
456	52.6	1.7	3982	6	CQ768869	CQ768869 Sequence
457	52.6	1.7	4460	6	CQ768867	CQ768867 Sequence
458	52.4	1.7	906	5	AY744921	AY744921 Petromyzo
459	52.4	1.7	10241	6	CQ868723	CQ868723 Sequence

	460	52.4	1.7	166182	10	AC084391	AC084391 Mus muscu
	461	52.2	1.7	443	6	CQ098976	CQ098976 Sequence
	462	52.2	1.7	443	6	CQ137898	CQ137898 Sequence
	463	52.2	1.7	443	6	CQ175119	CQ175119 Sequence
	464	52.2	1.7	443	6	CQ221268	CQ221268 Sequence
	465	52.2	1.7	443	6	CQ259393	CQ259393 Sequence
	466	52.2	1.7	443	6	CQ297084	CQ297084 Sequence
	467	52.2	1.7	443	6	CQ333463	CQ333463 Sequence
	468	52.2	1.7	4334	3	AF198084	AF198084 Drosophil
c	469	52.2	1.7	140415	5	CR392037	CR392037 Zebrafish
c	470	52.2	1.7	188534	9	AC022446	AC022446 Homo sapi
	471	52.2	1.7	197839	2	CR749771	CR749771 Danio rer
	472	52.2	1.7	230976	2	BX927201	BX927201 Danio rer
	473	52.2	1.7	235141	9	AC004615	AC004615 Homo sapi
	474	51.8	1.6	2879	5	AF124485	AF124485 Danio rer
	475	51.6	1.6	4126	3	BT009966	BT009966 Drosophil
	476	51.6	1.6	4340	6	CQ584163	CQ584163 Sequence
	477	51.4	1.6	1464	5	CR353284	CR353284 Gallus ga
c	478	51.4	1.6	163958	2	BX324005	BX324005 Danio rer
	479	51.4	1.6	208909	5	BX004975	BX004975 Zebrafish
	480	51.2	1.6	274	6	CQ112031	CQ112031 Sequence
	481	51.2	1.6	274	6	CQ150841	CQ150841 Sequence
	482	51.2	1.6	274	6	CQ184978	CQ184978 Sequence
	483	51.2	1.6	274	6	CQ234180	CQ234180 Sequence
	484	51.2	1.6	274	6	CQ271905	CQ271905 Sequence
	485	51.2	1.6	274	6	CQ309506	CQ309506 Sequence
	486	51.2	1.6	274	6	CQ346133	CQ346133 Sequence
	487	51	1.6	505	6	CQ832389	CQ832389 Sequence
	488	51	1.6	890	10	AF268594	AF268594 Rattus no
	489	51	1.6	2514	6	CQ716402	CQ716402 Sequence
	490	51	1.6	2719	6	AX743100	AX743100 Sequence
	491	51	1.6	2719	9	HSU33920	U33920 Human clone
	492	51	1.6	3540	9	BC042914	BC042914 Homo sapi
	493	50.8	1.6	2878	10	AK129362	AK129362 Mus muscu
	494	50.8	1.6	228902	2	AC098116	AC098116 Rattus no
	495	50.8	1.6	235551	2	AC130518	AC130518 Rattus no
c	496	50.6	1.6	273403	9	AC011498	AC011498 Homo sapi
	497	50.2	1.6	2452	3	TCATSEM	L26080 Tribolium c
	498	50.2	1.6	2504	6	AR040603	AR040603 Sequence
	499	50.2	1.6	2504	6	I47059	I47059 Sequence 63
	500	50	1.6	2400	6	CQ729847	CQ729847 Sequence
	501	50	1.6	2400	9	AB022317	AB022317 Homo sapi
	502	50	1.6	2507	9	BC018361	BC018361 Homo sapi
	503	49.4	1.6	2331	6	E27342	E27342 Novel polyp
	504	49.4	1.6	3871	6	AX376280	AX376280 Sequence
	505	49.4	1.6	3871	6	AX697241	AX697241 Sequence
	506	49.4	1.6	3871	9	AY358937	AY358937 Homo sapi
	507	49.4	1.6	3880	6	E27343	E27343 Novel polyp
	508	49.2	1.6	157502	5	AC144486	AC144486 Gasterost
	509	48.6	1.5	4041	5	BC080392	BC080392 Xenopus l
	510	48.4	1.5	1881	6	BD156840	BD156840 Primer fo
	511	48.4	1.5	1881	6	AX877772	AX877772 Sequence
	512	48.4	1.5	1881	9	AK001895	AK001895 Homo sapi
	513	48.4	1.5	2001	6	AR442653	AR442653 Sequence
	514	48.4	1.5	2010	6	AR137624	AR137624 Sequence
	515	48.4	1.5	2010	6	AX019702	AX019702 Sequence
	516	48.4	1.5	2035	6	CQ870008	CQ870008 Sequence

517	48.4	1.5	2498	6	AR148582	AR148582 Sequence
518	48.4	1.5	2498	6	AR349059	AR349059 Sequence
519	48.4	1.5	2594	9	AF071542	AF071542 Homo sapi
520	48.4	1.5	2636	6	E36227	E36227 Human semap
521	48.4	1.5	2636	6	AX001289	AX001289 Sequence
522	48.4	1.5	2636	6	AX154554	AX154554 Sequence
523	48.4	1.5	2636	9	AF030698	AF030698 Homo sapi
524	48.4	1.5	2660	6	CQ729594	CQ729594 Sequence
525	48.4	1.5	2661	6	BD171301	BD171301 Gene enco
526	48.4	1.5	2661	9	AF069493	AF069493 Homo sapi
c 527	48.4	1.5	5856	6	E36258	E36258 Human semap
c 528	48.4	1.5	5856	6	AX001322	AX001322 Sequence
529	48.4	1.5	6622	6	E36266	E36266 Human semap
530	48.4	1.5	6622	6	AX001330	AX001330 Sequence
531	48.4	1.5	7000	6	E36261	E36261 Human semap
532	48.4	1.5	7000	6	AX001325	AX001325 Sequence
533	48.4	1.5	7108	6	E36262	E36262 Human semap
534	48.4	1.5	7108	6	AX001326	AX001326 Sequence
535	48.4	1.5	7475	6	E36259	E36259 Human semap
536	48.4	1.5	7475	6	AX001323	AX001323 Sequence
537	48.4	1.5	8192	6	E36260	E36260 Human semap
538	48.4	1.5	8192	6	AX001324	AX001324 Sequence
c 539	48.2	1.5	156207	2	AC025507	AC025507 Homo sapi
540	48.2	1.5	165716	5	CR376858	CR376858 Zebrafish
c 541	48.2	1.5	182736	5	BX511146	BX511146 Zebrafish
542	48.2	1.5	198488	9	AC023794	AC023794 Homo sapi
c 543	48.2	1.5	202615	2	CR450766	CR450766 Danio rer
544	47.8	1.5	3988	10	MMZ93948	Z93948 M.musculus
545	47.8	1.5	4466	10	MMZ93947	Z93947 M.musculus
546	47.8	1.5	195311	10	AC121585	AC121585 Mus muscu
547	47.6	1.5	1481	6	I11900	I11900 Sequence 1
548	47.6	1.5	2558	3	AF134904	AF134904 Schistoce
549	47.6	1.5	110000	1	AP006840_22	Continuation (23 o
550	47.4	1.5	154341	5	CR381651	CR381651 Zebrafish
c 551	47.4	1.5	159726	2	CR356246	CR356246 Danio rer
552	47.4	1.5	187708	2	CR788293	CR788293 Danio rer
553	47.2	1.5	195962	2	AC058820	AC058820 Homo sapi
554	47.2	1.5	227555	10	AC108416	AC108416 Mus muscu
555	46.8	1.5	480	5	AF495525	AF495525 Gallus ga
c 556	46.8	1.5	2122	9	BC041165	BC041165 Homo sapi
c 557	46.8	1.5	2136	6	AX833644	AX833644 Sequence
c 558	46.8	1.5	2136	9	AK095556	AK095556 Homo sapi
559	46.8	1.5	181086	9	AL133215	AL133215 Human DNA
c 560	46.8	1.5	182546	2	AC148998	AC148998 Gasterost
c 561	46.6	1.5	123943	9	AC006208	AC006208 Homo sapi
c 562	46.6	1.5	214160	9	AC094021	AC094021 Homo sapi
c 563	46.4	1.5	10732	6	E32986	E32986 Gene encodi
564	46.2	1.5	540	6	AR123946	AR123946 Sequence
565	46.2	1.5	561	6	A01699	A01699 Synthetic D
566	46.2	1.5	561	6	A02358	A02358 Synthetic h
567	46.2	1.5	561	6	AR362902	AR362902 Sequence
568	46.2	1.5	655	6	AR066353	AR066353 Sequence
569	46.2	1.5	709	9	BC069540	BC069540 Homo sapi
570	46.2	1.5	1297	6	A01692	A01692 H.sapiens D
571	46.2	1.5	1297	6	A02353	A02353 cDNA of hum
572	46.2	1.5	1297	6	AR362900	AR362900 Sequence
573	46.2	1.5	1297	9	HUMLIFM	J03261 Human myelo

574	46.2	1.5	2065	6	AX747395	AX747395 Sequence
575	46.2	1.5	2065	9	AK092182	AK092182 Homo sapi
576	46.2	1.5	2144	9	HUMDSF02	M27053 Human diffe
577	46.2	1.5	3848	9	HSLIF	X13967 Human mRNA
578	46.2	1.5	3867	6	CQ730077	CQ730077 Sequence
579	46.2	1.5	3868	6	CQ870632	CQ870632 Sequence
580	46.2	1.5	3868	6	AX399180	AX399180 Sequence
581	46.2	1.5	4025	6	AX281658	AX281658 Sequence
582	46.2	1.5	7614	9	HUMALIFA	M63420 Human leuke
c 583	46.2	1.5	47188	9	AC004264	AC004264 Homo sapi
584	46	1.5	799	6	BD177665	BD177665 SBSEMN1 p
585	46	1.5	799	6	E35445	E35445 SBSEMN1 pol
586	46	1.5	799	6	AX003085	AX003085 Sequence
587	46	1.5	1913	9	AF053369	AF053369 Homo sapi
588	46	1.5	3560	6	AX781110	AX781110 Sequence
589	45.8	1.5	2446	3	AF216968	AF216968 Caenorhab
590	45.6	1.5	2615	5	AF022947	AF022947 Gallus ga
c 591	45.6	1.5	198907	2	AC109232	AC109232 Mus muscu
592	45.4	1.4	798	6	AX136614	AX136614 Sequence
593	45.4	1.4	798	6	BD123854	BD123854 Secretory
594	45.4	1.4	2194	6	AX136419	AX136419 Sequence
595	45.4	1.4	2194	6	BD123664	BD123664 Secretory
596	45.4	1.4	2194	9	AK075388	AK075388 Homo sapi
597	45.4	1.4	2615	8	AK072112	AK072112 Oryza sat
598	45.4	1.4	3369	6	CQ843521	CQ843521 Sequence
599	45.4	1.4	3369	9	AK126512	AK126512 Homo sapi
600	45.4	1.4	176979	8	AP001168	AP001168 Oryza sat
c 601	45.4	1.4	256584	2	AC133754	AC133754 Rattus no
c 602	45.2	1.4	249541	2	AC095672	AC095672 Rattus no
c 603	45.2	1.4	249774	2	AC126196	AC126196 Rattus no
604	45	1.4	45	6	AX697212	AX697212 Sequence
c 605	45	1.4	4069	9	AY148099	AY148099 Homo sapi
c 606	45	1.4	4282	6	AX254778	AX254778 Sequence
c 607	45	1.4	171987	9	AC079775	AC079775 Homo sapi
608	44.8	1.4	300	6	AX884556	AX884556 Sequence
609	44.8	1.4	300	6	BD024166	BD024166 Sequence
610	44.8	1.4	859	6	BD145948	BD145948 Primer fo
611	44.8	1.4	859	6	AX865886	AX865886 Sequence
612	44.8	1.4	1258	6	BD159156	BD159156 Primer fo
613	44.8	1.4	1258	6	AX881611	AX881611 Sequence
614	44.8	1.4	1258	9	AK021802	AK021802 Homo sapi
c 615	44.8	1.4	227182	2	AC099283	AC099283 Rattus no
c 616	44.2	1.4	110000	2	AC146850_2	Continuation (3 of
c 617	44.2	1.4	207757	10	AC022368	AC022368 Mus muscu
c 618	44.2	1.4	264205	10	AC121125	AC121125 Mus muscu
c 619	44	1.4	14751	1	AE001962	AE001962 Deinococc
c 620	44	1.4	183358	9	AC019041	AC019041 Homo sapi
c 621	44	1.4	231864	2	AC097246	AC097246 Rattus no
622	43.8	1.4	1278	10	AF164785	AF164785 Mus muscu
c 623	43.8	1.4	22947	9	AL606762	AL606762 Human DNA
c 624	43.8	1.4	36534	9	U73167	U73167 Homo sapien
625	43.8	1.4	36552	9	HSU90094	U90094 Human chrom
626	43.8	1.4	261384	2	AC115415	AC115415 Rattus no
c 627	43.6	1.4	149000	2	AC120842	AC120842 Mus muscu
628	43.6	1.4	170074	10	AL845160	AL845160 Mouse DNA
629	43.6	1.4	204062	2	AC091072	AC091072 Mus muscu
c 630	43.6	1.4	213698	2	AC120420	AC120420 Mus muscu

	631	43.4	1.4	133296	10	AL935323	AL935323 Mouse DNA
c	632	43.4	1.4	186826	5	BX000697	BX000697 Zebrafish
	633	43.2	1.4	34695	1	AY281352	AY281352 Unculture
c	634	43.2	1.4	52569	5	BX897713	BX897713 Zebrafish
	635	43.2	1.4	82561	2	AC139202	AC139202 Mus muscu
	636	43.2	1.4	152164	5	BX649527	BX649527 Zebrafish
	637	43.2	1.4	154624	2	BX544876	BX544876 Danio rer
	638	43.2	1.4	173134	5	AL935282	AL935282 Zebrafish
	639	43.2	1.4	173663	5	BX323861	BX323861 Zebrafish
	640	43.2	1.4	204502	5	BX469931	BX469931 Zebrafish
c	641	43.2	1.4	228700	2	CR450776	CR450776 Danio rer
	642	43.2	1.4	279277	2	AC015535	AC015535 Mus muscu
c	643	43	1.4	634	11	BV035820	BV035820 S212P6030
c	644	43	1.4	114084	5	BX942820	BX942820 Zebrafish
	645	43	1.4	139613	6	CQ869695	CQ869695 Sequence
	646	43	1.4	184366	10	AC121783	AC121783 Mus muscu
c	647	43	1.4	196735	2	BX294667	BX294667 Danio rer
	648	42.8	1.4	160901	9	CNS01DWJ	AL137228 Human chr
	649	42.8	1.4	299450	1	AP005938	AP005938 Bradyrhiz
	650	42.8	1.4	302174	1	AE017241	AE017241 Mycobacte
	651	42.6	1.4	1661	9	HSENO57	X76309 H.sapiens e
	652	42.6	1.4	2937	6	CQ728913	CQ728913 Sequence
c	653	42.6	1.4	110000	2	AC109862_1	Continuation (2 of
c	654	42.4	1.3	300	6	BD135648	BD135648 Observati
c	655	42.4	1.3	1539	6	AR117513	AR117513 Sequence
c	656	42.4	1.3	1539	6	BD250249	BD250249 Antisense
c	657	42.4	1.3	1539	6	AR228798	AR228798 Sequence
c	658	42.4	1.3	1539	9	HUMMAPKNS	L35253 Human p38 m
	659	42.4	1.3	6474	6	AX743098	AX743098 Sequence
	660	42.4	1.3	6474	9	AB002329	AB002329 Homo sapi
	661	42.4	1.3	33676	1	SCARD1GN	X84374 Saccharothr
	662	42.4	1.3	86000	2	AC136951	AC136951 Leishmani
c	663	42.4	1.3	164959	2	AC087823	AC087823 Homo sapi
	664	42.4	1.3	207636	2	AC019122	AC019122 Homo sapi
c	665	42.2	1.3	250	6	CQ150004	CQ150004 Sequence
c	666	42.2	1.3	250	6	CQ308622	CQ308622 Sequence
c	667	42.2	1.3	250	6	CQ345374	CQ345374 Sequence
	668	42.2	1.3	328	11	G00866	G00866 fruit fly S
	669	42.2	1.3	993	6	AX083324	AX083324 Sequence
	670	42.2	1.3	996	6	CQ727051	CQ727051 Sequence
	671	42.2	1.3	996	9	AY463154	AY463154 Homo sapi
	672	42.2	1.3	1200	9	AF212862	AF212862 Homo sapi
	673	42.2	1.3	1598	9	BC025273	BC025273 Homo sapi
	674	42.2	1.3	1606	6	AX083334	AX083334 Sequence
	675	42.2	1.3	1629	6	AR177377	AR177377 Sequence
	676	42.2	1.3	1629	6	BD131451	BD131451 cDNA enco
	677	42.2	1.3	1645	8	AK071437	AK071437 Oryza sat
	678	42.2	1.3	1965	6	AR451658	AR451658 Sequence
	679	42.2	1.3	1965	6	BD090514	BD090514 Plant opt
	680	42.2	1.3	2135	9	BC014981	BC014981 Homo sapi
	681	42.2	1.3	2192	9	BC001538	BC001538 Homo sapi
	682	42.2	1.3	2194	6	BD094120	BD094120 Shear str
	683	42.2	1.3	2199	9	BC012153	BC012153 Homo sapi
	684	42.2	1.3	2607	6	BD242857	BD242857 Secreted
	685	42.2	1.3	2864	9	AF306698	AF306698 Homo sapi
	686	42.2	1.3	3283	6	AX835315	AX835315 Sequence
	687	42.2	1.3	3283	9	AK098329	AK098329 Homo sapi

	688	42.2	1.3	15088	1	AE004831	AE004831 Pseudomon
c	689	42.2	1.3	143507	8	AC091774	AC091774 Oryza sat
c	690	42.2	1.3	145023	9	AC012621	AC012621 Homo sapi
c	691	42.2	1.3	164564	9	HUAC003108	AC003108 Human Chr
c	692	42.2	1.3	171965	8	AP003614	AP003614 Oryza sat
c	693	42.2	1.3	174234	10	AC117098	AC117098 Rattus no
	694	42.2	1.3	247910	1	AE017307	AE017307 Thermus t
c	695	42.2	1.3	259720	2	AC094497	AC094497 Rattus no
	696	42.2	1.3	303642	1	AE016923	AE016923 Chromobac
c	697	42	1.3	195110	9	AC107943	AC107943 Homo sapi
	698	41.8	1.3	2975	6	BD106505	BD106505 Human sem
	699	41.8	1.3	4996	9	BC030690	BC030690 Homo sapi
	700	41.8	1.3	5177	6	AR559312	AR559312 Sequence
	701	41.8	1.3	5177	6	AX743096	AX743096 Sequence
	702	41.8	1.3	5177	6	AX770552	AX770552 Sequence
	703	41.8	1.3	5177	9	AB000220	AB000220 Homo sapi
	704	41.8	1.3	5231	6	CQ491238	CQ491238 Sequence
	705	41.8	1.3	5231	6	CQ497106	CQ497106 Sequence
	706	41.8	1.3	110000	1	AP006840_13	Continuation (14 o
	707	41.8	1.3	110000	1	AP006840_14	Continuation (15 o
	708	41.8	1.3	205673	10	AC126688	AC126688 Mus muscu
c	709	41.8	1.3	226284	10	AC099609	AC099609 Mus muscu
	710	41.6	1.3	3202	11	BV177696	BV177696 sqnm96231
	711	41.6	1.3	10995	1	AE012474	AE012474 Xanthomon
	712	41.4	1.3	357	6	CQ815359	CQ815359 Sequence
c	713	41.4	1.3	187865	2	AC015559	AC015559 Homo sapi
c	714	41.4	1.3	230404	2	AC097160	AC097160 Rattus no
c	715	41.4	1.3	235185	2	AC098527	AC098527 Rattus no
	716	41.4	1.3	237974	2	AC094771	AC094771 Rattus no
	717	41.4	1.3	258786	2	AC125773	AC125773 Rattus no
c	718	41.4	1.3	301443	1	AE017239	AE017239 Mycobacte
	719	41.2	1.3	430	6	AR425159	AR425159 Sequence
	720	41.2	1.3	430	6	AX985853	AX985853 Sequence
	721	41.2	1.3	430	6	BD120712	BD120712 EST and e
	722	41.2	1.3	754	6	BD148621	BD148621 Primer fo
	723	41.2	1.3	754	6	AX868559	AX868559 Sequence
	724	41.2	1.3	786	6	BD147225	BD147225 Primer fo
	725	41.2	1.3	786	6	AX867163	AX867163 Sequence
	726	41.2	1.3	814	6	CQ780347	CQ780347 Sequence
	727	41.2	1.3	814	6	CQ782303	CQ782303 Sequence
	728	41.2	1.3	814	6	BD125056	BD125056 Primer fo
	729	41.2	1.3	814	6	BD127012	BD127012 Primer fo
	730	41.2	1.3	839	6	BD147394	BD147394 Primer fo
	731	41.2	1.3	839	6	AX867332	AX867332 Sequence
	732	41.2	1.3	2123	6	BD155987	BD155987 Primer fo
	733	41.2	1.3	2123	6	AX876167	AX876167 Sequence
	734	41.2	1.3	2123	9	AK027439	AK027439 Homo sapi
	735	41.2	1.3	2227	6	CQ782947	CQ782947 Sequence
	736	41.2	1.3	2227	6	BD127394	BD127394 Primer fo
	737	41.2	1.3	2227	9	AK074975	AK074975 Homo sapi
	738	41.2	1.3	2293	6	BD157826	BD157826 Primer fo
	739	41.2	1.3	2293	6	AX879422	AX879422 Sequence
	740	41.2	1.3	2293	9	AK027471	AK027471 Homo sapi
	741	41.2	1.3	2306	6	BD159853	BD159853 Primer fo
	742	41.2	1.3	2306	6	AX882662	AX882662 Sequence
	743	41.2	1.3	2306	9	AK027654	AK027654 Homo sapi
	744	41.2	1.3	3041	6	BD159617	BD159617 Primer fo

	745	41.2	1.3	3041	6	AX882248	AX882248 Sequence
	746	41.2	1.3	3041	9	AK027501	AK027501 Homo sapi
	747	41.2	1.3	3512	8	AK101861	AK101861 Oryza sat
	748	41.2	1.3	4281	6	BD183506	BD183506 Novel gen
	749	41.2	1.3	4529	9	AK074171	AK074171 Homo sapi
	750	41.2	1.3	7484	6	BD181563	BD181563 Novel gen
	751	41.2	1.3	7484	9	AB051556	AB051556 Homo sapi
	752	41.2	1.3	7804	9	AF517673	AF517673 Homo sapi
c	753	41.2	1.3	113196	9	HSJ697K14	AL121829 Human DNA
	754	41.2	1.3	127035	2	AC149255	AC149255 Papio anu
c	755	41.2	1.3	135195	2	AC151946	AC151946 Dasypus n
	756	41.2	1.3	139841	2	AC149170	AC149170 Papio anu
c	757	41.2	1.3	147313	8	AP005800	AP005800 Oryza sat
	758	41.2	1.3	161513	2	AL365262	AL365262 Homo sapi
	759	41.2	1.3	177251	9	AC109583	AC109583 Homo sapi
	760	41.2	1.3	177836	2	AC149559	AC149559 Papio anu
	761	41.2	1.3	290850	1	SCO939127	AL939127 Streptomy
	762	41.2	1.3	299925	1	AP005045	AP005045 Streptomy
c	763	41.2	1.3	301617	1	AE016911	AE016911 Chromobac
	764	41	1.3	334	6	AX884750	AX884750 Sequence
	765	41	1.3	334	6	BD024360	BD024360 Sequence
	766	41	1.3	334	6	BD076948	BD076948 5' EST of
	767	41	1.3	505	6	AR424142	AR424142 Sequence
	768	41	1.3	505	6	AX984836	AX984836 Sequence
	769	41	1.3	505	6	BD119695	BD119695 EST and e
	770	41	1.3	512	6	AR413702	AR413702 Sequence
	771	41	1.3	512	6	AX970536	AX970536 Sequence
	772	41	1.3	512	6	BD109255	BD109255 EST and e
	773	41	1.3	777	10	AF095155	AF095155 Mus muscu
	774	41	1.3	5502	9	AB023138	AB023138 Homo sapi
	775	41	1.3	5895	6	AX686475	AX686475 Sequence
	776	41	1.3	6147	6	AX704766	AX704766 Sequence
	777	41	1.3	91240	9	AC130566	AC130566 Homo sapi
c	778	41	1.3	119463	10	AL928942	AL928942 Mouse DNA
c	779	41	1.3	152135	9	AC011199	AC011199 Homo sapi
c	780	41	1.3	160739	9	AP001092	AP001092 Homo sapi
	781	41	1.3	167389	2	AC115926	AC115926 Mus muscu
	782	41	1.3	170114	9	AC044790	AC044790 Homo sapi
	783	41	1.3	196591	2	AC091082	AC091082 Homo sapi
	784	41	1.3	229937	2	AC137328	AC137328 Rattus no
	785	41	1.3	246177	10	AC132957	AC132957 Mus muscu
	786	41	1.3	247655	10	AC145549	AC145549 Mus muscu
	787	41	1.3	262886	2	AC121209	AC121209 Rattus no
	788	41	1.3	347368	2	AC096620	AC096620 Rattus no
c	789	40.8	1.3	1737	6	BD157253	BD157253 Primer fo
c	790	40.8	1.3	1737	6	AX878484	AX878484 Sequence
c	791	40.8	1.3	1737	9	AK027287	AK027287 Homo sapi
	792	40.8	1.3	3693	3	AY185495	AY185495 Blastocri
	793	40.8	1.3	81954	2	AC015133	AC015133 Drosophil
	794	40.8	1.3	110000	2	LMFLCHR32_06	Continuation (7 of
	795	40.8	1.3	174894	2	AC150793	AC150793 Bos tauru
	796	40.8	1.3	174906	9	AC067930	AC067930 Homo sapi
	797	40.8	1.3	179057	2	AF276758	AF276758 Homo sapi
	798	40.8	1.3	179941	9	AC105118	AC105118 Homo sapi
	799	40.8	1.3	186938	3	AC008331	AC008331 Drosophil
c	800	40.8	1.3	196346	2	AC151242	AC151242 Bos tauru
	801	40.8	1.3	308031	3	AE003621	AE003621 Drosophil

c 802	40.6	1.3	1251	6	AX750726	AX750726 Sequence
803	40.6	1.3	1788	1	BPU07800	U07800 Bordetella
c 804	40.6	1.3	1881	3	AY136274	AY136274 Antheraea
805	40.6	1.3	2443	10	BC029243	BC029243 Mus muscu
806	40.6	1.3	4555	10	BC007191	BC007191 Mus muscu
807	40.6	1.3	4597	10	RNO237670	AJ237670 Rattus no
808	40.6	1.3	40051	1	MSGY224	AD000004 Mycobacte
c 809	40.6	1.3	40907	9	AC007459	AC007459 Homo sapi
810	40.6	1.3	110000	1	AE000516_06	Continuation (7 of
811	40.6	1.3	123385	1	BX640452	BX640452 Bordetell
c 812	40.6	1.3	178035	2	AC068680	AC068680 Homo sapi
c 813	40.6	1.3	194632	9	AC096996	AC096996 Homo sapi
814	40.6	1.3	205702	10	AC140190	AC140190 Mus muscu
815	40.6	1.3	206230	10	AC084272	AC084272 Mus muscu
816	40.6	1.3	255260	1	BX640436	BX640436 Bordetell
817	40.6	1.3	257701	1	BX640422	BX640422 Bordetell
c 818	40.6	1.3	292100	1	SCO939121	AL939121 Streptomy
c 819	40.6	1.3	300880	1	AE016917	AE016917 Chromobac
820	40.6	1.3	304282	1	AE016910	AE016910 Chromobac
821	40.6	1.3	324050	1	BX248335	BX248335 Mycobacte
822	40.6	1.3	342416	1	BX842573	BX842573 Mycobacte
823	40.4	1.3	1056	5	BX934045	BX934045 Gallus ga
824	40.4	1.3	1749	5	AJ781409	AJ781409 Tetraodon
825	40.4	1.3	2621	6	E49239	E49239 Cell growth
826	40.4	1.3	2621	10	AF328140	AF328140 Mus muscu
827	40.4	1.3	6287	1	AF042281	AF042281 Ralstonia
828	40.4	1.3	12748	1	AE005759	AE005759 Caulobact
829	40.4	1.3	77330	9	AC090790	AC090790 Homo sapi
c 830	40.4	1.3	152530	9	AC011727	AC011727 Homo sapi
c 831	40.4	1.3	161788	9	AC009314	AC009314 Homo sapi
832	40.4	1.3	163952	2	AC149821	AC149821 Zea mays
c 833	40.4	1.3	167029	8	AP002540	AP002540 Oryza sat
c 834	40.4	1.3	169079	9	AC069185	AC069185 Homo sapi
c 835	40.4	1.3	176633	9	AC091901	AC091901 Homo sapi
836	40.4	1.3	178032	2	AC069370	AC069370 Homo sapi
c 837	40.4	1.3	198643	2	AC023335	AC023335 Homo sapi
c 838	40.4	1.3	253546	2	AC105507	AC105507 Rattus no
c 839	40.4	1.3	253910	10	AC100751	AC100751 Mus muscu
c 840	40.4	1.3	265361	2	AC125800	AC125800 Rattus no
841	40.2	1.3	1194	6	AR386658	AR386658 Sequence
842	40.2	1.3	1972	3	LMA243460	AJ243460 Leishmani
843	40.2	1.3	2650	1	PPPBAC358	X70139 P. putida e
844	40.2	1.3	4350	6	AX188564	AX188564 Sequence
c 845	40.2	1.3	115532	9	AL354754	AL354754 Human DNA
c 846	40.2	1.3	138203	1	AY310323	AY310323 Streptomy
c 847	40.2	1.3	172238	9	AC090942	AC090942 Homo sapi
848	40.2	1.3	182171	9	AC066589	AC066589 Homo sapi
c 849	40.2	1.3	190437	9	AC019077	AC019077 Homo sapi
c 850	40.2	1.3	191954	3	AC025726	AC025726 Caenorhab
c 851	40.2	1.3	208989	9	AC027124	AC027124 Homo sapi
852	40.2	1.3	228972	2	AC139930	AC139930 Rattus no
c 853	40.2	1.3	286550	1	SME591785	AL591785 Sinorhizo
854	40.2	1.3	300900	1	AP005939	AP005939 Bradyrhiz
c 855	40.2	1.3	346547	1	AP003012	AP003012 Mesorhizo
856	40	1.3	12326	1	AE004890	AE004890 Pseudomon
c 857	40	1.3	89170	10	AL731806	AL731806 Mouse DNA
c 858	40	1.3	110000	1	AE017282_00	AE017282 Methyloco

859	40	1.3	149249	9	AC079945	AC079945 Homo sapi
860	40	1.3	166128	8	AP005457	AP005457 Oryza sat
c 861	40	1.3	169422	9	AC093309	AC093309 Homo sapi
c 862	40	1.3	199323	2	AC099943	AC099943 Mus muscu
863	40	1.3	227330	10	AC020786	AC020786 Mus muscu
c 864	40	1.3	228147	10	AC090652	AC090652 Mus muscu
865	40	1.3	236039	2	AC121212	AC121212 Rattus no
866	40	1.3	236397	2	AC101880	AC101880 Mus muscu
867	40	1.3	274853	10	AC025353	AC025353 Mus muscu
868	39.8	1.3	1400	6	AX093390	AX093390 Sequence
869	39.8	1.3	1467	1	AF053937	AF053937 Pseudomon
870	39.8	1.3	1958	6	CQ716735	CQ716735 Sequence
871	39.8	1.3	2336	5	AF022946	AF022946 Gallus ga
872	39.8	1.3	2403	5	AJ720774	AJ720774 Gallus ga
c 873	39.8	1.3	6741	6	E32987	E32987 Gene encodi
c 874	39.8	1.3	35745	3	LMFL5174	AL445944 Leishmani
875	39.8	1.3	107868	9	AL445686	AL445686 Human DNA
876	39.8	1.3	111372	2	AL353145	AL353145 Homo sapi
c 877	39.8	1.3	134673	8	AP002860	AP002860 Oryza sat
878	39.8	1.3	163526	8	AP002522	AP002522 Oryza sat
879	39.8	1.3	168253	8	AP003045	AP003045 Oryza sat
880	39.8	1.3	191104	2	AC119483	AC119483 Rattus no
881	39.8	1.3	209068	10	AL603868	AL603868 Mouse DNA
882	39.8	1.3	227524	2	AC129956	AC129956 Bos tauru
883	39.8	1.3	301443	1	AE017239	AE017239 Mycobacte
c 884	39.8	1.3	308050	1	SCO939124	AL939124 Streptomy
c 885	39.8	1.3	349737	1	BX572597	BX572597 Rhodopseu
886	39.6	1.3	511	6	BD059601	BD059601 Secreted
887	39.6	1.3	1043	5	AF180295	AF180295 Alligator
888	39.6	1.3	1438	6	CQ587691	CQ587691 Sequence
889	39.6	1.3	1703	9	HSHBF2A	X74143 H.sapiens H
890	39.6	1.3	1772	8	CREATPS	J04219 C.reinhardt
891	39.6	1.3	2129	3	AY058756	AY058756 Drosophil
892	39.6	1.3	2142	9	AF180474	AF180474 Homo sapi
893	39.6	1.3	2787	9	HSM801420	AL133647 Homo sapi
894	39.6	1.3	2831	9	BC016474	BC016474 Homo sapi
895	39.6	1.3	2904	9	HSHBFG2	X78202 H.sapiens H
896	39.6	1.3	2913	8	CREATPC	M73493 Chlamydomon
c 897	39.6	1.3	3309	9	AF069072	AF069072 Homo sapi
898	39.6	1.3	4133	9	AB014591	AB014591 Homo sapi
899	39.6	1.3	4138	6	CQ717820	CQ717820 Sequence
900	39.6	1.3	4512	9	AK160386	AK160386 Homo sapi
901	39.6	1.3	49999	6	AX015915	AX015915 Sequence
c 902	39.6	1.3	102239	8	AP004043	AP004043 Oryza sat
903	39.6	1.3	155293	5	BX248384	BX248384 Zebrafish
904	39.6	1.3	178453	2	BX469917	BX469917 Danio rer
905	39.6	1.3	179481	2	AC148908	AC148908 Otolemur
c 906	39.6	1.3	181134	2	AC132350	AC132350 Mus muscu
c 907	39.6	1.3	182539	2	AC132443	AC132443 Mus muscu
908	39.6	1.3	198017	9	AC012314	AC012314 Homo sapi
909	39.6	1.3	200452	9	AC015804	AC015804 Homo sapi
c 910	39.6	1.3	205307	2	AC009968	AC009968 Homo sapi
911	39.6	1.3	207952	2	AC151020	AC151020 Callithri
c 912	39.6	1.3	221100	2	AC112841	AC112841 Rattus no
913	39.6	1.3	224391	2	AC148953	AC148953 Otolemur
914	39.6	1.3	235061	2	AC107257	AC107257 Rattus no
915	39.6	1.3	248550	1	SCO939120	AL939120 Streptomy

916	39.6	1.3	250672	2	AC096525	AC096525	Rattus no
c 917	39.6	1.3	252053	2	AC097148	AC097148	Rattus no
c 918	39.6	1.3	261136	2	AC111626	AC111626	Rattus no
c 919	39.6	1.3	265642	2	AC103455	AC103455	Rattus no
920	39.6	1.3	285663	2	AC111628	AC111628	Rattus no
c 921	39.4	1.3	318	11	BV144295	BV144295	PZA02417-
c 922	39.4	1.3	456	6	CQ098045	CQ098045	Sequence
c 923	39.4	1.3	456	6	CQ136907	CQ136907	Sequence
c 924	39.4	1.3	456	6	CQ174660	CQ174660	Sequence
c 925	39.4	1.3	456	6	CQ220231	CQ220231	Sequence
c 926	39.4	1.3	456	6	CQ258601	CQ258601	Sequence
c 927	39.4	1.3	456	6	CQ296041	CQ296041	Sequence
c 928	39.4	1.3	456	6	CQ332573	CQ332573	Sequence
929	39.4	1.3	1004	8	AK061357	AK061357	Oryza sat
c 930	39.4	1.3	1246	6	AX164174	AX164174	Sequence
931	39.4	1.3	1311	6	AX647515	AX647515	Sequence
932	39.4	1.3	1756	9	BC038980	BC038980	Homo sapi
933	39.4	1.3	1955	6	AX714845	AX714845	Sequence
934	39.4	1.3	1955	9	AK057470	AK057470	Homo sapi
c 935	39.4	1.3	11687	1	AE004662	AE004662	Pseudomon
936	39.4	1.3	23142	9	HUMGNOS48	D26607	Homo sapien
937	39.4	1.3	105841	8	AC092697	AC092697	Oryza sat
c 938	39.4	1.3	120450	9	AC093393	AC093393	Homo sapi
939	39.4	1.3	134102	8	AC074196	AC074196	Oryza sat
c 940	39.4	1.3	135214	9	AC004848	AC004848	Homo sapi
c 941	39.4	1.3	198411	10	AL731670	AL731670	Mouse DNA
c 942	39.4	1.3	200191	9	AL390027	AL390027	Human DNA
943	39.4	1.3	201226	10	AL806533	AL806533	Mouse DNA
c 944	39.4	1.3	234078	2	AC094883	AC094883	Rattus no
c 945	39.4	1.3	288669	2	AL390297	AL390297	Homo sapi
946	39.4	1.3	300029	8	AE017115	AE017115	Oryza sat
947	39.4	1.3	301617	1	AE016911	AE016911	Chromobac
948	39.2	1.2	364	6	AR425705	AR425705	Sequence
949	39.2	1.2	364	6	AX986399	AX986399	Sequence
950	39.2	1.2	364	6	BD121258	BD121258	EST and e
c 951	39.2	1.2	928	8	AK103030	AK103030	Oryza sat
952	39.2	1.2	1361	6	AR452833	AR452833	Sequence
c 953	39.2	1.2	1441	9	AK057733	AK057733	Homo sapi
954	39.2	1.2	1888	6	AR306559	AR306559	Sequence
955	39.2	1.2	1888	6	AX061633	AX061633	Sequence
956	39.2	1.2	1895	9	BC027884	BC027884	Homo sapi
957	39.2	1.2	1922	6	BD210061	BD210061	Human tra
958	39.2	1.2	1948	9	AK172768	AK172768	Homo sapi
c 959	39.2	1.2	2322	6	CQ870609	CQ870609	Sequence
c 960	39.2	1.2	2322	6	AX747240	AX747240	Sequence
c 961	39.2	1.2	2322	9	AK091896	AK091896	Homo sapi
c 962	39.2	1.2	2446	6	CQ851420	CQ851420	Sequence
c 963	39.2	1.2	2446	9	AK128663	AK128663	Homo sapi
c 964	39.2	1.2	3347	9	BC036549	BC036549	Homo sapi
c 965	39.2	1.2	3474	9	AY358107	AY358107	Homo sapi
c 966	39.2	1.2	9566	1	RP1W17A	L40585	Xanthomonas
967	39.2	1.2	28066	6	AX647845	AX647845	Sequence
968	39.2	1.2	55216	6	AR306445	AR306445	Sequence
c 969	39.2	1.2	55216	6	AR306445	AR306445	Sequence
c 970	39.2	1.2	82746	1	AF453501	AF453501	Actinosyn
c 971	39.2	1.2	110000	1	AP006618_48	Continuation (49 o	
972	39.2	1.2	110000	2	AC106346_1	Continuation (2 of	

973	39.2	1.2	110000	2	LMFLCHR36_07	Continuation (8 of
c 974	39.2	1.2	110000	8	AE016817_00	AE016817 Eremothec
975	39.2	1.2	120455	9	AL139254	AL139254 Human DNA
c 976	39.2	1.2	126141	2	AL356300	AL356300 Homo sapi
977	39.2	1.2	132107	8	AP005477	AP005477 Oryza sat
978	39.2	1.2	144255	8	AP004811	AP004811 Oryza sat
c 979	39.2	1.2	145590	8	AC109601	AC109601 Oryza sat
c 980	39.2	1.2	145912	8	AP003347	AP003347 Oryza sat
981	39.2	1.2	151986	8	AP005840	AP005840 Oryza sat
c 982	39.2	1.2	154831	2	AC019085	AC019085 Homo sapi
c 983	39.2	1.2	163377	8	AP004684	AP004684 Oryza sat
984	39.2	1.2	164856	9	AC027625	AC027625 Homo sapi
c 985	39.2	1.2	167560	8	AP003452	AP003452 Oryza sat
986	39.2	1.2	168396	2	AL590010	AL590010 Homo sapi
c 987	39.2	1.2	174487	9	AC073896	AC073896 Homo sapi
c 988	39.2	1.2	174521	2	AC127468	AC127468 Papio anu
989	39.2	1.2	174695	2	AC149448	AC149448 Papio anu
c 990	39.2	1.2	184762	2	AC023500	AC023500 Homo sapi
c 991	39.2	1.2	194377	2	AC021726	AC021726 Homo sapi
c 992	39.2	1.2	196650	2	AC118441	AC118441 Rattus no
c 993	39.2	1.2	217473	2	AC135154	AC135154 Rattus no
c 994	39.2	1.2	249291	2	AC109718	AC109718 Rattus no
995	39.2	1.2	251905	2	AC093682	AC093682 Homo sapi
996	39.2	1.2	272545	2	AC090533	AC090533 Mus muscu
997	39.2	1.2	299925	1	AP005043	AP005043 Streptomy
998	39	1.2	305	6	AX886356	AX886356 Sequence
999	39	1.2	305	6	BD025966	BD025966 Sequence
1000	39	1.2	472	6	AR424900	AR424900 Sequence
1001	39	1.2	472	6	AX985594	AX985594 Sequence
1002	39	1.2	472	6	BD120453	BD120453 EST and e
c1003	39	1.2	610	6	BD072443	BD072443 Secreted
1004	39	1.2	717	12	AY658165	AY658165 Synthetic
1005	39	1.2	1222	6	AR060393	AR060393 Sequence
1006	39	1.2	1222	6	I45973	I45973 Sequence 3
1007	39	1.2	1831	4	BTU65394	U65394 Bos taurus
1008	39	1.2	3117	9	BC000977	BC000977 Homo sapi
1009	39	1.2	3155	6	AX281693	AX281693 Sequence
1010	39	1.2	3315	6	CQ846005	CQ846005 Sequence
1011	39	1.2	3315	9	AK131490	AK131490 Homo sapi
1012	39	1.2	4097	4	BOVNOS	M95674 Bos taurus
1013	39	1.2	4097	6	A46717	A46717 Sequence 3
1014	39	1.2	4097	6	AR118634	AR118634 Sequence
1015	39	1.2	4097	6	AR141717	AR141717 Sequence
1016	39	1.2	4511	3	DM75B	X15586 D.melanogas
1017	39	1.2	4791	4	BTU63311	U63311 Bos taurus
1018	39	1.2	4791	6	AR164385	AR164385 Sequence
1019	39	1.2	4791	6	BD204900	BD204900 Compositi
1020	39	1.2	4791	6	AR205928	AR205928 Sequence
1021	39	1.2	5970	3	DME75A	X51548 Drosophila
1022	39	1.2	6083	3	AY489269	AY489269 Plodia in
1023	39	1.2	6282	3	DME75B	X51549 Drosophila
1024	39	1.2	6577	6	CQ590148	CQ590148 Sequence
c1025	39	1.2	11650	1	AE004914	AE004914 Pseudomon
c1026	39	1.2	12110	1	AE012125	AE012125 Xanthomon
c1027	39	1.2	14309	1	AE004759	AE004759 Pseudomon
1028	39	1.2	20250	1	AY204469	AY204469 Myxococcu
1029	39	1.2	31445	9	AL449263	AL449263 Human DNA

c1030	39	1.2	34094	6	BD235926	BD235926 Porcine a
c1031	39	1.2	34094	6	AR266357	AR266357 Sequence
c1032	39	1.2	34094	6	AX799763	AX799763 Sequence
c1033	39	1.2	34094	14	AB026117	AB026117 Porcine a
c1034	39	1.2	34094	14	AF083132	AF083132 Porcine a
c1035	39	1.2	34094	14	PAD237815	AJ237815 Porcine a
1036	39	1.2	35722	2	AC015427	AC015427 Drosophil
1037	39	1.2	131860	8	AC105770	AC105770 Oryza sat
c1038	39	1.2	152048	2	AC115343	AC115343 Rattus no
c1039	39	1.2	155749	2	AC135345	AC135345 Homo sapi
c1040	39	1.2	157135	2	AC064817	AC064817 Homo sapi
1041	39	1.2	158211	2	AC026853	AC026853 Homo sapi
c1042	39	1.2	159148	9	AL592424	AL592424 Human DNA
c1043	39	1.2	160740	9	AC091053	AC091053 Homo sapi
c1044	39	1.2	160842	2	AC124090	AC124090 Homo sapi
1045	39	1.2	164466	2	AC126353	AC126353 Homo sapi
c1046	39	1.2	168874	10	AC132135	AC132135 Mus muscu
c1047	39	1.2	170211	9	AC104360	AC104360 Homo sapi
1048	39	1.2	171678	3	AC010059	AC010059 Drosophil
1049	39	1.2	174566	9	AC068234	AC068234 Homo sapi
1050	39	1.2	175238	10	AL606903	AL606903 Mouse DNA
1051	39	1.2	177018	2	AC103584	AC103584 Bos tauru
1052	39	1.2	177613	2	AC124089	AC124089 Homo sapi
c1053	39	1.2	178353	2	AC012334	AC012334 Homo sapi
1054	39	1.2	179649	3	AC010045	AC010045 Drosophil
1055	39	1.2	180546	2	AC017046	AC017046 Homo sapi
c1056	39	1.2	182245	2	AC149842	AC149842 Papio anu
1057	39	1.2	186139	2	AC116540	AC116540 Drosophil
1058	39	1.2	188766	9	AC135329	AC135329 Homo sapi
1059	39	1.2	189050	1	AL646069	AL646069 Ralstonia
1060	39	1.2	192087	9	AC121324	AC121324 Homo sapi
c1061	39	1.2	195397	2	AC135718	AC135718 Homo sapi
1062	39	1.2	196827	9	AC124091	AC124091 Homo sapi
1063	39	1.2	202418	2	AC150815	AC150815 Callithri
c1064	39	1.2	208406	2	AC133405	AC133405 Rattus no
c1065	39	1.2	211009	8	AF326781	AF326781 Triticum
c1066	39	1.2	236760	2	AC132537	AC132537 Rattus no
c1067	39	1.2	253487	2	AC095252	AC095252 Rattus no
1068	39	1.2	268200	1	AP000061	AP000061 Aeropyrum
c1069	39	1.2	270418	1	AE017303	AE017303 Thermus t
c1070	39	1.2	275434	9	HSA400879	AJ400879 Homo sapi
1071	39	1.2	296500	1	SCO939128	AL939128 Streptomy
c1072	39	1.2	302050	3	AE003522	AE003522 Drosophil
1073	38.8	1.2	2092	8	AK069127	AK069127 Oryza sat
1074	38.8	1.2	3194	10	AF133208	AF133208 Mus muscu
1075	38.8	1.2	4938	1	PPU279003	AJ279003 Pseudomon
1076	38.8	1.2	7543	1	AF147448	AF147448 Pseudomon
1077	38.8	1.2	10245	1	AE004569	AE004569 Pseudomon
c1078	38.8	1.2	16964	1	AE004817	AE004817 Pseudomon
1079	38.8	1.2	110000	1	AE016822_05	Continuation (6 of
1080	38.8	1.2	110000	1	AP006618_36	Continuation (37 o
1081	38.8	1.2	120743	8	AP004082	AP004082 Oryza sat
1082	38.8	1.2	128150	2	AC148748	AC148748 Sorex ara
1083	38.8	1.2	151144	5	BX323575	BX323575 Zebrafish
1084	38.8	1.2	161126	8	NC80A10	BX294012 Neurospor
c1085	38.8	1.2	168862	9	AC022024	AC022024 Homo sapi
c1086	38.8	1.2	186121	5	AL929201	AL929201 Zebrafish

c1087	38.8	1.2	190860	2	AC073803	AC073803	Mus muscu
1088	38.8	1.2	196413	2	AC139927	AC139927	Rattus no
1089	38.8	1.2	197805	2	AC105307	AC105307	Bos tauru
c1090	38.8	1.2	199014	2	AC108293	AC108293	Rattus no
1091	38.8	1.2	199847	10	AL691431	AL691431	Mouse DNA
1092	38.8	1.2	215234	2	AC073745	AC073745	Mus muscu
1093	38.8	1.2	217744	2	BX323036	BX323036	Danio rer
c1094	38.8	1.2	237427	2	AC115488	AC115488	Rattus no
1095	38.8	1.2	242543	2	AC096128	AC096128	Rattus no
c1096	38.8	1.2	273285	1	AE017304	AE017304	Thermus t
c1097	38.8	1.2	281747	2	AC094865	AC094865	Rattus no
c1098	38.8	1.2	292200	1	SCO939129	AL939129	Streptomy
1099	38.8	1.2	296417	2	AC112730	AC112730	Rattus no
c1100	38.6	1.2	210	11	BV103732	BV103732	MARC 6937
1101	38.6	1.2	444	6	AX307710	AX307710	Sequence
c1102	38.6	1.2	1031	8	AK099137	AK099137	Oryza sat
c1103	38.6	1.2	1034	8	AK061436	AK061436	Oryza sat
1104	38.6	1.2	2135	10	S60316	S60316	DMR-B15=myo
1105	38.6	1.2	2261	10	S60314	S60314	DMR-B15=myo
1106	38.6	1.2	2432	10	S60313	S60313	DMR-B15=myo
1107	38.6	1.2	2477	10	MMRNASEME	X85994	M.musculus
1108	38.6	1.2	4717	6	AX463544	AX463544	Sequence
1109	38.6	1.2	4759	6	AX463530	AX463530	Sequence
1110	38.6	1.2	4783	6	E34509	E34509	Novel rpoA.
1111	38.6	1.2	4783	6	E34511	E34511	Novel ratA.
1112	38.6	1.2	4783	6	E34513	E34513	Novel utili
1113	38.6	1.2	4783	6	E34515	E34515	Human LIG-1
1114	38.6	1.2	4970	10	BC066852	BC066852	Mus muscu
1115	38.6	1.2	5287	9	AB050468	AB050468	Homo sapi
1116	38.6	1.2	13435	1	AE011670	AE011670	Xanthomon
1117	38.6	1.2	139628	2	AC150112	AC150112	Gallus ga
c1118	38.6	1.2	147924	2	AC036186	AC036186	Homo sapi
c1119	38.6	1.2	151986	8	AP005840	AP005840	Oryza sat
c1120	38.6	1.2	156655	2	AP002417	AP002417	Homo sapi
1121	38.6	1.2	156826	2	AC055767	AC055767	Homo sapi
c1122	38.6	1.2	162053	2	AC150193	AC150193	Gallus ga
1123	38.6	1.2	164403	9	AC027097	AC027097	Homo sapi
c1124	38.6	1.2	172185	2	AC068072	AC068072	Homo sapi
1125	38.6	1.2	174006	10	BX119994	BX119994	Mouse DNA
c1126	38.6	1.2	181340	2	AC009270	AC009270	Homo sapi
c1127	38.6	1.2	192063	9	AC099665	AC099665	Homo sapi
1128	38.6	1.2	202301	1	AE017286	AE017286	Desulfovi
c1129	38.6	1.2	247200	2	AC123270	AC123270	Rattus no
c1130	38.6	1.2	250709	2	AC135520	AC135520	Rattus no
c1131	38.6	1.2	266754	2	AC137277	AC137277	Rattus no
c1132	38.6	1.2	287536	2	AC093993	AC093993	Rattus no
c1133	38.6	1.2	299700	1	AP005944	AP005944	Bradyrhiz
1134	38.4	1.2	657	8	AK059037	AK059037	Oryza sat
1135	38.4	1.2	1056	6	AX455900	AX455900	Sequence
1136	38.4	1.2	1322	1	AY337170	AY337170	Unculture
1137	38.4	1.2	1534	8	AK059256	AK059256	Oryza sat
c1138	38.4	1.2	1550	10	BC057204	BC057204	Mus muscu
1139	38.4	1.2	1582	8	AK063635	AK063635	Oryza sat
c1140	38.4	1.2	1793	10	AF086830	AF086830	Mus muscu
1141	38.4	1.2	1897	8	AK068590	AK068590	Oryza sat
1142	38.4	1.2	1974	8	AK102523	AK102523	Oryza sat
1143	38.4	1.2	1977	8	AK106531	AK106531	Oryza sat

1144	38.4	1.2	1998	8	AK101878	AK101878 Oryza sat
1145	38.4	1.2	2493	6	AX455898	AX455898 Sequence
1146	38.4	1.2	2565	6	AX455899	AX455899 Sequence
1147	38.4	1.2	2568	6	AX468546	AX468546 Sequence
1148	38.4	1.2	2672	10	AF216805	AF216805 Rattus no
1149	38.4	1.2	2684	10	AF216806	AF216806 Rattus no
1150	38.4	1.2	2772	6	CQ730605	CQ730605 Sequence
1151	38.4	1.2	2792	9	BC035782	BC035782 Homo sapi
1152	38.4	1.2	2815	8	AY224496	AY224496 Oryza sat
1153	38.4	1.2	2870	10	AB019281	AB019281 Rattus no
1154	38.4	1.2	3097	10	AF216804	AF216804 Rattus no
1155	38.4	1.2	3336	8	AK121964	AK121964 Oryza sat
1156	38.4	1.2	3615	10	AF216807	AF216807 Rattus no
1157	38.4	1.2	3923	10	AK173279	AK173279 Mus muscu
1158	38.4	1.2	4187	10	BC059249	BC059249 Mus muscu
1159	38.4	1.2	10511	9	AF097738	AF097738 Homo sapi
1160	38.4	1.2	11673	6	CQ600338	CQ600338 Sequence
1161	38.4	1.2	11707	6	CQ609149	CQ609149 Sequence
c1162	38.4	1.2	12521	1	AE014717	AE014717 Bifidobac
1163	38.4	1.2	25150	1	AB070945	AB070945 Streptomy
1164	38.4	1.2	101075	8	CNS08CBU	AL928757 Oryza sat
c1165	38.4	1.2	106553	2	AC150982	AC150982 Zea mays
c1166	38.4	1.2	107819	8	CNS08C8J	AL731880 Oryza sat
1167	38.4	1.2	109008	9	AL590233	AL590233 Human DNA
1168	38.4	1.2	112897	2	OSIG00042	AL732347 Oryza sat
1169	38.4	1.2	113367	9	AC008178	AC008178 Homo sapi
c1170	38.4	1.2	134296	9	HS352H24	AL449215 Homo sapi
1171	38.4	1.2	141132	9	AC008250	AC008250 Homo sapi
c1172	38.4	1.2	144670	8	OSJN00084	AL606686 Oryza sat
c1173	38.4	1.2	145391	8	OSJN00092	AL606651 Oryza sat
1174	38.4	1.2	146442	8	AC125495	AC125495 Oryza sat
c1175	38.4	1.2	154018	2	AC062019	AC062019 Homo sapi
c1176	38.4	1.2	162568	8	AC136149	AC136149 Oryza sat
1177	38.4	1.2	166034	2	AC067913	AC067913 Homo sapi
c1178	38.4	1.2	174075	2	AC109241	AC109241 Mus muscu
1179	38.4	1.2	174373	3	AC093958	AC093958 Drosophil
1180	38.4	1.2	183922	2	AC005814	AC005814 Drosophil
1181	38.4	1.2	184349	9	AC113189	AC113189 Homo sapi
c1182	38.4	1.2	185278	9	AC023043	AC023043 Homo sapi
c1183	38.4	1.2	210624	2	AP001321	AP001321 Homo sapi
1184	38.4	1.2	210663	2	AC019525	AC019525 Drosophil
1185	38.4	1.2	213321	2	AC102988	AC102988 Rattus no
c1186	38.4	1.2	220283	2	AC103391	AC103391 Mus muscu
c1187	38.4	1.2	222457	9	AC108211	AC108211 Homo sapi
c1188	38.4	1.2	222871	2	AC108094	AC108094 Homo sapi
1189	38.4	1.2	231770	2	AC109171	AC109171 Mus muscu
c1190	38.4	1.2	238637	2	AC092254	AC092254 Mus muscu
c1191	38.4	1.2	245515	2	AC151275	AC151275 Mus muscu
c1192	38.4	1.2	247196	2	AC073822	AC073822 Mus muscu
c1193	38.4	1.2	300327	1	AE017228	AE017228 Mycobacte
c1194	38.4	1.2	300550	1	AP005030	AP005030 Streptomy
1195	38.4	1.2	300800	1	AP005036	AP005036 Streptomy
c1196	38.4	1.2	301068	1	AE017231	AE017231 Mycobacte
1197	38.4	1.2	311930	3	AE003480	AE003480 Drosophil
1198	38.4	1.2	346294	1	AP002999	AP002999 Mesorhizo
1199	38.4	1.2	347894	1	BX640431	BX640431 Bordetell
c1200	38.4	1.2	349980	6	AX492784	AX492784 Sequence

c1201	38.4	1.2	349980	6	AX553951	AX553951 Sequence
c1202	38.2	1.2	367	6	AX336220	AX336220 Sequence
c1203	38.2	1.2	367	6	AX336657	AX336657 Sequence
c1204	38.2	1.2	552	8	AB075378	AB075378 Oryza sat
1205	38.2	1.2	675	6	AR164340	AR164340 Sequence
1206	38.2	1.2	675	6	BD204855	BD204855 Compositi
1207	38.2	1.2	675	6	AR205883	AR205883 Sequence
c1208	38.2	1.2	1575	5	AF247675	AF247675 Gallus ga
1209	38.2	1.2	2173	8	AK072354	AK072354 Oryza sat
c1210	38.2	1.2	3510	1	MCA543648	AJ543648 Methyloco
1211	38.2	1.2	6520	4	BTU88532	U88532 Bos taurus
1212	38.2	1.2	11064	1	D63799	D63799 Thermus the
1213	38.2	1.2	16275	6	CQ584162	CQ584162 Sequence
c1214	38.2	1.2	34478	9	HUMLUCA19	AC000063 Human cos
1215	38.2	1.2	37507	6	CQ767414	CQ767414 Sequence
1216	38.2	1.2	37507	6	CQ774652	CQ774652 Sequence
1217	38.2	1.2	44567	6	AX695371	AX695371 Sequence
1218	38.2	1.2	77457	1	AF210249	AF210249 Streptomy
1219	38.2	1.2	82707	9	AC009363	AC009363 Homo sapi
1220	38.2	1.2	110000	1	AE017282_26	Continuation (27 o
c1221	38.2	1.2	123004	2	AC014962	AC014962 Drosophil
c1222	38.2	1.2	147392	9	AC023300	AC023300 Homo sapi
c1223	38.2	1.2	152435	10	AC121566	AC121566 Mus muscu
c1224	38.2	1.2	153792	2	AC099404	AC099404 Oryza sat
c1225	38.2	1.2	161970	9	AP005660	AP005660 Homo sapi
c1226	38.2	1.2	165592	10	AC122020	AC122020 Mus muscu
c1227	38.2	1.2	168981	10	AC124446	AC124446 Mus muscu
1228	38.2	1.2	169518	9	AC090826	AC090826 Homo sapi
1229	38.2	1.2	175275	2	AC111051	AC111051 Mus muscu
c1230	38.2	1.2	179997	2	AC093338	AC093338 Mus muscu
1231	38.2	1.2	186990	3	AC023678	AC023678 Drosophil
c1232	38.2	1.2	187708	2	CR788293	CR788293 Danio rer
1233	38.2	1.2	192389	9	AC007182	AC007182 Homo sapi
c1234	38.2	1.2	197878	3	AC093437	AC093437 Drosophil
c1235	38.2	1.2	198318	2	BX957253	BX957253 Danio rer
1236	38.2	1.2	204077	10	AC103407	AC103407 Mus muscu
1237	38.2	1.2	224733	2	AC098635	AC098635 Rattus no
c1238	38.2	1.2	234803	2	AC095884	AC095884 Rattus no
c1239	38.2	1.2	235930	10	AC131743	AC131743 Mus muscu
1240	38.2	1.2	236502	2	AC098186	AC098186 Rattus no
c1241	38.2	1.2	236913	2	AL161615	AL161615 Homo sapi
1242	38.2	1.2	256476	2	AC133985	AC133985 Rattus no
1243	38.2	1.2	291000	1	SCO939105	AL939105 Streptomy
c1244	38.2	1.2	303022	3	AE003542	AE003542 Drosophil
c1245	38.2	1.2	348457	2	AC127947	AC127947 Rattus no
1246	38	1.2	594	6	AX654720	AX654720 Sequence
1247	38	1.2	2325	6	E00897	E00897 DNA encodin
1248	38	1.2	2503	9	S72883	S72883 myotonin pr
c1249	38	1.2	2819	1	AZSNIFAFS	D13799 Azospirillu
1250	38	1.2	2982	6	CQ606905	CQ606905 Sequence
1251	38	1.2	3141	1	PSEACYII	M18278 Pseudomonas
1252	38	1.2	3768	1	SCU80063	U80063 Streptomyce
1253	38	1.2	25467	1	AB164642	AB164642 Streptomy
1254	38	1.2	36299	2	AC020209	AC020209 Drosophil
1255	38	1.2	47050	1	AJ582817	AJ582817 Streptomy
1256	38	1.2	80670	9	AC128683	AC128683 Homo sapi
c1257	38	1.2	82393	3	AC003923	AC003923 Drosophil

c1258	38	1.2	105830	10	AL606909	AL606909 Mouse DNA
c1259	38	1.2	110000	2	AP006489_1	Continuation (2 of
c1260	38	1.2	110000	2	BX255276_11	Continuation (12 o
1261	38	1.2	117724	2	AP004848	AP004848 Oryza sat
1262	38	1.2	123253	9	AC004971	AC004971 Homo sapi
1263	38	1.2	124814	9	AL161436	AL161436 Human DNA
c1264	38	1.2	129108	9	AC011482	AC011482 Homo sapi
1265	38	1.2	140219	10	AL603714	AL603714 Mouse DNA
1266	38	1.2	141121	10	AC099636	AC099636 Mus muscu
1267	38	1.2	144340	8	AP005110	AP005110 Oryza sat
1268	38	1.2	149135	2	AC149681	AC149681 Bos tauru
1269	38	1.2	153934	2	AC131027	AC131027 Canis fam
1270	38	1.2	153959	2	AC144526	AC144526 Homo sapi
c1271	38	1.2	157452	2	AC010190	AC010190 Homo sapi
1272	38	1.2	162139	9	AC147651	AC147651 Homo sapi
1273	38	1.2	167770	10	AC126445	AC126445 Mus muscu
c1274	38	1.2	178671	10	AC124632	AC124632 Mus muscu
1275	38	1.2	179305	2	AC144411	AC144411 Homo sapi
c1276	38	1.2	179724	9	AP003094	AP003094 Homo sapi
1277	38	1.2	184435	2	AC141618	AC141618 Homo sapi
c1278	38	1.2	190936	5	BX548158	BX548158 Zebrafish
1279	38	1.2	191909	2	AC148337	AC148337 Homo sapi
c1280	38	1.2	193314	2	AL603866	AL603866 Mus muscu
1281	38	1.2	194672	3	AC008360	AC008360 Drosophil
c1282	38	1.2	196490	10	AC126038	AC126038 Mus muscu
c1283	38	1.2	197943	2	AC129321	AC129321 Mus muscu
c1284	38	1.2	212808	2	AC150531	AC150531 Bos tauru
1285	38	1.2	218267	9	AC148667	AC148667 Macaca mu
c1286	38	1.2	225962	2	AC094695	AC094695 Rattus no
c1287	38	1.2	227245	9	AC008569	AC008569 Homo sapi
1288	38	1.2	228324	3	AE003700	AE003700 Drosophil
c1289	38	1.2	243187	2	AC134195	AC134195 Rattus no
1290	38	1.2	250636	2	AC110312	AC110312 Rattus no
1291	38	1.2	269862	2	CR450777	CR450777 Danio rer
c1292	38	1.2	299425	1	AP005037	AP005037 Streptomy
c1293	38	1.2	302300	1	AP005034	AP005034 Streptomy
1294	38	1.2	304517	1	AE016789	AE016789 Pseudomon
c1295	37.8	1.2	205	10	RATSIMPAL	M36626 Rat simple
c1296	37.8	1.2	307	11	BV144291	BV144291 PZA02417-
c1297	37.8	1.2	307	11	BV144292	BV144292 PZA02417-
c1298	37.8	1.2	315	11	BV144290	BV144290 PZA02417-
c1299	37.8	1.2	318	11	BV144297	BV144297 PZA02417-
c1300	37.8	1.2	320	11	BV144296	BV144296 PZA02417-
c1301	37.8	1.2	321	11	BV144289	BV144289 PZA02417-
c1302	37.8	1.2	322	11	BV144293	BV144293 PZA02417-
1303	37.8	1.2	646	11	PM7H3B	AL685226 Penicilli
1304	37.8	1.2	837	6	AR454024	AR454024 Sequence
1305	37.8	1.2	837	6	AR454025	AR454025 Sequence
1306	37.8	1.2	841	6	CQ780667	CQ780667 Sequence
1307	37.8	1.2	841	6	CQ782118	CQ782118 Sequence
1308	37.8	1.2	841	6	BD125376	BD125376 Primer fo
1309	37.8	1.2	841	6	BD126827	BD126827 Primer fo
1310	37.8	1.2	1065	10	AF212860	AF212860 Mus muscu
1311	37.8	1.2	1220	6	AR405953	AR405953 Sequence
1312	37.8	1.2	1221	9	AY136825	AY136825 Homo sapi
1313	37.8	1.2	1236	9	BC014245	BC014245 Homo sapi
1314	37.8	1.2	1257	6	BD269636	BD269636 Human sec

1315	37.8	1.2	1257	6	AX092390	AX092390	Sequence
1316	37.8	1.2	1257	6	AX376298	AX376298	Sequence
1317	37.8	1.2	1257	6	AX454660	AX454660	Sequence
1318	37.8	1.2	1257	6	AX459648	AX459648	Sequence
1319	37.8	1.2	1257	6	AX491138	AX491138	Sequence
1320	37.8	1.2	1257	6	AX697362	AX697362	Sequence
1321	37.8	1.2	1257	9	AY358914	AY358914	Homo sapi
1322	37.8	1.2	1284	6	AX829144	AX829144	Sequence
1323	37.8	1.2	1342	6	BD223153	BD223153	98 human
1324	37.8	1.2	1342	6	AR243851	AR243851	Sequence
1325	37.8	1.2	1471	8	AK106380	AK106380	Oryza sat
1326	37.8	1.2	1514	9	BC029590	BC029590	Homo sapi
c1327	37.8	1.2	1591	8	AK060742	AK060742	Oryza sat
c1328	37.8	1.2	1597	8	AF190770	AF190770	Oryza sat
1329	37.8	1.2	1653	5	AF205877	AF205877	Gallus ga
c1330	37.8	1.2	1677	8	AK069833	AK069833	Oryza sat
1331	37.8	1.2	2000	6	AX656098	AX656098	Sequence
c1332	37.8	1.2	2070	9	BC001723	BC001723	Homo sapi
c1333	37.8	1.2	2151	9	HSM803814	AL832506	Homo sapi
1334	37.8	1.2	2365	6	CQ783900	CQ783900	Sequence
1335	37.8	1.2	2365	6	BD127891	BD127891	Primer fo
1336	37.8	1.2	2365	9	AK075303	AK075303	Homo sapi
c1337	37.8	1.2	2445	8	AK100167	AK100167	Oryza sat
c1338	37.8	1.2	2821	6	AX835240	AX835240	Sequence
c1339	37.8	1.2	2821	9	AK098182	AK098182	Homo sapi
1340	37.8	1.2	3701	1	AF172724	AF172724	Caulobact
1341	37.8	1.2	5085	9	AF221759	AF221759	Homo sapi
1342	37.8	1.2	5713	9	D83785	D83785	Homo sapien
1343	37.8	1.2	9811	14	AF449714	AF449714	Cercopith
1344	37.8	1.2	10447	1	AE005692	AE005692	Caulobact
c1345	37.8	1.2	11283	1	AE005710	AE005710	Caulobact
c1346	37.8	1.2	33064	2	AY338477	AY338477	Streptomy
c1347	37.8	1.2	36655	9	HS399E4	AL031721	Human DNA
1348	37.8	1.2	72165	10	AL844574	AL844574	Mouse DNA
1349	37.8	1.2	72880	8	AP006375	AP006375	Lotus cor
1350	37.8	1.2	90497	10	AF260927	AF260927	Mus muscu
c1351	37.8	1.2	105589	2	AC092269	AC092269	Homo sapi
c1352	37.8	1.2	106544	6	CQ869794	CQ869794	Sequence
c1353	37.8	1.2	110000	1	AP006840_04	Continuation (5 of	
c1354	37.8	1.2	110000	2	AC138525_2	Continuation (3 of	
1355	37.8	1.2	111496	9	AC069351	AC069351	Homo sapi
1356	37.8	1.2	121607	8	AP003981	AP003981	Oryza sat
c1357	37.8	1.2	135175	8	AP004280	AP004280	Oryza sat
1358	37.8	1.2	138963	2	AC151908	AC151908	Mus muscu
1359	37.8	1.2	141686	9	AL355816	AL355816	Human DNA
1360	37.8	1.2	141833	9	AL442063	AL442063	Human DNA
c1361	37.8	1.2	144552	9	AC112723	AC112723	Homo sapi
1362	37.8	1.2	149051	2	AC138963	AC138963	Homo sapi
1363	37.8	1.2	150715	14	AY714813	AY714813	Cercopith
c1364	37.8	1.2	153287	8	AP006070	AP006070	Oryza sat
c1365	37.8	1.2	156514	8	AP003514	AP003514	Oryza sat
c1366	37.8	1.2	158063	9	AP001046	AP001046	Homo sapi
1367	37.8	1.2	160197	9	AP004221	AP004221	Homo sapi
1368	37.8	1.2	163794	2	AC138922	AC138922	Homo sapi
1369	37.8	1.2	166847	9	AC008393	AC008393	Homo sapi
1370	37.8	1.2	166892	9	AC007463	AC007463	Homo sapi
1371	37.8	1.2	167315	2	AC137501	AC137501	Homo sapi

1372	37.8	1.2	168860	9	AC098594	AC098594 Homo sapi
c1373	37.8	1.2	169089	9	AC008537	AC008537 Homo sapi
1374	37.8	1.2	171329	2	AC147785	AC147785 Pan trogl
1375	37.8	1.2	172424	2	AC150837	AC150837 Papio anu
c1376	37.8	1.2	174520	9	BS000234	BS000234 Pan trogl
c1377	37.8	1.2	175689	9	AC148703	AC148703 Macaca mu
1378	37.8	1.2	175839	9	AC004491	AC004491 Homo sapi
c1379	37.8	1.2	176922	9	AC012213	AC012213 Homo sapi
c1380	37.8	1.2	177163	9	AC138904	AC138904 Homo sapi
1381	37.8	1.2	179627	9	AC113426	AC113426 Homo sapi
1382	37.8	1.2	179947	10	AC122023	AC122023 Mus muscu
1383	37.8	1.2	181936	2	AC013387	AC013387 Homo sapi
1384	37.8	1.2	184706	2	AC013327	AC013327 Homo sapi
c1385	37.8	1.2	185165	2	AC134309	AC134309 Homo sapi
1386	37.8	1.2	186462	2	AL391727	AL391727 Homo sapi
c1387	37.8	1.2	186956	2	AC120346	AC120346 Mus muscu
c1388	37.8	1.2	187371	2	AC145229	AC145229 Homo sapi
c1389	37.8	1.2	189814	9	AC145866	AC145866 Pan trogl
1390	37.8	1.2	194757	2	AC068882	AC068882 Homo sapi
c1391	37.8	1.2	195646	9	AC093709	AC093709 Pan trogl
c1392	37.8	1.2	197000	2	AC124859	AC124859 Homo sapi
1393	37.8	1.2	197665	10	AC123940	AC123940 Mus muscu
c1394	37.8	1.2	200068	9	AC148691	AC148691 Macaca mu
c1395	37.8	1.2	201627	9	AC017068	AC017068 Homo sapi
1396	37.8	1.2	207751	2	AC112189	AC112189 Homo sapi
1397	37.8	1.2	213515	2	AC145231	AC145231 Homo sapi
1398	37.8	1.2	220349	2	AC136438	AC136438 Homo sapi
c1399	37.8	1.2	221557	2	AC146538	AC146538 Gasterost
c1400	37.8	1.2	224956	2	AC019008	AC019008 Mus muscu
c1401	37.8	1.2	228789	2	AC122236	AC122236 Mus muscu
1402	37.8	1.2	230510	9	AC084794	AC084794 Homo sapi
c1403	37.8	1.2	235751	2	AC146180	AC146180 Pan trogl
1404	37.8	1.2	237613	2	AC025769	AC025769 Homo sapi
c1405	37.8	1.2	238084	2	BX950172	BX950172 Danio rer
c1406	37.8	1.2	251096	10	AL596255	AL596255 Mouse DNA
1407	37.8	1.2	256417	2	AC079422	AC079422 Mus muscu
c1408	37.8	1.2	279011	9	AE006467	AE006467 Homo sapi
1409	37.8	1.2	300861	1	AE016777	AE016777 Pseudomon
1410	37.8	1.2	302898	1	AE017238	AE017238 Mycobacte
1411	37.8	1.2	321250	1	SCO939111	AL939111 Streptomy
c1412	37.8	1.2	340000	9	AP001751	AP001751 Homo sapi
c1413	37.8	1.2	349619	1	AP002996	AP002996 Mesorhizo
1414	37.6	1.2	599	11	G16014	G16014 human STS C
c1415	37.6	1.2	1297	1	S76058	S76058 MPKR=polyke
1416	37.6	1.2	1336	8	BT009312	BT009312 Triticum
c1417	37.6	1.2	2076	6	CQ490663	CQ490663 Sequence
c1418	37.6	1.2	2076	6	CQ496498	CQ496498 Sequence
1419	37.6	1.2	2400	6	CQ056276	CQ056276 Sequence
1420	37.6	1.2	2400	6	CQ075544	CQ075544 Sequence
1421	37.6	1.2	2400	6	CQ106523	CQ106523 Sequence
1422	37.6	1.2	2400	6	CQ145184	CQ145184 Sequence
1423	37.6	1.2	2400	6	CQ180624	CQ180624 Sequence
1424	37.6	1.2	2400	6	CQ204997	CQ204997 Sequence
1425	37.6	1.2	2400	6	CQ228365	CQ228365 Sequence
1426	37.6	1.2	2400	6	CQ266538	CQ266538 Sequence
1427	37.6	1.2	2400	6	CQ303495	CQ303495 Sequence
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1429	37.6	1.2	2530	1	SLU04630	U04630 Streptomyce
c1430	37.6	1.2	2581	6	CQ609150	CQ609150 Sequence
c1431	37.6	1.2	2655	6	CQ600339	CQ600339 Sequence
c1432	37.6	1.2	2684	9	BC059356	BC059356 Homo sapi
c1433	37.6	1.2	2854	1	SGAATA	X95916 Streptomyce
c1434	37.6	1.2	2862	9	AK122815	AK122815 Homo sapi
c1435	37.6	1.2	3973	3	BT010301	BT010301 Drosophil
c1436	37.6	1.2	4001	9	AK122942	AK122942 Homo sapi
c1437	37.6	1.2	4119	2	AC138418	AC138418 Homo sapi
c1438	37.6	1.2	4320	9	HSU60325	U60325 Human DNA p
c1439	37.6	1.2	4440	6	BD249887	BD249887 Diagnosti
c1440	37.6	1.2	4440	6	AX034450	AX034450 Sequence
c1441	37.6	1.2	4440	9	BC042571	BC042571 Homo sapi
c1442	37.6	1.2	4465	9	MIHSDNAPL	X98093 H.sapiens m
c1443	37.6	1.2	4503	9	BC050559	BC050559 Homo sapi
c1444	37.6	1.2	5520	3	AC084329	AC084329 Leishmani
c1445	37.6	1.2	5833	1	AF147703	AF147703 Streptomy
c1446	37.6	1.2	8699	9	HSU74651	U74651 Human DNA p
c1447	37.6	1.2	10276	1	AE012455	AE012455 Xanthomon
c1448	37.6	1.2	10524	1	AE011740	AE011740 Xanthomon
c1449	37.6	1.2	12905	1	AF055922	AF055922 Streptomy
c1450	37.6	1.2	21579	9	AC138417	AC138417 Homo sapi
1451	37.6	1.2	32331	9	AP001101	AP001101 Homo sapi
c1452	37.6	1.2	37487	6	AX695389	AX695389 Sequence
1453	37.6	1.2	53571	2	AC133632	AC133632 Homo sapi
1454	37.6	1.2	55114	9	HS1096J16	AL121721 Human DNA
c1455	37.6	1.2	59394	6	AX695860	AX695860 Sequence
c1456	37.6	1.2	64154	2	AL451003_3	Continuation (4 of
1457	37.6	1.2	100719	9	BX255925	BX255925 Human DNA
c1458	37.6	1.2	110000	1	AP006618_53	Continuation (54 o
c1459	37.6	1.2	110000	2	AL451003_2	Continuation (3 of
1460	37.6	1.2	110000	2	LMFLCHR36_03	Continuation (4 of
1461	37.6	1.2	122884	9	HS1158B12	AL034396 Human DNA
1462	37.6	1.2	126228	9	AC006543	AC006543 Homo sapi
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c1464	37.6	1.2	140507	10	AL772410	AL772410 Mouse DNA
c1465	37.6	1.2	142080	2	AC069260	AC069260 Homo sapi
c1466	37.6	1.2	156630	9	AC146025	AC146025 Pan trogl
1467	37.6	1.2	162392	9	AP001206	AP001206 Homo sapi
1468	37.6	1.2	163319	2	AC110512	AC110512 Mus muscu
c1469	37.6	1.2	163801	2	AC025224	AC025224 Homo sapi
1470	37.6	1.2	165433	8	CNS08C8S	AL731888 Oryza sat
1471	37.6	1.2	165704	9	AC007387	AC007387 Homo sapi
1472	37.6	1.2	167672	2	AC132806	AC132806 Homo sapi
1473	37.6	1.2	170612	9	AC005317	AC005317 Homo sapi
1474	37.6	1.2	170695	9	AC016134	AC016134 Homo sapi
1475	37.6	1.2	172505	9	AC124068	AC124068 Homo sapi
1476	37.6	1.2	177433	9	AP001458	AP001458 Homo sapi
c1477	37.6	1.2	177719	9	AC135048	AC135048 Homo sapi
1478	37.6	1.2	177990	2	AC090306	AC090306 Homo sapi
c1479	37.6	1.2	183846	9	AC073850	AC073850 Homo sapi
1480	37.6	1.2	184039	9	CNS018OX	AL109767 Human chr
c1481	37.6	1.2	184665	10	AL773563	AL773563 Mouse DNA
c1482	37.6	1.2	184799	2	AC037448	AC037448 Homo sapi
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1484	37.6	1.2	185079	2	AC135702	AC135702 Rattus no
c1485	37.6	1.2	187727	2	AC021142	AC021142 Homo sapi

1486	37.6	1.2	187741	2	AC087681	AC087681 Homo sapi
1487	37.6	1.2	189541	2	AC101785	AC101785 Mus muscu
1488	37.6	1.2	189758	2	CR450704	CR450704 Danio rer
1489	37.6	1.2	190253	2	AC067779	AC067779 Homo sapi
c1490	37.6	1.2	196413	2	AC139927	AC139927 Rattus no
1491	37.6	1.2	196733	10	AC090008	AC090008 Mus muclu
c1492	37.6	1.2	201821	2	AC129105	AC129105 Homo sapi
c1493	37.6	1.2	202414	2	AC135051	AC135051 Homo sapi
1494	37.6	1.2	202505	2	AC090232	AC090232 Homo sapi
1495	37.6	1.2	203050	1	AL646071	AL646071 Ralstonia
1496	37.6	1.2	208050	1	AL646083	AL646083 Ralstonia
c1497	37.6	1.2	209990	10	AC092751	AC092751 Genomic s
1498	37.6	1.2	211250	2	AC090702	AC090702 Homo sapi
c1499	37.6	1.2	213846	2	AC140254	AC140254 Mus muscu
1500	37.6	1.2	213916	2	AC073473	AC073473 Homo sapi

ALIGNMENTS

RESULT 1

AX697208

LOCUS AX697208 3143 bp DNA linear PAT 02-APR-2003

DEFINITION Sequence 276 from Patent WO0078961.

ACCESSION AX697208

VERSION AX697208.1 GI:29498147

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Ferrara,N., Stewart,T.A., Williams,P.M., Baker,K.P., Desnoyers,L.,
Eaton,D.L., Gao,W.Q., Pan,J., Botstein,D., Fong,S., Goddard,A.,
Godowski,P.J., Gurney,A.L., Smith,V., Tumas,D., Wood,W.I.,
Grimaldi,C.J., Hillan,K.J., Paoni,N.F., Roy,M.A. and Watanabe,C.K.

TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
the same

JOURNAL Patent: WO 0078961-A 276 28-DEC-2000;
Genentech Inc. (US)

FEATURES Location/Qualifiers
source 1. .3143
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Query Match 100.0%; Score 3143; DB 6; Length 3143;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3143; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGCTGAGGCACTGAGAGACCGGAAAGCCTGGCATTCCAGAGGGAGGGAAACGCAGCGGC 60
|||||

Db 1 GGGCTGAGGCACTGAGAGACCGGAAAGCCTGGCATTCCAGAGGGAGGGAAACGCAGCGGC 60

Qy 61 ATCCCCAGGCTCCAGAGCTCCCTGGTGACAGTCTGTGGCTGAGCATGGCCCTCCCAGCCC 120
|||||

Db	61	ATCCCCAGGCTCCAGAGCTCCCTGGTGACAGTCTGTGGCTGAGCATGGCCCTCCCAGCCC	120
Qy	121	TGGGCCTGGACCCCTGGAGCCTCCTGGGCCTTTTCCTCTTCCAAGTCTTCAGCTGCTGC	180
Db	121	TGGGCCTGGACCCCTGGAGCCTCCTGGGCCTTTTCCTCTTCCAAGTCTTCAGCTGCTGC	180
Qy	181	TGCCGACGACGACCGCGGGGGAGGCGGGCAGGGGCCCATGCCCAGGGTCAGATACTATG	240
Db	181	TGCCGACGACGACCGCGGGGGAGGCGGGCAGGGGCCCATGCCCAGGGTCAGATACTATG	240
Qy	241	CAGGGGATGAACGTAGGGCACTTAGCTTCTTCCACCAGAAGGGCCTCCAGGATTTTGACA	300
Db	241	CAGGGGATGAACGTAGGGCACTTAGCTTCTTCCACCAGAAGGGCCTCCAGGATTTTGACA	300
Qy	301	CTCTGCTCCTGAGTGGTGATGGAAATACTCTCTACGTGGGGGCTCGAGAAGCCATTCTGG	360
Db	301	CTCTGCTCCTGAGTGGTGATGGAAATACTCTCTACGTGGGGGCTCGAGAAGCCATTCTGG	360
Qy	361	CCTTGGATATCCAGGATCCAGGGGTCCCAGGCTAAAGAACATGATACCGTGGCCAGCCA	420
Db	361	CCTTGGATATCCAGGATCCAGGGGTCCCAGGCTAAAGAACATGATACCGTGGCCAGCCA	420
Qy	421	GTGACAGAAAAAGAGTGAATGTGCCTTTAAGAAGAAGAGCAATGAGACACAGTGTTC	480
Db	421	GTGACAGAAAAAGAGTGAATGTGCCTTTAAGAAGAAGAGCAATGAGACACAGTGTTC	480
Qy	481	ACTTCATCCGTGTCCTGGTTTCTTACAATGTCAACCATCTCTACACCTGCGGCACCTTCG	540
Db	481	ACTTCATCCGTGTCCTGGTTTCTTACAATGTCAACCATCTCTACACCTGCGGCACCTTCG	540
Qy	541	CCTTCAGCCCTGCTTGTACCTTCATTGAACCTCAAGATTCCTACCTGTTGCCATCTCGG	600
Db	541	CCTTCAGCCCTGCTTGTACCTTCATTGAACCTCAAGATTCCTACCTGTTGCCATCTCGG	600
Qy	601	AGGACAAGGTCATGGAGGAAAAGGCCAAAGCCCTTTGACCCGCTCACAAGCATAACGG	660
Db	601	AGGACAAGGTCATGGAGGAAAAGGCCAAAGCCCTTTGACCCGCTCACAAGCATAACGG	660
Qy	661	CTGTCTTGGTGGATGGGATGCTCTATTCTGGTACTATGAACAACCTTCCTGGGCAGTGAGC	720
Db	661	CTGTCTTGGTGGATGGGATGCTCTATTCTGGTACTATGAACAACCTTCCTGGGCAGTGAGC	720
Qy	721	CCATCCTGATGCGCACACTGGGATCCCAGCCTGTCTCAAGACCGACAACCTTCCTCCGCT	780
Db	721	CCATCCTGATGCGCACACTGGGATCCCAGCCTGTCTCAAGACCGACAACCTTCCTCCGCT	780
Qy	781	GGCTGCATCATGACGCCTCCTTTGTGGCAGCCATCCCTTCGACCCAGGTCGTCTACTTCT	840
Db	781	GGCTGCATCATGACGCCTCCTTTGTGGCAGCCATCCCTTCGACCCAGGTCGTCTACTTCT	840
Qy	841	TCTTCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAGAGGCTCCACACATCGCGGGTGG	900
Db	841	TCTTCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAGAGGCTCCACACATCGCGGGTGG	900
Qy	901	CTAGAGTCTGCAAGAATGACGTGGGCGGCGAAAAGCTGCTGCAGAAGAAGTGGACCACCT	960
Db	901	CTAGAGTCTGCAAGAATGACGTGGGCGGCGAAAAGCTGCTGCAGAAGAAGTGGACCACCT	960

Qy	961	TCCTGAAGGCCAGCTGCTCTGCACCCAGCCGGGGCAGCTGCCCTTCAACGTCATCCGCC	1020
Db	961	TCCTGAAGGCCAGCTGCTCTGCACCCAGCCGGGGCAGCTGCCCTTCAACGTCATCCGCC	1020
Qy	1021	ACGCGGTCTGCTCCCCGCCGATTCTCCCACAGCTCCCCACATCTACGCAGTCTTCACCT	1080
Db	1021	ACGCGGTCTGCTCCCCGCCGATTCTCCCACAGCTCCCCACATCTACGCAGTCTTCACCT	1080
Qy	1081	CCCAGTGGCAGGTTGGCGGGACCAGGAGCTCTGCGGTTTGTGCCTTCTCTCTTGGACA	1140
Db	1081	CCCAGTGGCAGGTTGGCGGGACCAGGAGCTCTGCGGTTTGTGCCTTCTCTCTTGGACA	1140
Qy	1141	TTGAACGTGTCTTTAAGGGGAAATACAAAGAGTTGAACAAAGAACTTCACGCTGGACTA	1200
Db	1141	TTGAACGTGTCTTTAAGGGGAAATACAAAGAGTTGAACAAAGAACTTCACGCTGGACTA	1200
Qy	1201	CTTATAGGGGCCCTGAGACCAACCCCGGCCAGGCAGTTGCTCAGTGGGCCCCCTCCTCTG	1260
Db	1201	CTTATAGGGGCCCTGAGACCAACCCCGGCCAGGCAGTTGCTCAGTGGGCCCCCTCCTCTG	1260
Qy	1261	ATAAGGCCCTGACCTTCATGAAGGACCATTTCCTGATGGATGAGCAAGTGGTGGGGACGC	1320
Db	1261	ATAAGGCCCTGACCTTCATGAAGGACCATTTCCTGATGGATGAGCAAGTGGTGGGGACGC	1320
Qy	1321	CCCTGCTGGTGAAATCTGGCGTGGAGTATACACGGCTTGCACTGGAGACAGCCAGGGCC	1380
Db	1321	CCCTGCTGGTGAAATCTGGCGTGGAGTATACACGGCTTGCACTGGAGACAGCCAGGGCC	1380
Qy	1381	TTGATGGGCACAGCCATCTTGTGATGTACCTGGGAACCACCACAGGGTCGCTCCACAAGG	1440
Db	1381	TTGATGGGCACAGCCATCTTGTGATGTACCTGGGAACCACCACAGGGTCGCTCCACAAGG	1440
Qy	1441	CTGTGGTAAGTGGGGACAGCAGTGCTCATCTGGTGGAAGAGATTGAGCTGTTCCCTGACC	1500
Db	1441	CTGTGGTAAGTGGGGACAGCAGTGCTCATCTGGTGGAAGAGATTGAGCTGTTCCCTGACC	1500
Qy	1501	CTGAACCTGTTGCAACCTGCAGCTGGCCCCACCCAGGGTGCAGTGTTGTAGGCTTCT	1560
Db	1501	CTGAACCTGTTGCAACCTGCAGCTGGCCCCACCCAGGGTGCAGTGTTGTAGGCTTCT	1560
Qy	1561	CAGGAGGTGTCTGGAGGGTGCCCCGAGCCAAGTGTAGTGTCTATGAGAGCTGTGTGGACT	1620
Db	1561	CAGGAGGTGTCTGGAGGGTGCCCCGAGCCAAGTGTAGTGTCTATGAGAGCTGTGTGGACT	1620
Qy	1621	GTGTCTTGGCCGGGACCCCCACTGTGCCTGGGACCCTGAGTCCCGAACCTGTTGCCTCC	1680
Db	1621	GTGTCTTGGCCGGGACCCCCACTGTGCCTGGGACCCTGAGTCCCGAACCTGTTGCCTCC	1680
Qy	1681	TGTCTGCCCCAACCTGAACTCCTGGAAGCAGGACATGGAGCGGGGAACCCAGAGTGGG	1740
Db	1681	TGTCTGCCCCAACCTGAACTCCTGGAAGCAGGACATGGAGCGGGGAACCCAGAGTGGG	1740
Qy	1741	CATGTGCCAGTGGCCCCATGAGCAGGAGCCTTCGGCCTCAGAGCCGCCCGCAAATCATT	1800
Db	1741	CATGTGCCAGTGGCCCCATGAGCAGGAGCCTTCGGCCTCAGAGCCGCCCGCAAATCATT	1800

Qy	1801	AAGAAGTCCTGGCTGTCCCCAACTCCATCCTGGAGCTCCCCTGCCCCACCTGTCAGCCT	1860
Db	1801	AAGAAGTCCTGGCTGTCCCCAACTCCATCCTGGAGCTCCCCTGCCCCACCTGTCAGCCT	1860
Qy	1861	TGGCCTCTTATTATTGGAGTCATGGCCAGCAGCAGTCCCAGAAGCCTCTTCCACTGTCT	1920
Db	1861	TGGCCTCTTATTATTGGAGTCATGGCCAGCAGCAGTCCCAGAAGCCTCTTCCACTGTCT	1920
Qy	1921	ACAATGGCTCCCTCTTGCTGATAGTGCAGGATGGAGTTGGGGGTCTCTACCACTGCTGGG	1980
Db	1921	ACAATGGCTCCCTCTTGCTGATAGTGCAGGATGGAGTTGGGGGTCTCTACCACTGCTGGG	1980
Qy	1981	CAACTGAGAATGGCTTTTCATACCCTGTGATCTCCTACTGGGTGGACAGCCAGGACCAGA	2040
Db	1981	CAACTGAGAATGGCTTTTCATACCCTGTGATCTCCTACTGGGTGGACAGCCAGGACCAGA	2040
Qy	2041	CCCTGGCCCTGGATCCTGAACTGGCAGGCATCCCCGGGAGCATGTGAAGGTCCCGTTGA	2100
Db	2041	CCCTGGCCCTGGATCCTGAACTGGCAGGCATCCCCGGGAGCATGTGAAGGTCCCGTTGA	2100
Qy	2101	CCAGGGTCAGTGGTGGGGCCGCCCTGGCTGCCAGCAGTCTACTGGCCCCACTTTGTCA	2160
Db	2101	CCAGGGTCAGTGGTGGGGCCGCCCTGGCTGCCAGCAGTCTACTGGCCCCACTTTGTCA	2160
Qy	2161	CTGTCACTGTCCTCTTTGCCTTAGTGCTTTCAGGAGCCCTCATCATCCTCGTGGCCTCCC	2220
Db	2161	CTGTCACTGTCCTCTTTGCCTTAGTGCTTTCAGGAGCCCTCATCATCCTCGTGGCCTCCC	2220
Qy	2221	CATTGAGAGCACTCCGGGCTCGGGGCAAGGTTTCAGGGCTGTGAGACCCTGCGCCCTGGGG	2280
Db	2221	CATTGAGAGCACTCCGGGCTCGGGGCAAGGTTTCAGGGCTGTGAGACCCTGCGCCCTGGGG	2280
Qy	2281	AGAAGGCCCCGTTAAGCAGAGAGCAACACCTCCAGTCTCCAAGGAATGCAGGACCTCTG	2340
Db	2281	AGAAGGCCCCGTTAAGCAGAGAGCAACACCTCCAGTCTCCAAGGAATGCAGGACCTCTG	2340
Qy	2341	CCAGTGATGTGGACGCTGACAACAACCTGCCTAGGCACTGAGGTAGCTTAAACTCTAGGCA	2400
Db	2341	CCAGTGATGTGGACGCTGACAACAACCTGCCTAGGCACTGAGGTAGCTTAAACTCTAGGCA	2400
Qy	2401	CAGGCCGGGGCTGCGGTGCAGGCACCTGGCCATGCTGGCTGGGCGGCCCAAGCACAGCCC	2460
Db	2401	CAGGCCGGGGCTGCGGTGCAGGCACCTGGCCATGCTGGCTGGGCGGCCCAAGCACAGCCC	2460
Qy	2461	TGACTAGGATGACAGCAGCACAAAAGACCACCTTTCTCCCCTGAGAGGAGCTTCTGCTAC	2520
Db	2461	TGACTAGGATGACAGCAGCACAAAAGACCACCTTTCTCCCCTGAGAGGAGCTTCTGCTAC	2520
Qy	2521	TCTGCATCACTGATGACACTCAGCAGGGTGATGCACAGCAGTCTGCCTCCCCTATGGGAC	2580
Db	2521	TCTGCATCACTGATGACACTCAGCAGGGTGATGCACAGCAGTCTGCCTCCCCTATGGGAC	2580
Qy	2581	TCCCTTCTACCAAGCACATGAGCTCTCTAACAGGGTGGGGGCTACCCCAGACCTGCTCC	2640
Db	2581	TCCCTTCTACCAAGCACATGAGCTCTCTAACAGGGTGGGGGCTACCCCAGACCTGCTCC	2640
Qy	2641	TAACTGATATTGAAGAACCTGGAGAGGATCCTTCAGTTCTGGCCATTCCAGGGACCCTC	2700

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Qy	2701		CAGAAACACAGTGTTCAGAGACCCATAAAAAACCTGCCTGTCCCAGGACCCATATGGTAA	2760
Db	2701		CAGAAACACAGTGTTCAGAGACCCATAAAAAACCTGCCTGTCCCAGGACCCATATGGTAA	2760
Qy	2761		TGAACACCAAACATCTAAACAATCATATGCTAACATGCCACTCCTGGAAACTCCACTCTG	2820
Db	2761		TGAACACCAAACATCTAAACAATCATATGCTAACATGCCACTCCTGGAAACTCCACTCTG	2820
Qy	2821		AAGCTGCCGCTTTGGACACCAACACTCCCTTCTCCCAGGGTCATGCAGGGATCTGCTCCC	2880
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Qy	2881		TCCTGCTTCCCTTACCAGTCGTGCACCGCTGACTCCCAGGAAGTCTTTCCTGAAGTCTGA	2940
Db	2881		TCCTGCTTCCCTTACCAGTCGTGCACCGCTGACTCCCAGGAAGTCTTTCCTGAAGTCTGA	2940
Qy	2941		CCACCTTTCTTCTTGCTTCAGTTGGGGCAGACTCTGATCCCTTCTGCCCTGGCAGAATGG	3000
Db	2941		CCACCTTTCTTCTTGCTTCAGTTGGGGCAGACTCTGATCCCTTCTGCCCTGGCAGAATGG	3000
Qy	3001		CAGGGGTAATCTGAGCCTTCTTCACTCCTTTACCCTAGCTGACCCCTTACCTCTCCCCC	3060
Db	3001		CAGGGGTAATCTGAGCCTTCTTCACTCCTTTACCCTAGCTGACCCCTTACCTCTCCCCC	3060
Qy	3061		TCCCTTTTCCTTTGTTTTGGGATTAGAGAACTGCTTGTGTCAGAGACTGTTTATTTTTTAT	3120
Db	3061		TCCCTTTTCCTTTGTTTTGGGATTAGAGAACTGCTTGTGTCAGAGACTGTTTATTTTTTAT	3120
Qy	3121		TAAAAATATAAGGCTTAAAAAAA	3143
Db	3121		TAAAAATATAAGGCTTAAAAAAA	3143

RESULT 2

AY358531

LOCUS AY358531 3143 bp mRNA linear PRI 03-OCT-2003

DEFINITION Homo sapiens clone DNA71166 semaphorin B (UNQ783) mRNA, complete cds.

ACCESSION AY358531

VERSION AY358531.1 GI:37182184

KEYWORDS FLI_CDNA.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 3143)

AUTHORS Clark,H.F., Gurney,A.L., Abaya,E., Baker,K., Baldwin,D., Brush,J., Chen,J., Chow,B., Chui,C., Crowley,C., Currell,B., Deuel,B., Dowd,P., Eaton,D., Foster,J., Grimaldi,C., Gu,Q., Hass,P.E., Heldens,S., Huang,A., Kim,H.S., Klimowski,L., Jin,Y., Johnson,S., Lee,J., Lewis,L., Liao,D., Mark,M., Robbie,E., Sanchez,C., Schoenfeld,J., Seshagiri,S., Simmons,L., Singh,J., Smith,V., Stinson,J., Vagts,A., Vandlen,R., Watanabe,C., Wieand,D., Woods,K., Xie,M.H., Yansura,D., Yi,S., Yu,G., Yuan,J., Zhang,M., Zhang,Z.,

Qy	181	TGCCGACGACGACCGCGGGGGAGGCGGGCAGGGGCCCATGCCCAGGGTCAGATACTATG	240
Db	181	TGCCGACGACGACCGCGGGGGAGGCGGGCAGGGGCCCATGCCCAGGGTCAGATACTATG	240
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Qy	301	CTCTGCTCCTGAGTGGTGATGGAAATACTCTCTACGTGGGGGCTCGAGAAGCCATTCTGG	360
Db	301	CTCTGCTCCTGAGTGGTGATGGAAATACTCTCTACGTGGGGGCTCGAGAAGCCATTCTGG	360
Qy	361	CCTTGGATATCCAGGATCCAGGGGTCCCAGGCTAAAGAACATGATACCGTGGCCAGCCA	420
Db	361	CCTTGGATATCCAGGATCCAGGGGTCCCAGGCTAAAGAACATGATACCGTGGCCAGCCA	420
Qy	421	GTGACAGAAAAAGAGTGAATGTGCCTTTAAGAAGAAGAGCAATGAGACACAGTGTTC	480
Db	421	GTGACAGAAAAAGAGTGAATGTGCCTTTAAGAAGAAGAGCAATGAGACACAGTGTTC	480
Qy	481	ACTTCATCCGTGTCTGGTTTCTTACAATGTCACCCATCTCTACACCTGCGGCACCTTCG	540
Db	481	ACTTCATCCGTGTCTGGTTTCTTACAATGTCACCCATCTCTACACCTGCGGCACCTTCG	540
Qy	541	CCTTCAGCCCTGCTTGTACCTTCATTGAACTTCAAGATTCTACCTGTTGCCCATCTCGG	600
Db	541	CCTTCAGCCCTGCTTGTACCTTCATTGAACTTCAAGATTCTACCTGTTGCCCATCTCGG	600
Qy	601	AGGACAAGGTCATGGAGGAAAAGGCCAAAGCCCCTTTGACCCGCTCACAAGCATACGG	660
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Qy	661	CTGTCTTGGTGGATGGGATGCTCTATTCTGGTACTATGAACAACTTCCTGGGCAGTGAGC	720
Db	661	CTGTCTTGGTGGATGGGATGCTCTATTCTGGTACTATGAACAACTTCCTGGGCAGTGAGC	720
Qy	721	CCATCCTGATGCGCACACTGGGATCCCAGCCTGTCCTCAAGACCGACAACCTTCCTCCGCT	780
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Qy	781	GGCTGCATCATGACGCCTCCTTTGTGGCAGCCATCCCTTCGACCCAGGTCGTCTACTTCT	840
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Db	1321	CCCTGCTGGTGAAATCTGGCGTGGAGTATACACGGCTTGCACTGGAGACAGCCAGGGCC	1380
Qy	1381	TTGATGGGCACAGCCATCTTGTCTGTACCTGGGAACCACCACAGGGTCGCTCCACAAGG	1440
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Qy	1441	CTGTGGTAAGTGGGGACAGCAGTGTCTCATCTGGTGGAAGAGATTTCAGCTGTTCCCTGACC	1500
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Db	1561	CAGGAGGTGTCTGGAGGGTGCCCCGAGCCAACCTGTAGTGTCTATGAGAGCTGTGTGGACT	1620
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Qy	1681	TGTCTGCCCCAACCTGAACTCCTGGAAGCAGGACATGGAGCGGGGGAACCCAGAGTGGG	1740
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Qy	1741	CATGTGCCAGTGGCCCCATGAGCAGGAGCCTTCGGCCTCAGAGCCGCCCGCAAATCATTA	1800
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Qy	1801	AAGAAGTCCTGGCTGTCCCCAACTCCATCCTGGAGCTCCCCTGCCCCACCTGTCAGCCT	1860
Db	1801	AAGAAGTCCTGGCTGTCCCCAACTCCATCCTGGAGCTCCCCTGCCCCACCTGTCAGCCT	1860
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Qy	1981		CAACTGAGAATGGCTTTTCATACCCTGTGATCTCCTACTGGGTGGACAGCCAGGACCAGA	2040
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Qy	2641		TAACTGATATTGAAGAACCTGGAGAGGATCCTTCAGTTCTGGCCATTCCAGGGACCCTC	2700
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Db 2701 CAGAAACACAGTGTTCAGAGACCCTAAAAACCTGCCTGTCCCAGGACCCTATGGTAA 2760

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Qy 2821 AAGCTGCCGCTTTGGACACCAACACTCCCTTCTCCCAGGGTCATGCAGGGATCTGCTCCC 2880
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Qy 2941 CCACCTTTCTTCTTGCTTCAGTTGGGGCAGACTCTGATCCCTTCTGCCCTGGCAGAATGG 3000
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Qy 3121 TAAAAATATAAGGCTTAAAAAAA 3143
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RESULT 3

BC020974

LOCUS BC020974 3257 bp mRNA linear PRI 30-JUN-2004

DEFINITION Homo sapiens sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4A, mRNA (cDNA clone MGC:9542 IMAGE:3847802), complete cds.

ACCESSION BC020974

VERSION BC020974.1 GI:18088092

KEYWORDS MGC.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 3257)

AUTHORS Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
 Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
 Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
 Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
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 Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
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 Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
 Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
 McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
 Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
 Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,

Fahey,J., Helton,E., Kettelman,M., Madan,A., Rodrigues,S.,
 Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
 Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
 Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
 Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
 Schnierch,A., Schein,J.E., Jones,S.J. and Marra,M.A.

TITLE Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

PUBMED 12477932

REFERENCE 2 (bases 1 to 3257)

AUTHORS Strausberg,R.

TITLE Direct Submission

JOURNAL Submitted (03-JAN-2002) National Institutes of Health, Mammalian
 Gene Collection (MGC), Cancer Genomics Office, National Cancer
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
 USA

REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>

COMMENT Contact: MGC help desk
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Sequencing Group at the Stanford Human Genome
 Center, Stanford University School of Medicine, Stanford, CA 94305
 Web site: <http://www-shgc.stanford.edu>
 Contact: (Dickson, Mark) mcd@paxil.stanford.edu
 Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
 R. M.

Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Series: IRAK Plate: 20 Row: i Column: 24
 This clone was selected for full length sequencing because it
 passed the following selection criteria: matched mRNA gi: 21361913.

FEATURES

source Location/Qualifiers

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ORIGIN

Query Match 97.6%; Score 3068.4; DB 9; Length 3257;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3069; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db	1907	 TGTCCCCAACTCCATCCTGGAGCTCCCCTGCCCCACCTGTCAGCCTTGGCCTCTTATTA	1966
Qy	1874	TTGGAGTCATGGCCCAGCAGCAGTCCCAGAAGCCTCTTCCACTGTCTACAATGGCTCCCT	1933
Db	1967	 TTGGAGTCATGGCCCAGCAGCAGTCCCAGAAGCCTCTTCCACTGTCTACAATGGCTCCCT	2026
Qy	1934	CTTGCTGATAGTGCAGGATGGAGTTGGGGGTCTCTACCAGTGTGGGCAACTGAGAATGG	1993
Db	2027	 CTTGCTGATAGTGCAGGATGGAGTTGGGGGTCTCTACCAGTGTGGGCAACTGAGAATGG	2086
Qy	1994	CTTTTCATACCCTGTGATCTCCTACTGGGTGGACAGCCAGGACCAGACCCTGGCCCTGGA	2053
Db	2087	 CTTTTCATACCCTGTGATCTCCTACTGGGTGGACAGCCAGGACCAGACCCTGGCCCTGGA	2146
Qy	2054	TCCTGAACTGGCAGGCATCCCCGGGAGCATGTGAAGGTCCCGTTGACCAGGGTCAGTGG	2113
Db	2147	 TCCTGAACTGGCAGGCATCCCCGGGAGCATGTGAAGGTCCCGTTGACCAGGGTCAGTGG	2206
Qy	2114	TGGGGCCGCCCTGGCTGCCCAGCAGTCCCTACTGGCCCCACTTTGTCACTGTCACTGTCT	2173
Db	2207	 TGGGGCCGCCCTGGCTGCCCAGCAGTCCCTACTGGCCCCACTTTGTCACTGTCACTGTCT	2266
Qy	2174	CTTTGCCTTAGTGCTTTTCAGGAGCCCTCATCATCCTCGTGGCCTCCCCATTGAGAGCACT	2233
Db	2267	 CTTTGCCTTAGTGCTTTTCAGGAGCCCTCATCATCCTCGTGGCCTCCCCATTGAGAGCACT	2326
Qy	2234	CCGGGCTCGGGGCAAGGTTTCAGGGCTGTGAGACCCTGCGCCCTGGGGAGAAGGCCCGTT	2293
Db	2327	 CCGGGCTCGGGGCAAGGTTTCAGGGCTGTGAGACCCTGCGCCCTGGGGAGAAGGCCCGTT	2386
Qy	2294	AAGCAGAGAGCAACACCTCCAGTCTCCCAAGGAATGCAGGACCTCTGCCAGTGATGTGGA	2353

Db	2387	AAGCAGAGAGCAACACCTCCAGTCTCCCAAGGAATGCAGGACCTCTGCCAGTGATGTGGA	2446
Qy	2354	CGCTGACAACAACCTGCCTAGGCACTGAGGTAGCTTAAACTCTAGGCACAGGCCGGGGCTG	2413
Db	2447	CGCTGACAACAACCTGCCTAGGCACTGAGGTAGCTTAAACTCTAGGCACAGGCCGGGGCTG	2506
Qy	2414	CGGTGCAGGCACCTGGCCATGCTGGCTGGGCGGCCCAAGCACAGCCCTGACTAGGATGAC	2473
Db	2507	CGGTGCAGGCACCTGGCCATGCTGGCTGGGCGGCCCAAGCACAGCCCTGACTAGGATGAC	2566
Qy	2474	AGCAGCACAAAAGACCACCTTTCTCCCCTGAGAGGAGCTTCTGCTACTCTGCATCACTGA	2533
Db	2567	AGCAGCACAAAAGACCACCTTTCTCCCCTGAGAGGAGCTTCTGCTACTCTGCATCACTGA	2626
Qy	2534	TGACACTCAGCAGGGTGATGCACAGCAGTCTGCCTCCCCTATGGGACTCCCTTCTACCAA	2593
Db	2627	TGACACTCAGCAGGGTGATGCACAGCAGTCTGCCTCCCCTATGGGACTCCCTTCTACCAA	2686
Qy	2594	GCACATGAGCTCTCTAACAGGGTGGGGGCTACCCCCAGACCTGCTCCTACACTGATATTG	2653
Db	2687	GCACATGAGCTCTCTAACAGGGTGGGGGCTACCCCCAGACCTGCTCCTACACTGATATTG	2746
Qy	2654	AAGAACCTGGAGAGGATCCTTCAGTTCTGGCCATTCCAGGGACCCTCCAGAAACACAGTG	2713
Db	2747	AAGAACCTGGAGAGGATCCTTCAGTTCTGGCCATTCCAGGGACCCTCCAGAAACACAGTG	2806
Qy	2714	TTTCAAGAGACCCTAAAAAACCTGCCTGTCCCAGGACCCTATGGTAATGAACACCAAACA	2773
Db	2807	TTTCAAGAGACCCTAAAAAACCTGCCTGTCCCAGGACCCTATGGTAATGAACACCAAACA	2866
Qy	2774	TCTAAACAATCATATGCTAACATGCCACTCCTGGAACTCCACTCTGAAGCTGCCGCTTT	2833
Db	2867	TCTAAACAATCATATGCTAACATGCCACTCCTGGAACTCCACTCTGAAGCTGCCGCTTT	2926
Qy	2834	GGACACCAACACTCCCTTCTCCCAGGGTCATGCAGGGATCTGCTCCCTCCTGCTTCCCTT	2893
Db	2927	GGACACCAACACTCCCTTCTCCCAGGGTCATGCAGGGATCTGCTCCCTCCTGCTTCCCTT	2986
Qy	2894	ACCAGTCGTGCACCGCTGACTCCCAGGAAGTCTTTCCTGAAGTCTGACCACCTTCTTCT	2953
Db	2987	ACCAGTCGTGCACCGCTGACTCCCAGGAAGTCTTTCCTGAAGTCTGACCACCTTCTTCT	3046
Qy	2954	TGCTTCAGTTGGGGCAGACTCTGATCCCTTCTGCCCTGGCAGAATGGCAGGGGTAATCTG	3013
Db	3047	TGCTTCAGTTGGGGCAGACTCTGATCCCTTCTGCCCTGGCAGAATGGCAGGGGTAATCTG	3106
Qy	3014	AGCCTTCTTCACTCCTTTACCCTAGCTGACCCCTTCACCTCTCCCCCTCCCTTTTCCTTT	3073
Db	3107	AGCCTTCTTCACTCCTTTACCCTAGCTGACCCCTTCACCTCTCCCCCTCCCTTTTCCTTT	3166
Qy	3074	GTTTTGGGATTTCAGAAAACCTGCTTGTGAGAGACTGTTTATTTTTTATTAAAAATATAAGG	3133
Db	3167	GTTTTGGGATTTCAGAAAACCTGCTTGTGAGAGACTGTTTATTTTTTATTAAAAATATAAGG	3226
Qy	3134	CTTAAAAAAA	3143
Db	3227	CTTAAAAAAA	3236

RESULT 4

AB029394

LOCUS AB029394 3252 bp mRNA linear PRI 06-JAN-2001

DEFINITION Homo sapiens mRNA for SEMB, complete cds.

ACCESSION AB029394

VERSION AB029394.1 GI:12248381

KEYWORDS SEMB.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 3252)

AUTHORS Seki,N., Hattori,A., Hayashi,A., Kozuma,S., Muramatsu,M.,
Miyajima,N. and Saito,T.

TITLE Human semaphorin B

JOURNAL Published Only in DataBase (2001)

REFERENCE 2 (bases 1 to 3252)

AUTHORS Seki,N., Hattori,A., Hayashi,A., Kozuma,S., Muramatsu,M.,
Miyajima,N. and Saito,T.

TITLE Direct Submission

JOURNAL Submitted (28-JUN-1999) Toshiyuki Saito, National Institute of
Radiological Sciences, Genome Research Group; Inage-ku Anagawa
4-9-1, Chiba, Chiba 263-8555, Japan (E-mail:t_saito@nirs.go.jp,
Tel:81-43-201-3135, Fax:81-43-251-9818)

FEATURES Location/Qualifiers

source

1. .3252

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

gene

1. .3252

/gene="SEMB"

CDS

209. .2497

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/db_xref="GI:12248382"

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MKDHFLMDEQVVGTPLLVKSGVEYTRLAVETAQGLDGHSHLVMYLGTGSLHKAVVS
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ORIGIN

Query Match 96.8%; Score 3041.4; DB 9; Length 3252;

Best Local Similarity 99.4%; Pred. No. 0;

Qy	888	ACATCGCGGGTGGCTAGAGTCTGCAAGAATGACGTGGGCGGGCGAAAAGCTGCTGCAGAAG	947
Db	992	ACATCGCGGGTGGCTAGAGTCTGCAAGAATGACGTGGGCGGGCGAAAAGCTGCTGCAGAAG	1051
Qy	948	AAGTGGACCACCTTCCTGAAGGCCAGCTG--CTCTGCACCCAGCCGGGGCAGCTGCCCT	1005
Db	1052	AAGTGGACCACCTTCCTGAAGGCCAGCTGCTCTCTGCACCCAGCCGGGGCAGCTGCCCT	1111
Qy	1006	TCAACGTCATCCGCCACGCGGTCTGCTCCCCGCCGATTCTCCACAGCTCCCCACATCT	1065
Db	1112	TCAACGTCATCCGCCACGCGGTCTGCTCCCCGCCGATTCTCCACAGCTCCCCACATCT	1171
Qy	1066	ACGCAGTCTTCACCTCCAGT-GGCAGGTTGGCGGGACCAGGAGCTCTGCGGTTTGTGCC	1124
Db	1172	ACGCAGTCTTCACCTCCAGTGGGCAGGTTGGCGGGACCAGGAGCTCTGCGGTTTGTGCC	1231
Qy	1125	TTCTCTCTCTTGACATTGAACGTGTCTTTAAGGGGAAATACAAAGAGTTGAACAAAGAA	1184
Db	1232	TTCTCTCTCTTGACATTGAACGTGTCTTTAAGGGGAAATTCAAAGAGTTGAACAAAGAA	1291
Qy	1185	ACTTCACGCTGGACTACTTATAGGGGCCCTGAGACCAACCCCCGGCCAGGCAGTTGCTCA	1244
Db	1292	ACTTCACGCTGGACTACTTATAGGGGCCCTGAGACCAACCCCCGGCCAGGCAGTTGCTCA	1351
Qy	1245	GTGGGCCCCCTCCTCTGATAAGGCCCTGACCTTCATGAAGGACCATTTCTGATGGATGAG	1304
Db	1352	GTGGGCCCCCTCCTCTGATAAGGCCCTGACCTTCATGAAGGACCATTTCTGATGGATGAG	1411
Qy	1305	CAAGTGGTGGGGACGCCCCCTGCTGGTGAAATCTGGCGTGGAGTATACACGGCTTGCAGTG	1364
Db	1412	CAAGTGGTGGGGACGCCCCCTGCTGGTGAAATCTGGCGTGGAGTATACACGGCTTGCAGTG	1471
Qy	1365	GAGACAGCCCAGGGCCTTGATGGGCACAGCCATCTTGTCATGTACCTGGGAACCACCACA	1424
Db	1472	GAGACAGCCCAGGGCCTTGATGGGCACAGCCATCTTGTCATGTACCTGGGAACCACCACA	1531
Qy	1425	GGGTCGCTCCACAAGGCTGTGGTAAGTGGGGACAGCAGTGCTCATCTGGTGGAAGAGATT	1484
Db	1532	GGGTCGCTCCACAAGGCTGTGGTAAGTGGGGACAGCAGTGCTCATCTGGTGGAAGAGATT	1591
Qy	1485	CAGCTGTTCCCTGACCCTGAACCTGTTGCAACCTGCAGCTGGCCCCACCCAGGGTGCA	1544
Db	1592	CAGCTGTTCCCTGACCCTGAACCTGTTGCAACCTGCAGCTGGCCCCACCCAGGGTGCA	1651
Qy	1545	GTGTTTGTAGGCTTCTCAGGAGGTGTCTGGAGGGTGCCCCGAGCCAACTGTAGTGTCTAT	1604
Db	1652	GTGTTTGTAGGCTTCTCAGGAGGTGTCTGGAGGGTGCCCCGAGCCAACTGTAGTGTCTAT	1711
Qy	1605	GAGAGCTGTGTGGACTGTGTCCTTGCCCGGGACCCCCACTGTGCCTGGGACCCTGAGTCC	1664
Db	1712	GAGAGCTGTGTGGACTGTGTCCTTGCCCGGGACCCCCACTGTGCCTGGGACCCTGAGTCC	1771
Qy	1665	CGAACCTGTTGCCTCCTGTCTGCCCCAACCTGAACTCCTGGAAGCAGGACATGGAGCGG	1724
Db	1772	CGAACCTGTTGCCTCCTGTCTGCCCCAACCTGAACTCCTGGAAGCAGGACATGGAGCGG	1831

Qy	1725	GGGAACCCAGAGTGGGCATGTGCCAGTGGCCCCATGAGCAGGAGCCTTCGGCCTCAGAGC	1784
Db	1832	GGGAACCCAGAGTGGGCATGTGCCAGTGGCCCCATGAGCAGGAGCCTTCGGCCTCAGAGC	1891
Qy	1785	CGCCCCGAAATCATTAAAGAAGTCCTGGCTGTCCCCAACTCCATCCTGGAGCTCCCCTGC	1844
Db	1892	CGCCCCGAAATCATTAAAGAAGTCCTGGCTGTCCCCAACTCCATCCTGGAGCTCCCCTGC	1951
Qy	1845	CCCCACCTGTCAGCCTTGGCCTCTTATTATTGGAGTCATGGCCCAGCAGCAGTCCCAGAA	1904
Db	1952	CCCCACCTGTCAGCCTTGGCCTCTTATTATTGGAGTCATGGCCCAGCAGCAGTCCCAGAA	2011
Qy	1905	GCCTCTTCCACTGTCTACAATGGCTCCCTCTTGCTGATAGTGCAGGATGGAGTTGGGGGT	1964
Db	2012	GCCTCTTCCACTGTCTACAATGGCTCCCTCTTGCTGATAGTGCAGGATGGAGTTGGGGGT	2071
Qy	1965	CTCTACCACTGCTGGGCAACTGAGAATGGCTTTTCATACCCTGTGATCTCCTACTGGGTG	2024
Db	2072	CTCTACCACTGCTGGGCAACTGAGAATGGCTTTTCATACCCTGTGATCTCCTACTGGGTG	2131
Qy	2025	GACAGCCAGGACCAGACCCTGGCCCTGGATCCTGAACTGGCAGGCATCCCCGGGAGCAT	2084
Db	2132	GACAGCCAGGACCAGACCCTGGCCCTGGATCCTGAACTGGCAGGCATCCCCGGGAGCAT	2191
Qy	2085	GTGAAGGTCCCGTTGACCAGGGTCAGTGGTGGGGCCGCCCTGGCTGCCCAGCAGTCTTAC	2144
Db	2192	GTGAAGGTCCCGTTGACCAGGGTCAGTGGTGGGGCCGCCCTGGCTGCCCAGCAGTCTTAC	2251
Qy	2145	TGGCCCCACTTTGTCACTGTCACTGTCCTCTTTGCCTTAGTGCTTTTCAGGAGCCCTCATC	2204
Db	2252	TGGCCCCACTTTGTCACTGTCACTGTCCTCTTTGCCTTAGTGCTTTTCAGGAGCCCTCATC	2311
Qy	2205	ATCCTCGTGGCCTCCCCATTGAGAGCACTCCGGGCTCGGGGCAAGGTTTCAGGGCTGTGAG	2264
Db	2312	ATCCTCGTGGCCTCCCCATTGAGAGCACTCCGGGCTCGGGGCAAGGTTTCAGGGCTGTGAG	2371
Qy	2265	ACCCTGCGCCCTGGGGAGAAGGCCCCGTTAAGCAGAGAGCAACACCTCCAGTCTCCCAAG	2324
Db	2372	ACCCTGCGCCCTGGGGAGAAGGCCCCGTTAAGCAGAGAGCAACACCTCCAGTCTCCCAAG	2431
Qy	2325	GAATGCAGGACCTCTGCCAGTGATGTGGACGCTGACAACAACCTAGGCACTGAGGTA	2384
Db	2432	GAATGCAGGACCTCTGCCAGTGATGTGGACGCTGACAACAACCTAGGCACTGAGGTA	2491
Qy	2385	GCTTAAACTCTAGGCACAGGCCGGGGCTGCGGTGCAGGCACCTGGCCATGCTGGCTGGGC	2444
Db	2492	GCTTAAACTCTAGGCACAGGCCGGGGCTGCGGTGCAGGCACCTGGCCATGCTGGCTGGGC	2551
Qy	2445	GGCCCAAGCACAGCCCTGACTAGGATGACAGCAGCACAAAAGACCACCTTTCTCCCCTGA	2504
Db	2552	GGCCCAAGCACAGCCCTGACTAGGATGACAGCAGCACAAAAGACCACCTTTCTCCCCTGA	2611
Qy	2505	GAGGAGCTTCTGCTACTCTGCATCACTGATGACACTCAGCAGGGTGATGCACAGCAGTCT	2564
Db	2612	GAGGAGCTTCTGCTACTCTGCATCACTGATGACACTCAGCAGGGTGATGCACAGCAGTCT	2671
Qy	2565	GCCTCCCCTATGGGACTCCCTTCTACCAAGCACATGAGCTCTCTAACAGGGTGGGGGCTA	2624

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Db      2672 GCCTCCCCTATGGGACTCCCTTCTACCAAGCACATGAGCTCTCTAACAGGGTGGGGGCTA 2731
Qy      2625 CCCCCAGACCTGCTCCTACACTGATATTGAAGAACCTGGAGAGGATCCTTCAGTTCTGGC 2684
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Db      2732 CCCCCAGACCTGCTCCTACACTGATATTGAAGAACCTGGAGAGGATCCTTCAGTTCTGGC 2791
Qy      2685 CATTCCAGGGACCCTCCAGAAACACAGTGTTCAGAGACCCTAAAAACCTGCCTGTCC 2744
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Db      2792 CATTCCAGGGACCCTCCAGAAACACAGTGTTCAGAGACCCTAAAAACCTGCCTGTCC 2851
Qy      2745 CAGGACCCTATGGTAATGAACACCAAACATCTAAACAATCATATGCTAACATGCCACTCC 2804
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Db      2852 CAGGACCCTATGGTAATGAACACCAAACATCTAAACAATCATATGCTAACATGCCACTCC 2911
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Db      2912 TGGAAACTCCACTCTGAAGCTGCCGCTTTGGACACCAACACTCCCTTCTCCCAGGGTCAT 2971
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Db      2972 GCAGGGATCTGCTCCCTCCTGCTTCCCTTACCAGTCGTGCACCGCTGACTCCCAGGAAGT 3031
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Qy      2985 TGCCCTGGCAGAATGGCAGGGGTAATCTGAGCCTTCTTCACTCCTTTACCCTAGCTGACC 3044
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Qy      3045 CCTTCACCTCTCCCCCTCCCTTTTCTTTGTTTTGGGATTTCAGAAAACCTGCTTGTTCAGAG 3104
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Db      3152 CCTTCACCTCTCCCCCTCCCTTTTCTTTGTTTTGGGATTTCAGAAAACCTGCTTGTTCAGAG 3211
Qy      3105 ACTGTTTATTTTTTTATTAAAAATATAAGGCTTA 3137
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RESULT 5

AR564550

LOCUS AR564550 3104 bp DNA linear PAT 08-OCT-2004

DEFINITION Sequence 17 from patent US 6764677.

ACCESSION AR564550

VERSION AR564550.1 GI:53979961

KEYWORDS .

SOURCE Unknown.

ORGANISM Unknown.

Unclassified.

REFERENCE 1 (bases 1 to 3104)

AUTHORS Sharp, J.D. and Barnes, T.M.

TITLE Tango 294, a lipase-like protein

JOURNAL Patent: US 6764677-A 17 20-JUL-2004;

FEATURES Location/Qualifiers

source 1. .3104

/organism="unknown"

ORIGIN

Query Match 96.7%; Score 3040.8; DB 6; Length 3104;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 3053; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

Qy	89	CAGTCTGTGGCTGAGCATGGCCCTCCCAGCCCTGGGCCTGGACCCCTGGAGCCTCCTGGG	148
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Qy	149	CCTTTTCCTCTTCCAACCTGCTTCAGCTGCTGCTGCCGACGACGACCGCGGGGGGAGGCGG	208
Db	76	CCTTTTCCTCTTCCAACCTGCTTCAGCTGCTGCTGCCGACGACGACCGCGGGGGGAGGCGG	135
Qy	209	GCAGGGGCCCCATGCCCAGGGTCAGATACTATGCAGGGGATGAACGTAGGGCACTTAGCTT	268
Db	136	GCAGGGGCCCCATGCCCAGGGTCAGATACTATGCAGGGGATGAACGTAGGGCACTTAGCTT	195
Qy	269	CTTCCACCAGAAGGGCCTCCAGGATTTTGACACTCTGCTCCTGAGTGGTGATGGAAATAC	328
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Qy	329	TCTCTACGTGGGGGCTCGAGAAGCCATTCTGGCCTTGGATATCCAGGATCCAGGGGTCCC	388
Db	256	TCTCTACGTGGGGGCTCGAGAAGCCATTCTGGCCTTGGATATCCAGGATCCAGGGGTCCC	315
Qy	389	CAGGCTAAAGAACATGATACCGTGGCCAGCCAGTGACAGAAAAAAGAGTGAATGTGCCTT	448
Db	316	CAGGCTAAAGAACATGATACCGTGGCCAGCCAGTGACAGAAAAAAGAGTGAATGTGCCTT	375
Qy	449	TAAGAAGAAGAGCAATGAGACACAGTGTTTCAACTTCATCCGTGTCCTGGTTTCTTACAA	508
Db	376	TAAGAAGAAGAGCAATGAGACACAGTGTTTCAACTTCATCCGTGTCCTGGTTTCTTACAA	435
Qy	509	TGTCACCCATCTCTACACCTGCGGCACCTTCGCCTTCAGCCCTGCTTGTACCTTCATTGA	568
Db	436	TGTCACCCATCTCTACACCTGCGGCACCTTCGCCTTCAGCCCTGCTTGTACCTTCATTGA	495
Qy	569	ACTTCAAGATTCTACCTGTTGCCCATCTCGGAGGACAAGGTCATGGAGGGAAAAGGCCA	628
Db	496	ACTTCAAGATTCTACCTGTTGCCCATCTCGGAGGACAAGGTCATGGAGGGAAAAGGCCA	555
Qy	629	AAGCCCCCTTTGACCCCGCTCACAAGCATAACGGCTGTCTTGGTGGATGGGATGCTCTATTC	688
Db	556	AAGCCCCCTTTGACCCCGCTCACAAGCATAACGGCTGTCTTGGTGGATGGGATGCTCTATTC	615
Qy	689	TGGTACTATGAACAACCTTCTGGGCAGTGAGCCCATCCTGATGCGCACACTGGGATCCCA	748
Db	616	TGGTACTATGAACAACCTTCTGGGCAGTGAGCCCATCCTGATGCGCACACTGGGATCCCA	675
Qy	749	GCCTGTCTCTAAGACCGACAACCTTCTCCGCTGGCTGCATCATGACGCCTCCTTTGTGGC	808
Db	676	GCCTGTCTCTAAGACCGACAACCTTCTCCGCTGGCTGCATCATGACGCCTCCTTTGTGGC	735
Qy	809	AGCCATCCCTTCGACCCAGGTTCGTCTACTTCTTCTTCGAGGAGACAGCCAGCGAGTTTGA	868

Db	736	AGCCATCCCTTCGACCCAGGTCGTCTACTTCTTCTTCGAGGAGACAGCCAGCGAGTTTGA	795
Qy	869	CTTCTTTGAGAGGCTCCACACATCGCGGGTGGCTAGAGTCTGCAAGAATGACGTGGGCGG	928
Db	796	CTTCTTTGAGAGGCTCCACACATCGCGGGTGGCTAGAGTCTGCAAGAATGACGTGGGCGG	855
Qy	929	CGAAAAGCTGCTGCAGAAGAAGTGGACCACCTTCCTGAAGGCCAGCTGCTCTGCACCCA	988
Db	856	CGAAAAGCTGCTGCAGAAGAAGTGGACCACCTTCCTGAAGGCCAGCTGCTCTGCACCCA	915
Qy	989	GCCGGGGCAGCTGCCCTTCAACGTCATCCGCCACGCGGTCTGCTCCCCGCCGATTCTCC	1048
Db	916	GCCGGGGCAGCTGCCCTTCAACGTCATCCGCCACGCGGTCTGCTCCCCGCCGATTCTCC	975
Qy	1049	CACAGCTCCCCACATCTACGCAGTCTTCACCTCCCAGTGGCAGGTTGGCGGGACCAGGAG	1108
Db	976	CACAGCTCCCCACATCTACGCAGTCTTCACCTCCCAGTGGCAGGTTGGCGGGACCAGGAG	1035
Qy	1109	CTCTGCGGTTTGTGCCTTCTCTCTCTTGGACATTGAACGTGTCTTTAAGGGGAAATACAA	1168
Db	1036	CTCTGCGGTTTGTGCCTTCTCTCTCTTGGACATTGAACGTGTCTTTAAGGGGAAATACAA	1095
Qy	1169	AGAGTTGAACAAAGAACTTCACGCTGGACTACTTATAGGGGCCCTGAGACCAACCCCCG	1228
Db	1096	AGAGTTGAACAAAGAACTTCACGCTGGACTACTTATAGGGGCCCTGAGACCAACCCCCG	1155
Qy	1229	GCCAGGCAGTTGCTCAGTGGGCCCCCTCCTCTGATAAGGCCCTGACCTTCATGAAGGACCA	1288
Db	1156	GCCAGGCAGTTGCTCAGTGGGCCCCCTCCTCTGATAAGGCCCTGACCTTCATGAAGGACCA	1215
Qy	1289	TTTCCTGATGGATGAGCAAGTGGTGGGGACGCCCCCTGCTGGTGAAATCTGGCGTGGAGTA	1348
Db	1216	TTTCCTGATGGATGAGCAAGTGGTGGGGACGCCCCCTGCTGGTGAAATCTGGCGTGGAGTA	1275
Qy	1349	TACACGGCTTGCAAGTGGAGACAGCCAGGGCCTTGATGGGCACAGCCATCTTGTTCATGTA	1408
Db	1276	TACACGGCTTGCAAGTGGAGACAGCCAGGGCCTTGATGGGCACAGCCATCTTGTTCATGTA	1335
Qy	1409	CCTGGGAACCACCACAGGGTCGCTCCACAAGGCTGTGGTAAGTGGGGACAGCAGTGCTCA	1468
Db	1336	CCTGGGAACCACCACAGGGTCGCTCCACAAGGCTGTGGTAAGTGGGGACAGCAGTGCTCA	1395
Qy	1469	TCTGGTGGAAGAGATTAGCTGTTCCCTGACCCTGAACCTGTTGCAACCTGCAGCTGGC	1528
Db	1396	TCTGGTGGAAGAGATTAGCTGTTCCCTGACCCTGAACCTGTTGCAACCTGCAGCTGGC	1455
Qy	1529	CCCCACCCAGGGTGCAGTGTGGTAGGCTTCTCAGGAGGTGTCTGGAGGGTGCCCCGAGC	1588
Db	1456	CCCCACCCAGGGTGCAGTGTGGTAGGCTTCTCAGGAGGTGTCTGGAGGGTGCCCCGAGC	1515
Qy	1589	CAACTGTAGTGTCTATGAGAGCTGTGTGGACTGTGTCCTTGCCCGGGACCCCCACTGTGC	1648
Db	1516	CAACTGTAGTGTCTATGAGAGCTGTGTGGACTGTGTCCTTGCCCGGGACCCCCACTGTGC	1575
Qy	1649	CTGGGACCCTGAGTCCCGAACCTGTTGCCTCCTGTCTGCCCCAACCTGAACTCCTGGAA	1708
Db	1576	CTGGGACCCTGAGTCCCGAACCTGTTGCCTCCTGTCTGCCCCAACCTGAACTCCTGGAA	1635

Qy	1709	GCAGGACATGGAGCGGGGAACCCAGAGTGGGCATGTGCCAGTGGCCCCATGAGCAGGAG	1768
Db	1636	GCAGGACATGGAGCGGGGAACCCAGAGTGGGCATGTGCCAGTGGCCCCATGAGCAGGAG	1695
Qy	1769	CCTTCGGCCTCAGAGCCGCCCGCAAATCATTAAAGAAGTCCTGGCTGTCCCCAACTCCAT	1828
Db	1696	CCTTCGGCCTCAGAGCCGCCCGCAAATCATTAAAGAAGTCCTGGCTGTCCCCAACTCCAT	1755
Qy	1829	CCTGGAGCTCCCCTGCCCCACCTGTCAGCCTTGGCCTCTTATTATTGGAGTCATGGCCC	1888
Db	1756	CCTGGAGCTCCCCTGCCCCACCTGTCAGCCTTGGCCTCTTATTATTGGAGTCATGGCCC	1815
Qy	1889	AGCAGCAGTCCCAGAAGCCTCTTCCACTGTCTACAATGGCTCCCTCTTGCTGATAGTGCA	1948
Db	1816	AGCAGCAGTCCCAGAAGCCTCTTCCACTGTCTACAATGGCTCCCTCTTGCTGATAGTGCA	1875
Qy	1949	GGATGGAGTTGGGGTCTCTACCACTGCTGGGCAACTGAGAATGGCTTTTCATACCCTGT	2008
Db	1876	GGATGGAGTTGGGGTCTCTACCACTGCTGGGCAACTGAGAATGGCTTTTCATACCCTGT	1935
Qy	2009	GATCTCCTACTGGGTGGACAGCCAGGACCAGACCCTGGCCCTGGATCCTGAACTGGCAGG	2068
Db	1936	GATCTCCTACTGGGTGGACAGCCAGGACCAGACCCTGGCCCTGGATCCTGAACTGGCAGG	1995
Qy	2069	CATCCCCGGGAGCATGTGAAGGTCCCGTTGACCAGGGTCAGTGGTGGGGCCGCCCTGGC	2128
Db	1996	CATCCCCGGGAGCATGTGAAGGTCCCGTTGACCAGGGTCAGTGGTGGGGCCGCCCTGGC	2055
Qy	2129	TGCCCAGCAGTCCTACTGGCCCCACTTTGTCACTGTCACTGTCCTCTTTGCCTTAGTGCT	2188
Db	2056	TGCCCAGCAGTCCTACTGGCCCCACTTTGTCACTGTCACTGTCCTCTTTGCCTTAGTGCT	2115
Qy	2189	TTCAGGAGCCCTCATCATCCTCGTGGCCTCCCCATTGAGAGCACTCCGGGCTCGGGGCAA	2248
Db	2116	TTCAGGAGCCCTCATCATCCTCGTGGCCTCCCCATTGAGAGCACTCCGGGCTCGGGGCAA	2175
Qy	2249	GGTTCAGGGCTGTGAGACCCTGCGCCCTGGGGAGAAGGCCCCGTTAAGCAGAGAGCAACA	2308
Db	2176	GGTTCAGGGCTGTGAGACCCTGCGCCCTGGGGAGAAGGCCCCGTTAAGCAGAGAGCAACA	2235
Qy	2309	CCTCCAGTCTCCCAAGGAATGCAGGACCTCTGCCAGTGATGTGGACGCTGACAACAACTG	2368
Db	2236	CCTCCAGTCTCCCAAGGAATGCAGGACCTCTGCCAGTGATGTGGACGCTGACAACAACTG	2295
Qy	2369	CCTAGGCACTGAGGTAGCTTAAACTCTAGGCACAGGCCGGGGCTGCGGTGCAGGCACCTG	2428
Db	2296	CCTAGGCACTGAGGTAGCTTAAACTCTAGGCACAGGCCGGGGCTGCGGTGCAGGCACCTG	2355
Qy	2429	GCCATGCTGGCTGGGCGGCCCAAGCACAGCCCTGACTAGGATGACAGCAGCACAAAAGAC	2488
Db	2356	GCCATGCTGGCTGGGCGGCCCAAGCACAGCCCTGACTAGGATGACAGCAGCACAAAAGAC	2415
Qy	2489	CACCTTTCTCCCCTGAGAGGAGCTTCTGCTACTCTGCATCACTGATGACACTCAGCAGGG	2548
Db	2416	CACCTTTCTCCCCTGAGAGGAGCTTCTGCTACTCTGCATCACTGATGACACTCAGCAGGG	2475

Qy	2549	TGATGCACAGCAGTCTGCCTCCCCTATGGGACTCCCTTCTACCAAGCACATGAGCTCTCT	2608
Db	2476	TGATGCACAGCAGTCTGCCTCCCCTATGGGACTCCCTTCTACCAAGCACATGAGCTCTCT	2535
Qy	2609	AACAGGGTGGGGGCTACCCCCAGACCTGCTCCTACACTGATATTGAAGAACCTGGAGAGG	2668
Db	2536	AACAGGGTGGGGGCTACCCCCAGACCTGCTCCTACACTGATATTGAAGAACCTGGAGAGG	2595
Qy	2669	ATCCTTCAGTTCTGGCCATTCCAGGGACCCTCCAGAAACACAGTGTTCAGAGACCCT-	2727
Db	2596	ATCCTTCAGTTCTGGCCATTCCAGGGACCCTCCAGAAACACAGTGTTCAGAGATCCTA	2655
Qy	2728	AAAAAACCTGCCTGTCCCAGGACCCTATGGTAATGAACACCAAACATCTAAACAATCATA	2787
Db	2656	AAAAAACCTGCCTGTCCCAGGACCCTATGGTAATGAACACCAAACATCTAAACAATCATA	2715
Qy	2788	TGCTAACATGCCACTCCTGGAACTCCACTCTGAAGCTGCCGCTTTGGACACCAACACTC	2847
Db	2716	TGCTAACATGCCACTCCTGGAACTCCACTCTGAAGCTGCCGCTTTGGACACCAACACTC	2775
Qy	2848	CCTTCTCCCAGGGTCATGCAGGGATCTGCTCCCTCCTGCTTCCCTTACCAGTCGTGCACC	2907
Db	2776	CCTTCTCCCAGGGTCATGCAGGGATCTGCTCCCTCCTGCTTCCCTTACCAGTCGTGCACC	2835
Qy	2908	GCTGACTCCCAGGAAGTCTTTCCTGAAGTCTGACCACCTTTCCTTCTTGCTTCAGTTGGGG	2967
Db	2836	GCTGACTCCCAGGAAGTCTTTCCTGAAGTCTGACCACCTTTCCTTCTTGCTTCAGTTGGGG	2895
Qy	2968	CAGACTCTGATCCCTTCTGCCCTGGCAGAATGGCAGGGGTAATCTGAGCCTTCTTCACTC	3027
Db	2896	CAGACTCTGATCCCTTCTGCCCTGGCAGAATGGCAGGGGTAATCTGAGCCTTCTTCACTC	2955
Qy	3028	CTTTACCCTAGCTGACCCCTTCACCTCTCCCCCTCCCTTTTCCTTTGTTTTGGGATTTCAG	3087
Db	2956	CTTTACCCTAGCTGACCCCTTCACCTCTCCCCCTCCCTTTTCCTTTGTTTTGGGATTTCAG	3015
Qy	3088	AAAACCTGCTTGTCAGAGACTGTTTATTTTTTTATTAAAAATATAAGGCTTAAAAAAA	3143
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RESULT 6

BD249136

LOCUS	BD249136	3191 bp	DNA	linear	PAT 17-JUL-2003
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DEFINITION 27 human secreted proteins.

ACCESSION BD249136

VERSION BD249136.1 GI:33058906

KEYWORDS JP 2002538841-A/10.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 3191)

AUTHORS Ruben,S.M., Ni,J., Ebner,R., Rosen,C.A., Shi,Y., Birse,C., Florence,K., Komatsoulis,G., Lafleur,D.W., Moore,P.A., Olsen,H.S. and Young,P.E.

TITLE 27 human secreted proteins

JOURNAL Patent: JP 2002538841-A 10 19-NOV-2002;
HUMAN GENOME SCIENCES INC

COMMENT OS Homo sapiens (human)
PN JP 2002538841-A/10
PD 19-NOV-2002
PF 16-MAR-2000 JP 2000605787
PR 18-MAR-1999 US 60/125055
PI STEVEN M RUBEN, JIAN NI, REINHARD EBNER, CRAIG
A ROSEN, YANGGU SHI,
PI CHARLES BIRSE, KIMBERLY FLORENCE, GEORGE KOMATSOULIS, DAVID W PI
LAFLEUR,
PI PAUL A MOORE, HENRIK S OLSEN, PAUL E YOUNG
PC C12N15/09, A61K31/711, A61K38/00, A61K48/00, A61P9/00, A61P17/00,
PC A61P19/02,
PC A61P25/02, A61P25/16, A61P25/18, A61P25/22, A61P25/24, A61P25/28,
PC A61P27/02,
PC A61P29/00, A61P29/00, A61P31/04, A61P31/12, A61P35/00, A61P37/00,
PC A61P43/00,
PC C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/10 PC
, C12P21/02, C12Q1/02,
PC C12Q1/68, G01N33/15, G01N33/50, G01N33/53, G01N33/566, C12N15/00,
PC C12N5/00,
PC A61K37/02
CC n equals a, t, g, or c
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FH Key Location/Qualifiers
FT source 1. .3191
FT /organism='Homo sapiens (human)'.
FEATURES Location/Qualifiers
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ORIGIN

Query Match 96.6%; Score 3035.8; DB 6; Length 3191;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 3031; Conservative 9; Mismatches 1; Indels 0; Gaps 0;

Qy 103 GCATGGCCCTCCCAGCCCTGGGCCTGGACCCCTGGAGCCTCCTGGGCCTTTTCTCTTCC 162
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Qy 163 AACTGCTTCAGCTGCTGCTGCCGACGACGACCGCGGGGGAGGCGGGCAGGGGCCCCATGC 222
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Db 138 AACTGCTTCAGCTGCTGCTGCCGACGACGACCGCGGGGGAGGCGGGCAGGGGCCCCATGC 197

Qy 223 CCAGGGTCAGATACTATGCAGGGGATGAACGTAGGGCACTTAGCTTCTTCCACCAGAAGG 282
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Qy 283 GCCTCCAGGATTTTGACACTCTGCTCCTGAGTGGTGATGGAAATACTCTCTACGTGGGGG 342
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Db	258	GCCTCCAGGATTTTGACACTCTGCTCCTGAGTGGTGATGGAAATACTCTCTACGTGGGGG	317
Qy	343	CTCGAGAAGCCATTCTGGCCTTGGATATCCAGGATCCAGGGGTCCCCAGGCTAAAGAACA	402
Db	318	CTCGAGAAGCCATTCTGGCCTTGGATATCCAGGATCCAGGGGTCCCCAGGCTAAAGAACA	377
Qy	403	TGATACCGTGGCCAGCCAGTGACAGAAAAAAGAGTGAATGTGCCTTTAAGAAGAAGAGCA	462
Db	378	TGATACCGTGGCCAGCCAGTGACAGAAAAAAGAGTGAATGTGCCTTTAAGAAGAAGAGCA	437
Qy	463	ATGAGACACAGTGTTCACCTTCATCCGTGTCTGGTTTCTTACAATGTCACCCATCTCT	522
Db	438	ATGAGACACAGTGTTCACCTTCATCCGTGTCTGGTTTCTTACAATGTCACCCATCTCT	497
Qy	523	ACACCTGCGGCACCTTCGCCTTCAGCCCTGCTTGTACCTTCATTGAACTTCAAGATTCCCT	582
Db	498	ACACCTGCGGCACCTTCGCCTTCAGCCCTGCTTGTACCTTCATTGAACTTCAAGATTCCCT	557
Qy	583	ACCTGTTGCCCATCTCGGAGGACAAGGTCATGGAGGGAAAAGGCCAAAGCCCCCTTTGACC	642
Db	558	ACCTGTTGCCCATCTCGGAGGACAAGGTCATGGAGGGAAAAGGCCAAAGCCCCCTTTGACC	617
Qy	643	CCGCTCACAAGCATACGGCTGTCTTGGTGGATGGGATGCTCTATTCTGGTACTATGAACA	702
Db	618	CCGCTCACAAGCATACGGCTGTCTTGGTGGATGGGATGCTCTATTCTGGTACTATGAACA	677
Qy	703	ACTTCCTGGGCAGTGAGCCCATCCTGATGCGCACACTGGGATCCCAGCCTGTCCTCAAGA	762
Db	678	ACTTCCTGGGCAGTGAGCCCATCCTGATGCGCACACTGGGATCCCAGCCTGTCCTCAAGA	737
Qy	763	CCGACAACTTCCTCCGCTGGCTGCATCATGACGCCTCCTTTGTGGCAGCCATCCCTTCGA	822
Db	738	CCGACAACTTCCTCCGCTGGCTGCATCATGACGCCTCCTTTGTGGCAGCCATCCCTTCGA	797
Qy	823	CCCAGGTCGTCTACTTCTTCTTCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAGAGGC	882
Db	798	CCCAGGTCGTCTACTTCTTCTTCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAGAGGC	857
Qy	883	TCCACACATCGCGGGTGGCTAGAGTCTGCAAGAATGACGTGGGCGGGCGAAAAGCTGCTGC	942
Db	858	TCCACACATCGCGGGTGGCTAGAGTCTGCAAGAATGACGTGGGCGGGCGAAAAGCTGCTGC	917
Qy	943	AGAAGAAGTGGACCACCTTCCTGAAGGCCAGCTGCTCTGCACCCAGCCGGGGCAGCTGC	1002
Db	918	AGAAGAAGTGGACCACCTTCCTGAAGGCCAGCTGCTCTGCACCCAGCCGGGGCAGCTGC	977
Qy	1003	CCTTCAACGTCATCCGCCACGCGGTCTGCTCCCCGCCGATTCTCCCACAGCTCCCCACA	1062
Db	978	CCTTCAACGTCATCCGCCACGCGGTCTGCTCCCCGCCGATTCTCCCACAGCTCCCCACA	1037
Qy	1063	TCTACGCAGTCTTCACCTCCCAGTGGCAGGTTGGCGGGACCAGGAGCTCTGCGGTTTGTG	1122
Db	1038	TCTACGCAGTCTTCACCTCCCAGTGGCAGGTTGGCGGGACCAGGAGCTCTGCGGTTTGTG	1097
Qy	1123	CCTTCTCTCTCTTGGACATTGAACGTGTCTTTAAGGGGAAATACAAAGAGTTGAACAAAG	1182
Db	1098	CCTTCTCTCTCTTGGACATTGAACGTGTCTTTAAGGGGAAATACAAAGAGTTGAACAAAG	1157

Qy	1183	AAACTTCACGCTGGACTACTTATAGGGGCCCTGAGACCAACCCCCGGCCAGGCAGTTGCT	1242
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Db	1158	AAACTTCACGCTGGACTACTTATAGGGGCCCTGAGACCAACCCCCGGSCAGGCAGTTGCT	1217
Qy	1243	CAGTGGGCCCCCTCCTCTGATAAGGCCCTGACCTTCATGAAGGACCATTTCTGATGGATG	1302
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Db	1218	YARTGGGCCCCCTYCTCTGATAAGGCCCTGACCTTCATGAAGGACCATTTCTGATGGATG	1277
Qy	1303	AGCAAGTGGTGGGGACGCCCCTGCTGGTGAAATCTGGCGTGGAGTATACACGGCTTGCAG	1362
Db	1278	AGCAAGTGGTGGGGACGCCCCTGCTGGTGAAATCTGGCGTGGAGTATACACGGCTTGCAG	1337
Qy	1363	TGGAGACAGCCAGGGCCTTGATGGGCACAGCCATCTTGTCATGTACCTGGGAACCACCA	1422
Db	1338	TGGAGACAGCCAGGGCCTTGATGGGCACAGCCATCTTGTCATGTACCTGGGAACCACCA	1397
Qy	1423	CAGGGTCGCTCCACAAGGCTGTGGTAAGTGGGGACAGCAGTGCTCATCTGGTGGAAGAGA	1482
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Qy	1483	TTCAGCTGTTCCCTGACCCTGAACCTGTTTCGCAACCTGCAGCTGGCCCCACCCAGGGTG	1542
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Db	1458	TTCAGCTGYTCCCTGACCCTGAACCTGTTTCGCAACCTGCAGCTGGCCCCACCCAGGGTG	1517
Qy	1543	CAGTGTTTGTAGGCTTCTCAGGAGGTGTCTGGAGGGTGCCCCGAGCCAACTGTAGTGTCT	1602
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Db	1518	CAGTGTTTGKAGGCTTCTYAGGAGGTGTCTGRAGGGTGCCCCGAGCCAACTGTAGTGTCT	1577
Qy	1603	ATGAGAGCTGTGTGGACTGTGTCCTTGCCCGGGACCCCCACTGTGCCTGGGACCCTGAGT	1662
Db	1578	ATGAGAGCTGTGTGGACTGTGTCCTTGCCCGGGACCCCCACTGTGCCTGGGACCCTGAGT	1637
Qy	1663	CCCGAACCTGTTGCCTCCTGTCTGCCCCAACCTGAACTCCTGGAAGCAGGACATGGAGC	1722
Db	1638	CCCGAACCTGTTGCCTCCTGTCTGCCCCAACCTGAACTCCTGGAAGCAGGACATGGAGC	1697
Qy	1723	GGGGGAACCCAGAGTGGGCATGTGCCAGTGGCCCCATGAGCAGGAGCCTTCGGCCTCAGA	1782
Db	1698	GGGGGAACCCAGAGTGGGCATGTGCCAGTGGCCCCATGAGCAGGAGCCTTCGGCCTCAGA	1757
Qy	1783	GCCGCCCCGAAATCATTAAGAAGTCCTGGCTGTCCCCAACTCCATCCTGGAGCTCCCCT	1842
Db	1758	GCCGCCCCGAAATCATTAAGAAGTCCTGGCTGTCCCCAACTCCATCCTGGAGCTCCCCT	1817
Qy	1843	GCCCCACCTGTCAGCCTTGGCCTCTTATTATTGGAGTCATGGCCCAGCAGCAGTCCCAG	1902
Db	1818	GCCCCACCTGTCAGCCTTGGCCTCTTATTATTGGAGTCATGGCCCAGCAGCAGTCCCAG	1877
Qy	1903	AAGCCTCTTCCACTGTCTACAATGGCTCCCTCTTGCTGATAGTGCAGGATGGAGTTGGGG	1962
Db	1878	AAGCCTCTTCCACTGTCTACAATGGCTCCCTCTTGCTGATAGTGCAGGATGGAGTTGGGG	1937
Qy	1963	GTCTCTACCAGTGCTGGGCAACTGAGAATGGCTTTTCATACCCTGTGATCTCCTACTGGG	2022
Db	1938	GTCTCTACCAGTGCTGGGCAACTGAGAATGGCTTTTCATACCCTGTGATCTCCTACTGGG	1997

Qy	2023	TGGACAGCCAGGACCAGACCCTGGCCCTGGATCCTGAACTGGCAGGCATCCCCGGGAGC	2082
Db	1998	TGGACAGCCAGGACCAGACCCTGGCCCTGGATCCTGAACTGGCAGGCATCCCCGGGAGC	2057
Qy	2083	ATGTGAAGGTCCCGTTGACCAGGGTCAGTGGTGGGGCCGCCCTGGCTGCCAGCAGTCCT	2142
Db	2058	ATGTGAAGGTCCCGTTGACCAGGGTCAGTGGTGGGGCCGCCCTGGCTGCCAGCAGTCCT	2117
Qy	2143	ACTGGCCCCACTTTGTCACTGTCACCTCTTGCCTTAGTGCTTTCAGGAGCCCTCA	2202
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Qy	2203	TCATCCTCGTGGCCTCCCCATTGAGAGCACTCCGGGCTCGGGGCAAGGTTTCAGGGCTGTG	2262
Db	2178	TCATCCTCGTGGCCTCCCCATTGAGAGCACTCCGGGCTCGGGGCAAGGTTTCAGGGCTGTG	2237
Qy	2263	AGACCCTGCGCCCTGGGGAGAAGGCCCCGTTAAGCAGAGAGCAACACCTCCAGTCTCCCA	2322
Db	2238	AGACCCTGCGCCCTGGGGAGAAGGCCCCGTTAAGCAGAGAGCAACACCTCCAGTCTCCCA	2297
Qy	2323	AGGAATGCAGGACCTCTGCCAGTGATGTGGACGCTGACAACAACCTGCCTAGGCACTGAGG	2382
Db	2298	AGGAATGCAGGACCTCTGCCAGTGATGTGGACGCTGACAACAACCTGCCTAGGCACTGAGG	2357
Qy	2383	TAGCTTAACTCTAGGCACAGGCCGGGGCTGCGGTGCAGGCACCTGGCCATGCTGGCTGG	2442
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Qy	2443	GCGGCCCAAGCACAGCCCTGACTAGGATGACAGCAGCACAAAAGACCACCTTTCTCCCT	2502
Db	2418	GCGGCCCAAGCACAGCCCTGACTAGGATGACAGCAGCACAAAAGACCACCTTTCTCCCT	2477
Qy	2503	GAGAGGAGCTTCTGCTACTCTGCATCACTGATGACACTCAGCAGGGTGATGCACAGCAGT	2562
Db	2478	GAGAGGAGCTTCTGCTACTCTGCATCACTGATGACACTCAGCAGGGTGATGCACAGCAGT	2537
Qy	2563	CTGCCTCCCCTATGGGACTCCCTTCTACCAAGCACATGAGCTCTCTAACAGGGTGGGGGC	2622
Db	2538	CTGCCTCCCCTATGGGACTCCCTTCTACCAAGCACATGAGCTCTCTAACAGGGTGGGGGC	2597
Qy	2623	TACCCCCAGACCTGCTCCTACACTGATATTGAAGAACCTGGAGAGGATCCTTCAGTTCTG	2682
Db	2598	TACCCCCAGACCTGCTCCTACACTGATATTGAAGAACCTGGAGAGGATCCTTCAGTTCTG	2657
Qy	2683	GCCATTCCAGGGACCCTCCAGAAACACAGTGTTTCAAGAGACCCTAAAAACCTGCCTGT	2742
Db	2658	GCCATTCCAGGGACCCTCCAGAAACACAGTGTTTCAAGAGACCCTAAAAACCTGCCTGT	2717
Qy	2743	CCCAGGACCCTATGGTAATGAACACCAAACATCTAAACAATCATATGCTAACATGCCACT	2802
Db	2718	CCCAGGACCCTATGGTAATGAACACCAAACATCTAAACAATCATATGCTAACATGCCACT	2777
Qy	2803	CCTGGAAACTCCACTCTGAAGCTGCCGCTTTGGACACCAACACTCCCTTCTCCCAGGGTC	2862
Db	2778	CCTGGAAACTCCACTCTGAAGCTGCCGCTTTGGACACCAACACTCCCTTCTCCCAGGGTC	2837
Qy	2863	ATGCAGGGATCTGCTCCCTCCTGCTTCCCTTACCAGTCGTGCACCGCTGACTCCCAGGAA	2922

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Db      2838 ATGCAGGGATCTGCTCCCTCCTGCTTCCCTTACCAGTCGTGCACCGCTGACTCCCAGGAA 2897
Qy      2923 GTCTTTCCTGAAGTCTGACCACCTTTCTTCTTGCTTCAGTTGGGGCAGACTCTGATCCCT 2982
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Db      2898 GTCTTYCCTGAAGTCTGACCACCTTTCTTCTTGCTTCAGTTGGGGCAGACTCTGATCCCT 2957
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RESULT 7

AX746794

LOCUS AX746794 2981 bp mRNA linear PAT 20-JUN-2003

DEFINITION Sequence 319 from Patent EP1308459.

ACCESSION AX746794

VERSION AX746794.1 GI:32131182

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Isogai,T., Sugiyama,T., Otsuki,T., Wakamatsu,A., Sato,H., Ishii,S.,
Yamamoto,J.I., Isono,Y., Hio,Y., Otsuka,K., Nagai,K., Irie,R.,
Tamechika,I., Seki,N., Yoshikawa,T., Otsuka,M., Nagahari,K. and
Masuho,Y.

TITLE Full-length cDNA sequences

JOURNAL Patent: EP 1308459-A 319 07-MAY-2003;
Helix Research Institute (JP) ; Research Association for
Biotechnology (JP)

FEATURES Location/Qualifiers

source 1. .2981
/organism="Homo sapiens"
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ORIGIN

Query Match 85.3%; Score 2682.2; DB 6; Length 2981;
Best Local Similarity 96.5%; Pred. No. 0;
Matches 2793; Conservative 0; Mismatches 3; Indels 99; Gaps 1;

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Db	412	-----	411
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Db	412	-----GAACTTCAAGATTCCTACCTGTTGCCCATCTCGGA	446
Qy	602	GGACAAGGTCATGGAGGGAAAAGGCCAAAGCCCCTTTGACCCCGCTCACAAGCATAACGGC	661
Db	447	GGACAAGGTCATGGAGGGAAAAGGCCAAAGCCCCTTTGACCCCGCTCACAAGCATAACGGC	506
Qy	662	TGTCTTGGTGGATGGGATGCTCTATTCTGGTACTATGAACAACTTCCTGGGCAGTGAGCC	721
Db	507	TGTCTTGGTGGATGGGATGCTCTATTCTGGTACTATGAACAACTTCCTGGGCAGTGAGCC	566
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Qy	782	GCTGCATCATGACGCCTCCTTTGTGGCAGCCATCCCTTCGACCCAGGTTCGTCTACTTCTT	841
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Qy	1082	CCAGTGGCAGGTTGGCGGGACCAGGAGCTCTGCGGTTTGTGCCTTCTCTCTCTTGGACAT	1141
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Qy	1142	TGAACGTGTCTTTAAGGGGAAATACAAAGAGTTGAACAAAGAACTTCACGCTGGACTAC	1201
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Qy	1202	TTATAGGGGCCCTGAGACCAACCCCCGGCCAGGCAGTTGCTCAGTGGGCCCCCTCCTCTGA	1261
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Db	1107	TAAGGCCCTGACCTTCATGAAGGACCATTTCTGATGGATGAGCAAGTGGTGGGGACGCC	1166
Qy	1322	CCTGCTGGTGAATCTGGCGTGGAGTATACACGGCTTGCACTGGAGACAGCCCAGGGCCT	1381
Db	1167	CCTGCTGGTGAATCTGGCGTGGAGTATACACGGCTTGCACTGGAGACAGCCCAGGGCCT	1226
Qy	1382	TGATGGGCACAGCCATCTTGTCATGTACCTGGGAACCACCACAGGGTCGCTCCACAAGGC	1441
Db	1227	TGATGGGCACAGCCATCTTGTCATGTACCTGGGAACCACCACAGGGTCGCTCCACAAGGC	1286
Qy	1442	TGTGGTAAGTGGGGACAGCAGTGCTCATCTGGTGGAAGAGATTAGCTGTTCCCTGACCC	1501
Db	1287	TGTGGTAAGTGGGGACAGCAGTGCTCATCTGGTGGAAGAGATTAGCTGTTCCCTGACCC	1346
Qy	1502	TGAACCTGTTTCGCAACCTGCAGCTGGCCCCCACCAGGGTGCAGTGTTTGTAGGCTTCTC	1561
Db	1347	TGAACCTGTTTCGCAACCTGCAGCTGGCCCCCACCAGGGTGCAGTGTTTGTAGGCTTCTC	1406
Qy	1562	AGGAGGTGTCTGGAGGGTGCCCCGAGCCAACTGTAGTGTCTATGAGAGCTGTGTGGACTG	1621
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Qy	1622	TGTCCTTGCCCCGGGACCCCCACTGTGCCTGGGACCCTGAGTCCCGAACCTGTTGCCTCCT	1681
Db	1467	TGTCCTTGCCCCGGGACCCCCACTGTGCCTGGGACCCTGAGTCCCGAACCTGTTGCCTCCT	1526
Qy	1682	GTCTGCCCCAACCTGAACTCCTGGAAGCAGGACATGGAGCGGGGGAACCCAGAGTGGGC	1741
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Qy	1802	AGAAGTCCTGGCTGTCCCCAACTCCATCCTGGAGCTCCCCTGCCCCACCTGTCAGCCTT	1861
Db	1647	AGAAGTCCTGGCTGTCCCTAACTCCATCCTGGAGCTCCCCTGCCCCACCTGTCAGCCTT	1706
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Db	1707	GGCCTCTTATTATTGGAGTCATGGCCCAGCAGCAGTCCCAGAAGCCTCTTCCACTGTCTA	1766
Qy	1922	CAATGGCTCCCTCTTGCTGATAGTGCAGGATGGAGTTGGGGGTCTCTACCACTGCTGGGC	1981
Db	1767	CAATGGCTCCCTCTTGCTGATAGTGCAGGATGGAGTTGGGGGTCTCTACCACTGCTGGGC	1826
Qy	1982	AACTGAGAATGGCTTTTCATACCCTGTGATCTCCTACTGGGTGGACAGCCAGGACCAGAC	2041
Db	1827	AACTGAGAATGGCTTTTCATACCCTGTGATCTCCTACTGGGTGGGCAGCCAGGACCAGAC	1886

Qy	2042	CCTGGCCCTGGATCCTGAACTGGCAGGCATCCCCGGGAGCATGTGAAGGTCCCGTTGAC	2101
Db	1887	CCTGGCCCTGGATCCTGAACTGGCAGGCATCCCCGGGAGCATGTGAAGGTCCCGTTGAC	1946
Qy	2102	CAGGGTCAGTGGTGGGGCCGCCCTGGCTGCCCAGCAGTCCTACTGGCCCCACTTTGTCAC	2161
Db	1947	CAGGGTCAGTGGTGGGGCCGCCCTGGCTGCCCAGCAGTCCTACTGGCCCCACTTTGTCAC	2006
Qy	2162	TGTCACTGTCCTCTTTGCCTTAGTGCTTTT CAGGAGCCCTCATCATCCTCGTGGCCTCCCC	2221
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Qy	2222	ATTGAGAGCACTCCGGGCTCGGGGCAAGGTT CAGGGCTGTGAGACCCTGCGCCCTGGGGA	2281
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Qy	2282	GAAGGCCCGTTAAGCAGAGAGCAACACCTCCAGTCTCCCAAGGAATGCAGGACCTCTGC	2341
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Db	2367	CTGCATCACTGATGACACTCAGCAGGGTGATGCACAGCAGTCTGCCTCCCCTATGGGACT	2426
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Qy	2702	AGAAACACAGTGTTTCAAGAGACCCTAAAAAACCTGCCTGTCCCAGGACCCTATGGTAAT	2761
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Qy	2822	AGCTGCCGCTTTGGACACCAACACTCCCTTCTCCCAGGGTCATGCAGGGATCTGCTCCCT	2881
Db	2667	AGCTGCCGCTTTGGACACCAACACTCCCTTCTCCCAGGGTCATGCAGGGATCTGCTCCCT	2726
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RESULT 8

AK091127

LOCUS AK091127 2981 bp mRNA linear PRI 30-JAN-2004

DEFINITION Homo sapiens cDNA FLJ33808 fis, clone CTONG2001749, highly similar to SEMAPHORIN 4A PRECURSOR.

ACCESSION AK091127

VERSION AK091127.1 GI:21749423

KEYWORDS oligo capping; fis (full insert sequence).

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1

AUTHORS

Ota,T., Suzuki,Y., Nishikawa,T., Otsuki,T., Sugiyama,T., Irie,R., Wakamatsu,A., Hayashi,K., Sato,H., Nagai,K., Kimura,K., Makita,H., Sekine,M., Obayashi,M., Nishi,T., Shibahara,T., Tanaka,T., Ishii,S., Yamamoto,J., Saito,K., Kawai,Y., Isono,Y., Nakamura,Y., Nagahari,K., Murakami,K., Yasuda,T., Iwayanagi,T., Wagatsuma,M., Shiratori,A., Sudo,H., Hosoiri,T., Kaku,Y., Kodaira,H., Kondo,H., Sugawara,M., Takahashi,M., Kanda,K., Yokoi,T., Furuya,T., Kikkawa,E., Omura,Y., Abe,K., Kamihara,K., Katsuta,N., Sato,K., Tanikawa,M., Yamazaki,M., Ninomiya,K., Ishibashi,T., Yamashita,H., Murakawa,K., Fujimori,K., Tanai,H., Kimata,M., Watanabe,M., Hiraoka,S., Chiba,Y., Ishida,S., Ono,Y., Takiguchi,S., Watanabe,S., Yosida,M., Hotuta,T., Kusano,J., Kanehori,K., Takahashi-Fujii,A., Hara,H., Tanase,T., Nomura,Y., Togiya,S., Komai,F., Hara,R., Takeuchi,K., Arita,M., Imose,N., Musashino,K., Yuuki,H., Oshima,A., Sasaki,N., Aotsuka,S., Yoshikawa,Y., Matsunawa,H., Ichihara,T., Shiohata,N., Sano,S., Moriya,S., Momiyama,H., Satoh,N., Takami,S., Terashima,Y., Suzuki,O., Nakagawa,S., Senoh,A., Mizoguchi,H., Goto,Y., Shimizu,F., Wakebe,H., Hishigaki,H., Watanabe,T., Sugiyama,A., Takemoto,M., Kawakami,B., Yamazaki,M., Watanabe,K., Kumagai,A., Itakura,S., Fukuzumi,Y., Fujimori,Y., Komiyama,M., Tashiro,H., Tanigami,A., Fujiwara,T., Ono,T., Yamada,K., Fujii,Y., Ozaki,K., Hirao,M., Ohmori,Y., Kawabata,A., Hikiji,T., Kobatake,N., Inagaki,H., Ikema,Y., Okamoto,S., Okitani,R., Kawakami,T., Noguchi,S., Itoh,T., Shigeta,K., Senba,T., Matsumura,K.,

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 Nagase,T., Nomura,N., Kikuchi,H., Masuho,Y., Yamashita,R.,
 Nakai,K., Yada,T., Nakamura,Y., Ohara,O., Isogai,T. and Sugano,S.

TITLE Complete sequencing and characterization of 21,243 full-length
 human cDNAs

JOURNAL Nat. Genet. 36 (1), 40-45 (2004)

PUBMED 14702039

REFERENCE 2

AUTHORS Nishi,T., Ota,T., Nakagawa,S., Senoh,A., Mizuguchi,H., Inagaki,H.,
 Sugiyama,T., Irie,R., Otsuki,T., Sato,H., Wakamatsu,A., Ishii,S.,
 Yamamoto,J., Isono,Y., Kawai-Hio,Y., Saito,K., Nishikawa,T.,
 Kimura,K., Yamashita,H., Matsuo,K., Nakamura,Y., Sekine,M.,
 Kikuchi,H., Kanda,K., Wagatsuma,M., Murakawa,K., Kanehori,K.,
 Takahashi-Fujii,A., Oshima,A., Sugiyama,A., Kawakami,B., Suzuki,Y.,
 Sugano,S., Nagahari,K., Masuho,Y., Nagai,K. and Isogai,T.

TITLE NEDO human cDNA sequencing project

JOURNAL Unpublished

REFERENCE 3 (bases 1 to 2981)

AUTHORS Isogai,T. and Yamamoto,J.

TITLE Direct Submission

JOURNAL Submitted (04-JUL-2002) Takao Isogai, FLJ Project (HRI Team); 2-6-7
 Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan
 (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)

COMMENT NEDO human cDNA sequencing project supported by Ministry of
 Economy, Trade and Industry of Japan; cDNA full insert sequencing:
 Research Association for Biotechnology (RAB); cDNA library
 construction: Helix Research Institute (HRI) (supported by Japan
 Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB,
 HRI, and Biotechnology Center, National Institute of Technology and
 Evaluation; clone selection for full insert sequencing: HRI and
 RAB; annotation: HRI and RAB.

FEATURES Location/Qualifiers

source 1. .2981
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 /db_xref="taxon:9606"
 /clone="CTONG2001749"
 /tissue_type="tongue, tumor tissue"
 /clone_lib="CTONG2"
 /note="cloning vector: pME18SFL3"

ORIGIN

Query Match 85.3%; Score 2682.2; DB 9; Length 2981;
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 Matches 2793; Conservative 0; Mismatches 3; Indels 99; Gaps 1;

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Db 186 AGGGGATGAACGTAGGGCACTTAGCTTCTTCCACCAGAAGGGCCTCCAGGATTTTGACAC 245

Qy 302 TCTGCTCCTGAGTGGTGATGGAAATACTCTCTACGTGGGGGCTCGAGAAGCCATTCTGGC 361
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Db 246 TCTGCTCCTGAGTGGTGATGGAAATACTCTCTACGTGGGGGCTCGAGAAGCCATTCTGGC 305

Qy 362 CTTGGATATCCAGGATCCAGGGGTCCCCAGGCTAAAGAACATGATACCGTGGCCAGCCAG 421

Db	306		CTTGGATATCCAGGATCCAGGGGTCCCCAGGCTAAAGAACATGATACCGTGGCCAGCCAG	365
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Db	366		TGACAGAAAAAAGAGTGAATGTGCCTTTAAGAAGAAGAGCAATGAG-----	411
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Db	927		CCAGTGGCAGGTTGGCGGGACCAGGAGCTCTGCGGTTTGTGCCTTCTCTCTCTTGGACAT	986
Qy	1142		TGAACGTGTCTTTAAGGGGAAATACAAAGAGTTGAACAAAGAACTTCACGCTGGACTAC	1201
Db	987		TGAACGTGTCTTTAAGGGGAAATACAAAGAGTTGAACAAAGAACTTCACGCTGGACTAC	1046
Qy	1202		TTATAGGGGCCCTGAGACCAACCCCCGGCCAGGCAGTTGCTCAGTGGGCCCCCTCCTCTGA	1261

Db	1047	TTATAGGGGCCCTGAGACCAACCCCCGGCCAGGCAGTTGCTCAGTGGGCCCCCTCCTCTGA	1106
Qy	1262	TAAGGCCCTGACCTTCATGAAGGACCATTTCTGATGGATGAGCAAGTGGTGGGGACGCC	1321
Db	1107	TAAGGCCCTGACCTTCATGAAGGACCATTTCTGATGGATGAGCAAGTGGTGGGGACGCC	1166
Qy	1322	CCTGCTGGTGAAATCTGGCGTGGAGTATACACGGCTTGCAGTGGAGACAGCCCAGGGCCT	1381
Db	1167	CCTGCTGGTGAAATCTGGCGTGGAGTATACACGGCTTGCAGTGGAGACAGCCCAGGGCCT	1226
Qy	1382	TGATGGGCACAGCCATCTTGTCATGTACCTGGGAACCACCACAGGGTCGCTCCACAAGGC	1441
Db	1227	TGATGGGCACAGCCATCTTGTCATGTACCTGGGAACCACCACAGGGTCGCTCCACAAGGC	1286
Qy	1442	TGTGGTAAGTGGGGACAGCAGTGCTCATCTGGTGGAGAGATTAGCTGTTCCCTGACCC	1501
Db	1287	TGTGGTAAGTGGGGACAGCAGTGCTCATCTGGTGGAGAGATTAGCTGTTCCCTGACCC	1346
Qy	1502	TGAACCTGTTTCGCAACCTGCAGCTGGCCCCCACCAGGGTGCAGTGTTTGTAGGCTTCTC	1561
Db	1347	TGAACCTGTTTCGCAACCTGCAGCTGGCCCCCACCAGGGTGCAGTGTTTGTAGGCTTCTC	1406
Qy	1562	AGGAGGTGTCTGGAGGGTGCCCCGAGCCAACTGTAGTGTCTATGAGAGCTGTGTGGACTG	1621
Db	1407	AGGAGGTGTCTGGAGGGTGCCCCGAGCCAACTGTAGTGTCTATGAGAGCTGTGTGGACTG	1466
Qy	1622	TGTCCTTGCCCCGGGACCCCCACTGTGCCTGGGACCCTGAGTCCCGAACCTGTTGCCTCCT	1681
Db	1467	TGTCCTTGCCCCGGGACCCCCACTGTGCCTGGGACCCTGAGTCCCGAACCTGTTGCCTCCT	1526
Qy	1682	GTCTGCCCCCAACCTGAACTCCTGGAAGCAGGACATGGAGCGGGGGAACCCAGAGTGGGC	1741
Db	1527	GTCTGCCCCCAACCTGAACTCCTGGAAGCAGGACATGGAGCGGGGGAACCCAGAGTGGGC	1586
Qy	1742	ATGTGCCAGTGGCCCCATGAGCAGGAGCCTTCGGCCTCAGAGCCGCCGCAAATCATTA	1801
Db	1587	ATGTGCCAGTGGCCCCATGAGCAGGAGCCTTCGGCCTCAGAGCCGCCGCAAATCATTA	1646
Qy	1802	AGAAGTCCTGGCTGTCCCCAACTCCATCCTGGAGCTCCCCTGCCCCACCTGTCAGCCTT	1861
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Qy	1862	GGCCTCTTATTATTGGAGTCATGGCCCAGCAGCAGTCCCAGAAGCCTCTTCCACTGTCTA	1921
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Db	1767	CAATGGCTCCCTCTTGCTGATAGTGCAGGATGGAGTTGGGGGTCTCTACCAGTGCTGGGC	1826
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Db	1827	AACTGAGAATGGCTTTTCATACCCTGTGATCTCCTACTGGGTGGGCAGCCAGGACCAGAC	1886
Qy	2042	CCTGGCCCTGGATCCTGAACTGGCAGGCATCCCCGGGAGCATGTGAAGGTCCCGTTGAC	2101
Db	1887	CCTGGCCCTGGATCCTGAACTGGCAGGCATCCCCGGGAGCATGTGAAGGTCCCGTTGAC	1946

Qy	2102	CAGGGTCAGTGGTGGGGCCGCCCTGGCTGCCCAGCAGTCCTACTGGCCCCACTTTGTCAC	2161
Db	1947	CAGGGTCAGTGGTGGGGCCGCCCTGGCTGCCCAGCAGTCCTACTGGCCCCACTTTGTCAC	2006
Qy	2162	TGTCACTGTCCTCTTTGCCTTAGTGCTTTTCAGGAGCCCTCATCATCCTCGTGGCCTCCCC	2221
Db	2007	TGTCACTGTCCTCTTTGCCTTAGTGCTTTTCAGGAGCCCTCATCATCCTCGTGGCCTCCCC	2066
Qy	2222	ATTGAGAGCACTCCGGGCTCGGGGCAAGGTTTCAGGGCTGTGAGACCCTGCGCCCTGGGGA	2281
Db	2067	ATTGAGAGCACTCCGGGCTCGGGGCAAGGTTTCAGGGCTGTGAGACCCTGCGCCCTGGGGA	2126
Qy	2282	GAAGGCCCCGTTAAGCAGAGAGCAACACCTCCAGTCTCCCAAGGAATGCAGGACCTCTGC	2341
Db	2127	GAAGGCCCCGTTAAGCAGAGAGCAACACCTCCAGTCTCCCAAGGAATGCAGGACCTCTGC	2186
Qy	2342	CAGTGATGTGGACGCTGACAACAACCTGCCTAGGCACTGAGGTAGCTTAAACTCTAGGCAC	2401
Db	2187	CAGTGATGTGGACGCTGACAACAACCTGCCTAGGCACTGAGGTAGCTTAAACTCTAGGCAC	2246
Qy	2402	AGGCCGGGGCTGCGGTGCAGGCACCTGGCCATGCTGGCTGGGCGGGCCCAAGCACAGCCCT	2461
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Db	2487	ACACTGATATTGAAGAACCTGGAGAGGATCCTTCAGTTCTGGCCATTCCAGGGACCCTCC	2546
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RESULT 9

AX512887

LOCUS AX512887 2768 bp DNA linear PAT 03-OCT-2002

DEFINITION Sequence 35 from Patent WO02062841.

ACCESSION AX512887

VERSION AX512887.1 GI:23504046

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Tang,T.Y., Yue,H., Gandhi,A.R., Yao,M.G., Warren,B.A., Ding,L.,
 Duggan,B.M., Xu,Y., Yang,J., Thangavelu,K., Lal,P.G.,
 Honchell,C.D., Walia,N.K., Lee,S., Lee,E.A., Richardson,T.W.,
 Baughn,M.R. and Elliott,V.S.

TITLE Secreted proteins

JOURNAL Patent: WO 02062841-A 35 15-AUG-2002;

Incyte Genomics, Inc. (US)

FEATURES Location/Qualifiers

source 1. .2768
 /organism="Homo sapiens"
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ORIGIN

Query Match 78.8%; Score 2476.4; DB 6; Length 2768;
 Best Local Similarity 96.5%; Pred. No. 0;
 Matches 2580; Conservative 0; Mismatches 1; Indels 93; Gaps 1;

Qy 74 AGAGCTCCCTGGTGACAGTCTGTGGCTGAGCATGGCCCTCCCAGCCCTGGGCCTGGACCC 133
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 Db 169 AGAGCTCCCTGGTGACAGTCTGTGGCTGAGCATGGCCCTCCCAGCCCTGGGCCTGGACCC 228

Qy 134 CTGGAGCCTCCTGGGCCTTTTCTCTTCCAAGTCTTCAGCTGCTGCTGCCGACGACGAC 193
 |||
 Db 229 CTGGAGCCTCCTGGGCCTTTTCTCTTCCAAGTCTTCAGCTGCTGCTGCCGACGACGAC 288

Qy 194 CGCGGGGGGAGGCGGGCAGGGGCCCATGCCAGGGTCAGATACTATGCAGGGGATGAACG 253

Db	289	 CGCGGGGGGAGGCGGGCAGGGGCCCATGCCAGGGTCAGATACTATGCAGGGGATGAACG	348
Qy	254	TAGGGCACTTAGCTTCTTCCACCAGAAGGGCCTCCAGGATTTTGACACTCTGCTCCTGAG	313
Db	349	 TAGGGCACTTAGCTTCTTCCACCAGAAGGGCCTCCAGGATTTTGACACTCTGCTCCTGAG	408
Qy	314	TGGTGATGGAATACTCTCTACGTGGGGGCTCGAGAAGCCATTCTGGCCTTGGATATCCA	373
Db	409	 TGGTGATGGAATACTCTCTACGTGGGGGCTCGAGAAGCCATTCTGGCCTTGGATATCCA	468
Qy	374	GGATCCAGGGGTCCCCAGGCTAAAGAACATGATACCGTGGCCAGCCAGTGACAGAAAAAA	433
Db	469	 GGATCCAGGGGTCCCCAGGCTAAAGAACATGATACCGTGGCCAGCCAGTGACAGAAAAAA	528
Qy	434	GAGTGAATGTGCCTTTAAGAAGAAGAGCAATGAGACACAGTGTTTCAACTTCATCCGTGT	493
Db	529	 GAGTGAATGTGCCTTTAAGAAGAAGAGCAATGAGACACAGTGTTTCAACTTCATCCGTGT	588
Qy	494	CCTGGTTTCTTACAATGTCACCCATCTCTACACCTGCGGCACCTTCGCCTTCAGCCCTGC	553
Db	589	 CCTGGTTTCTTACAATGTCACCCATCTCTACACCTGCGGCACCTTCGCCTTCAGCCCTGC	648
Qy	554	TTGTACCTTCATTGAACTTCAAGATTCCTACCTGTTGCCCATCTCGGAGGACAAGGTCAT	613
Db	649	 TTGTACCTTCATTGAACTTCAAGATTCCTACCTGTTGCCCATCTCGGAGGACAAGGTCAT	708
Qy	614	GGAGGGAAAAGGCCAAAGCCCCCTTTGACCCCGCTCACAAGCATACGGCTGTCTTGGTGGA	673
Db	709	 GGAGGGAAAAGGCCAAAGCCCCCTTTGACCCCGCTCACAAGCATACGGCTGTCTTGGTGGA	768
Qy	674	TGGGATGCTCTATTCTGGTACTATGAACAACCTCCTGGGCAGTGAGCCCATCCTGATGCG	733
Db	769	 TGGGATGCTCTATTCTGGTACTATGAACAACCTCCTGGGCAGTGAGCCCATCCTGATGCG	828
Qy	734	CACACTGGGATCCCAGCCTGTCTCAAGACCGACAACCTCCTCCGCTGGCTGCATCATGA	793
Db	829	 CACACTGGGATCCCAGCCTGTCTCAAGACCGACAACCTCCTCCGCTGGCTGCATCATGA	888
Qy	794	CGCCTCCTTTGTGGCAGCCATCCCTTCGACCCAGGTCGTCTACTTCTTCTTCGAGGAGAC	853
Db	889	 CGCCTCCTTTGTGGCAGCCATCCCTTCGACCCAGGTCGTCTACTTCTTCTTCGAGGAGAC	948
Qy	854	AGCCAGCGAGTTTGACTTCTTTGAGAGGCTCCACACATCGCGGGTGGCTAGAGTCTGCAA	913
Db	949	 AGCCAGCGAGTTTGACTTCTTTGAGAGGCTCCACACATCGCGGGTGGCTAGAGTCTGCAA	1008
Qy	914	GAATGACGTGGGCGGCGAAAAGCTGCTGCAGAAGAAGTGGACCACCTTCCTGAAGGCCCA	973
Db	1009	 GAATGACGTGGGCGGCGAAAAGCTGCTGCAGAAGAAGTGGACCACCTTCCTGAAGGCCCA	1068
Qy	974	GCTGCTCTGCACCCAGCCGGGGCAGTGCCCTTCAACGTCATCCGCCACGCGGTCTGCT	1033
Db	1069	 GCTGCTCTGCACCCAGCCGGGGCAGTGCCCTTCAACGTCATCCGCCACGCGGTCTGCT	1128
Qy	1034	CCCCGCCGATTCTCCACAGCTCCCCACATCTACGCAGTCTTCACCTCCCAGTGGCAGGT	1093

Db	1129	CCCCGCCGATTCTCCACAGCTCCCCACATCTACGCAGTCTTCACCTCCCAGTGGCAGGT	1188
Qy	1094	TGGCGGGACCAGGAGCTCTGCGGTTTGTGCCTTCTCTCTCTTGGACATTGAACGTGTCTT	1153
Db	1189	TGGCGGGACCAGGAGCTCTGCGGTTTGTGCCTTCTCTCTCTTGGACATTGAACGTGTCTT	1248
Qy	1154	TAAGGGGAAATACAAAGAGTTGAACAAAGAACTTCACGCTGGACTACTTATAGGGGCCC	1213
Db	1249	TAAGGGGAAATACAAAGAGTTGAACAAAGAACTTCACGCTGGACTACTTATAGGGGCCC	1308
Qy	1214	TGAGACCAACCCCCGGCCAGGCAGTTGCTCAGTGGGCCCCCTCCTCTGATAAGGCCCTGAC	1273
Db	1309	TGAGACCAACCCCCGGCCAGGCAGTTGCTCAGTGGGCCCCCTCCTCTGATAAGGCCCTGAC	1368
Qy	1274	CTTCATGAAGGACCATTTTCCTGATGGATGAGCAAGTGGTGGGGACGCCCTGCTGGTGAA	1333
Db	1369	CTTCATGAAGGACCATTTTCCTGATGGATGAGCAAGTGGTGGGGACGCCCTGCTGGTGAA	1428
Qy	1334	ATCTGGCGTGGAGTATACACGGCTTGCAGTGGAGACAGCCCAGGGCCTTGATGGGCACAG	1393
Db	1429	ATCTGGCGTGGAGTATACACGGCTTGCAGTGGAGACAGCCCAGGGCCTTGATGGGCACAG	1488
Qy	1394	CCATCTTGTCATGTACCTGGGAACCACCACAGGGTCGCTCCACAAGGCTGTGGTAAGTGG	1453
Db	1489	CCATCTTGTCATGTACCTGGGAACCACCACAGGGTCGCTCCACAAGGCTGT-----	1539
Qy	1454	GGACAGCAGTGCTCATCTGGTGGAGAGATTAGCTGTTCCCTGACCCTGAACCTGTTTCG	1513
Db	1540	-----	1539
Qy	1514	CAACCTGCAGCTGGCCCCCACCAGGGTGCAGTGTTTGTAGGCTTCTCAGGAGGTGTCTG	1573
Db	1540	-----GGGTGCAGTGTTTGTAGGCTTCTCAGGAGGTGTCTG	1575
Qy	1574	GAGGGTGCCCCGAGCCAACGTAGTGTCTATGAGAGCTGTGTGGACTGTGTCTTGCCCCG	1633
Db	1576	GAGGGTGCCCCGAGCCAACGTAGTGTCTATGAGAGCTGTGTGGACTGTGTCTTGCCCCG	1635
Qy	1634	GGACCCCCACTGTGCCTGGGACCCTGAGTCCCGAACCTGTTGCCTCCTGTCTGCCCCAA	1693
Db	1636	GGACCCCCACTGTGCCTGGGACCCTGAGTCCCGAACCTGTTGCCTCCTGTCTGCCCCAA	1695
Qy	1694	CCTGAACCTCCTGGAAGCAGGACATGGAGCGGGGGAACCCAGAGTGGGCATGTGCCAGTGG	1753
Db	1696	CCTGAACCTCCTGGAAGCAGGACATGGAGCGGGGGAACCCAGAGTGGGCATGTGCCAGTGG	1755
Qy	1754	CCCCATGAGCAGGAGCCTTCGGCCTCAGAGCCGCCCGCAAATCATTAAGAAGTCCTGGC	1813
Db	1756	CCCCATGAGCAGGAGCCTTCGGCCTCAGAGCCGCCCGCAAATCATTAAGAAGTCCTGGC	1815
Qy	1814	TGTCCCCAACTCCATCCTGGAGCTCCCCTGCCCCACCTGTCAGCCTTGGCCTCTTATTA	1873
Db	1816	TGTCCCCAACTCCATCCTGGAGCTCCCCTGCCCCACCTGTCAGCCTTGGCCTCTTATTA	1875
Qy	1874	TTGGAGTCATGGCCCAGCAGCAGTCCCAGAAGCCTCTTCCACTGTCTACAATGGCTCCCT	1933
Db	1876	TTGGAGTCATGGCCCAGCAGCAGTCCCAGAAGCCTCTTCCACTGTCTACAATGGCTCCCT	1935

Qy	1934	CTTGCTGATAGTGCAGGATGGAGTTGGGGGTCTCTACCAAGTCTGGGCAACTGAGAATGG	1993
Db	1936	CTTGCTGATAGTGCAGGATGGAGTTGGGGGTCTCTACCAAGTCTGGGCAACTGAGAATGG	1995
Qy	1994	CTTTTCATACCCTGTGATCTCCTACTGGGTGGACAGCCAGGACCAGACCCTGGCCCTGGA	2053
Db	1996	CTTTTCATACCCTGTGATCTCCTACTGGGTGGACAGCCAGGACCAGACCCTGGCCCTGGA	2055
Qy	2054	TCCTGAACTGGCAGGCATCCCCGGGAGCATGTGAAGGTCCCGTTGACCAGGGTCAGTGG	2113
Db	2056	TCCTGAACTGGCAGGCATCCCCGGGAGCATGTGAAGGTCCCGTTGACCAGGGTCAGTGG	2115
Qy	2114	TGGGGCCGCCCTGGCTGCCCAGCAGTCCTACTGGCCCCACTTTGTCACTGTCACTGTCCT	2173
Db	2116	TGGGGCCGCCCTGGCTGCCCAGCAGTCCTACTGGCCCCACTTTGTCACTGTCACTGTCCT	2175
Qy	2174	CTTTGCCTTAGTGCTTTTCAGGAGCCCTCATCATCCTCGTGGCCTCCCCATTGAGAGCACT	2233
Db	2176	CTTTGCCTTAGTGCTTTTCAGGAGCCCTCATCATCCTCGTGGCCTCCCCATTGAGAGCACT	2235
Qy	2234	CCGGGCTCGGGGCAAGGTTTCAGGGCTGTGAGACCCTGCGCCCTGGGGAGAAGGCCCGTT	2293
Db	2236	CCGGGCTCGGGGCAAGGTTTCAGGGCTGTGAGACCCTGCGCCCTGGGGAGAAGGCCCGTT	2295
Qy	2294	AAGCAGAGAGCAACACCTCCAGTCTCCCAAGGAATGCAGGACCTCTGCCAGTGATGTGGA	2353
Db	2296	AAGCAGAGAGCAACACCTCCAGTCTCCCAAGGAATGCAGGACCTCTGCCAGTGATGTGGA	2355
Qy	2354	CGCTGACAACAACCTGCCTAGGCACTGAGGTAGCTTAAACTCTAGGCACAGGCCGGGGCTG	2413
Db	2356	CGCTGACAACAACCTGCCTAGGCACTGAGGTAGCTTAAACTCTAGGCACAGGCCGGGGCTG	2415
Qy	2414	CGGTGCAGGCACCTGGCCATGCTGGCTGGGCGGGCCCAAGCACAGCCCTGACTAGGATGAC	2473
Db	2416	CGGTGCAGGCACCCGGCCATGCTGGCTGGGCGGGCCCAAGCACAGCCCTGACTAGGATGAC	2475
Qy	2474	AGCAGCACAAAAGACCACCTTTCTCCCCTGAGAGGAGCTTCTGCTACTCTGCATCACTGA	2533
Db	2476	AGCAGCACAAAAGACCACCTTTCTCCCCTGAGAGGAGCTTCTGCTACTCTGCATCACTGA	2535
Qy	2534	TGACACTCAGCAGGGTGATGCACAGCAGTCTGCCTCCCCTATGGGACTCCCTTCTACCAA	2593
Db	2536	TGACACTCAGCAGGGTGATGCACAGCAGTCTGCCTCCCCTATGGGACTCCCTTCTACCAA	2595
Qy	2594	GCACATGAGCTCTCTAACAGGGTGGGGGCTACCCCCAGACCTGCTCCTACACTGATATTG	2653
Db	2596	GCACATGAGCTCTCTAACAGGGTGGGGGCTACCCCCAGACCTGCTCCTACACTGATATTG	2655
Qy	2654	AAGAACCTGGAGAGGATCCTTCAGTTCTGGCCATTCCAGGGACCCTCCAGAAACACAGTG	2713
Db	2656	AAGAACCTGGAGAGGATCCTTCAGTTCTGGCCATTCCAGGGACCCTCCAGAAACACAGTG	2715
Qy	2714	TTTCAAGAGACCCTAAAAACCTGCCTGTCCCAG	2747
Db	2716	TTTCAAGAGACCCTAAAAACCTGCCTGTCCCAG	2749

RESULT 10

CQ716130

LOCUS CQ716130 2286 bp DNA linear PAT 03-FEB-2004

DEFINITION Sequence 2064 from Patent WO02068579.

ACCESSION CQ716130

VERSION CQ716130.1 GI:42276987

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Venter,C.J., Adams,M.C., Li,P.W. and Myers,E.W.

TITLE Kits, such as nucleic acid arrays, comprising a majority of
humanexons or transcripts, for detecting expression and other uses
thereofJOURNAL Patent: WO 02068579-A 2064 06-SEP-2002;
PE Corporation (NY) (US)

FEATURES Location/Qualifiers

source 1. .2286
/organism="Homo sapiens"
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ORIGIN

Query Match 72.7%; Score 2284.4; DB 6; Length 2286;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2285; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db       1  ATGGCCCTCCCAGCCCTGGGCCTGGACCCCTGGAGCCTCCTGGGCCTTTTCCTCTTCCAA 60

Qy      165 CTGCTTCAGCTGCTGCTGCCGACGACGACCGCGGGGGAGGCGGGCAGGGGCCCATGCCC 224
          |||
Db       61 CTGCTTCAGCTGCTGCTGCCGACGACGACCGCGGGGGAGGCGGGCAGGGGCCCATGCCC 120

Qy      225 AGGGTCAGATACTATGCAGGGGATGAACGTAGGGCACTTAGCTTCTTCCACCAGAAGGGC 284
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Db      121 AGGGTCAGATACTATGCAGGGGATGAACGTAGGGCACTTAGCTTCTTCCACCAGAAGGGC 180

Qy      285 CTCCAGGATTTTGACACTCTGCTCCTGAGTGGTGATGGAAATACTCTCTACGTGGGGGCT 344
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Db      181 CTCCAGGATTTTGACACTCTGCTCCTGAGTGGTGATGGAAATACTCTCTACGTGGGGGCT 240

Qy      345 CGAGAAGCCATTCTGGCCTTGGATATCCAGGATCCAGGGGTCCCCAGGCTAAAGAACATG 404
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Db      241 CGAGAAGCCATTCTGGCCTTGGATATCCAGGATCCAGGGGTCCCCAGGCTAAAGAACATG 300

Qy      405 ATACCGTGGCCAGCCAGTGACAGAAAAAGAGTGAATGTGCCTTTAAGAAGAAGAGCAAT 464
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Db      301 ATACCGTGGCCAGCCAGTGACAGAAAAAGAGTGAATGTGCCTTTAAGAAGAAGAGCAAT 360

Qy      465 GAGACACAGTGTTCACCTTCATCCGTGTCCTGGTTTCTTACAATGTCACCCATCTCTAC 524
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Db      361 GAGACACAGTGTTCACCTTCATCCGTGTCCTGGTTTCTTACAATGTCACCCATCTCTAC 420
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Qy	525	ACCTGCGGCACCTTCGCCTTCAGCCCTGCTTGTACCTTCATTGAACTTCAAGATTCTCTAC	584
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Qy	585	CTGTTGCCCATCTCGGAGGACAAGGTCATGGAGGGAAAAGGCCAAAGCCCCTTTGACCCC	644
Db	481	CTGTTGCCCATCTCGGAGGACAAGGTCATGGAGGGAAAAGGCCAAAGCCCCTTTGACCCC	540
Qy	645	GCTCACAAGCATACGGCTGTCTTGGTGGATGGGATGCTCTATTCTGGTACTATGAACAAC	704
Db	541	GCTCACAAGCATACGGCTGTCTTGGTGGATGGGATGCTCTATTCTGGTACTATGAACAAC	600
Qy	705	TTCCTGGGCAGTGAGCCCATCCTGATGCGCACACTGGGATCCCAGCCTGTCCTCAAGACC	764
Db	601	TTCCTGGGCAGTGAGCCCATCCTGATGCGCACACTGGGATCCCAGCCTGTCCTCAAGACC	660
Qy	765	GACAACTTCCTCCGCTGGCTGCATCATGACGCCTCCTTTGTGGCAGCCATCCCTTCGACC	824
Db	661	GACAACTTCCTCCGCTGGCTGCATCATGACGCCTCCTTTGTGGCAGCCATCCCTTCGACC	720
Qy	825	CAGGTCGTCTACTTCTTCTTCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAGAGGCTC	884
Db	721	CAGGTCGTCTACTTCTTCTTCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAGAGGCTC	780
Qy	885	CACACATCGCGGGTGGCTAGAGTCTGCAAGAATGACGTGGGCGGGCGAAAAGCTGCTGCAG	944
Db	781	CACACATCGCGGGTGGCTAGAGTCTGCAAGAATGACGTGGGCGGGCGAAAAGCTGCTGCAG	840
Qy	945	AAGAAGTGGACCACCTTCCTGAAGGCCAGCTGCTCTGCACCCAGCCGGGGCAGCTGCCC	1004
Db	841	AAGAAGTGGACCACCTTCCTGAAGGCCAGCTGCTCTGCACCCAGCCGGGGCAGCTGCCC	900
Qy	1005	TTCAACGTCATCCGCCACGCGGTCTGCTCCCCGCCGATTCTCCCACAGCTCCCCACATC	1064
Db	901	TTCAACGTCATCCGCCACGCGGTCTGCTCCCCGCCGATTCTCCCACAGCTCCCCACATC	960
Qy	1065	TACGCAGTCTTCACCTCCCAGTGGCAGGTTGGCGGGACCAGGAGCTCTGCGGTTTGTGCC	1124
Db	961	TACGCAGTCTTCACCTCCCAGTGGCAGGTTGGCGGGACCAGGAGCTCTGCGGTTTGTGCC	1020
Qy	1125	TTCTCTCTCTTGGACATTGAACGTGTCTTTAAGGGGAAATACAAAGAGTTGAACAAAGAA	1184
Db	1021	TTCTCTCTCTTGGACATTGAACGTGTCTTTAAGGGGAAATACAAAGAGTTGAACAAAGAA	1080
Qy	1185	ACTTCACGCTGGACTACTTATAGGGGCCCTGAGACCAACCCCCGGCCAGGCAGTTGCTCA	1244
Db	1081	ACTTCACGCTGGACTACTTATAGGGGCCCTGAGACCAACCCCCGGCCAGGCAGTTGCTCA	1140
Qy	1245	GTGGGCCCCCTCCTCTGATAAGGCCCTGACCTTCATGAAGGACCATTTCCTGATGGATGAG	1304
Db	1141	GTGGGCCCCCTCCTCTGATAAGGCCCTGACCTTCATGAAGGACCATTTCCTGATGGATGAG	1200
Qy	1305	CAAGTGGTGGGGACGCCCCCTGCTGGTGAAATCTGGCGTGGAGTATACACGGCTTGCAGTG	1364
Db	1201	CAAGTGGTGGGGACGCCCCCTGCTGGTGAAATCTGGCGTGGAGTATACACGGCTTGCAGTG	1260

Qy	1365	GAGACAGCCCAGGGCCTTGATGGGCACAGCCATCTTGT	CATGTACCTGGGAACCACCACA	1424
Db	1261	GAGACAGCCCAGGGCCTTGATGGGCACAGCCATCTTGT	CATGTACCTGGGAACCACCACA	1320
Qy	1425	GGGTCGCTCCACAAGGCTGTGGTAAGTGGGGACAGCAGT	GCTCATCTGGTGGAAGAGATT	1484
Db	1321	GGGTCGCTCCACAAGGCTGTGGTAAGTGGGGACAGCAGT	GCTCATCTGGTGGAAGAGATT	1380
Qy	1485	CAGCTGTTCCCTGACCCTGAACCTGTTGCAACCTGCAGCT	GGCCCCACCCAGGGTGCA	1544
Db	1381	CAGCTGTTCCCTGACCCTGAACCTGTTGCAACCTGCAGCT	GGCCCCACCCAGGGTGCA	1440
Qy	1545	GTGTTTGTAGGCTTCTCAGGAGGTGTCTGGAGGGTGCCCC	GAGCCAACTGTAGTGTCTAT	1604
Db	1441	GTGTTTGTAGGCTTCTCAGGAGGTGTCTGGAGGGTGCCCC	GAGCCAACTGTAGTGTCTAT	1500
Qy	1605	GAGAGCTGTGTGGACTGTGTCCTTGCCCGGGACCCCCACT	GTGCCTGGGACCCTGAGTCC	1664
Db	1501	GAGAGCTGTGTGGACTGTGTCCTTGCCCGGGACCCCCACT	GTGCCTGGGACCCTGAGTCC	1560
Qy	1665	CGAACCTGTTGCCTCCTGTCTGCCCCAACCTGAACTCCT	GGAAGCAGGACATGGAGCGG	1724
Db	1561	CGAACCTGTTGCCTCCTGTCTGCCCCAACCTGAACTCCT	GGAAGCAGGACATGGAGCGG	1620
Qy	1725	GGGAACCCAGAGTGGGCATGTGCCAGTGGCCCCATGAGC	AGGAGCCTTCGGCCTCAGAGC	1784
Db	1621	GGGAACCCAGAGTGGGCATGTGCCAGTGGCCCCATGAGC	AGGAGCCTTCGGCCTCAGAGC	1680
Qy	1785	CGCCCGCAAATCATTAAGAAGTCTGGCTGTCCCCAACT	CCATCCTGGAGCTCCCCTGC	1844
Db	1681	CGCCCGCAAATCATTAAGAAGTCTGGCTGTCCCCAACT	CCATCCTGGAGCTCCCCTGC	1740
Qy	1845	CCCCACCTGTCAGCCTTGGCCTCTTATTATTGGAGTCAT	GGCCCAGCAGCAGTCCCAGAA	1904
Db	1741	CCCCACCTGTCAGCCTTGGCCTCTTATTATTGGAGTCAT	GGCCCAGCAGCAGTCCCAGAA	1800
Qy	1905	GCCTCTTCCACTGTCTACAATGGCTCCCTCTTGCTGATA	GTGCAGGATGGAGTTGGGGGT	1964
Db	1801	GCCTCTTCCACTGTCTACAATGGCTCCCTCTTGCTGATA	GTGCAGGATGGAGTTGGGGGT	1860
Qy	1965	CTCTACCACTGCTGGGCAACTGAGAATGGCTTTTCATACC	CTGTGATCTCCTACTGGGTG	2024
Db	1861	CTCTACCACTGCTGGGCAACTGAGAATGGCTTTTCATACC	CTGTGATCTCCTACTGGGTG	1920
Qy	2025	GACAGCCAGGACCAGACCCTGGCCCTGGATCCTGAACT	GGCAGGCATCCCCGGGAGCAT	2084
Db	1921	GACAGCCAGGACCAGACCCTGGCCCTGGATCCTGAACT	GGCAGGCATCCCCGGGAGCAT	1980
Qy	2085	GTGAAGGTCCCGTTGACCAGGGTCAGTGGTGGGGCCGCC	CTGGCTGCCCAGCAGTCCTAC	2144
Db	1981	GTGAAGGTCCCGTTGACCAGGGTCAGTGGTGGGGCCGCC	CTGGCTGCCCAGCAGTCCTAC	2040
Qy	2145	TGGCCCCACTTTGTCACTGTCACTGTCCTCTTTGCCTTA	GTGCTTTTCAGGAGCCCTCATC	2204
Db	2041	TGGCCCCACTTTGTCACTGTCACTGTCCTCTTTGCCTTA	GTGCTTTTCAGGAGCCCTCATC	2100
Qy	2205	ATCCTCGTGGCCTCCCCATTGAGAGCACTCCGGGCTCG	GGGGCAAGGTTTCAGGGCTGTGAG	2264

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Db      2101 ATCCTCGTGGCCTCCCATTTGAGAGCACTCCGGGCTCGGGGCAAGGTTTCAGGGCTGTGAG 2160
Qy      2265 ACCCTGCGCCCTGGGGAGAAGGCCCCGTTAAGCAGAGAGCAACACCTCCAGTCTCCCAAG 2324
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Db      2161 ACCCTGCGCCCTGGGGAGAAGGCCCCGTTAAGCAGAGAGCAACACCTCCAGTCTCCCAAG 2220
Qy      2325 GAATGCAGGACCTCTGCCAGTGATGTGGACGCTGACAACAACCTGCCTAGGCACTGAGGTA 2384
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Db      2221 GAATGCAGGACCTCTGCCAGTGATGTGGACGCTGACAACAACCTGCCTAGGCACTGAGGTA 2280
Qy      2385 GCTTAA 2390
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RESULT 11

AR564551

LOCUS AR564551 2283 bp DNA linear PAT 08-OCT-2004

DEFINITION Sequence 18 from patent US 6764677.

ACCESSION AR564551

VERSION AR564551.1 GI:53979962

KEYWORDS .

SOURCE Unknown.

ORGANISM Unknown.

Unclassified.

REFERENCE 1 (bases 1 to 2283)

AUTHORS Sharp, J.D. and Barnes, T.M.

TITLE Tango 294, a lipase-like protein

JOURNAL Patent: US 6764677-A 18 20-JUL-2004;

FEATURES Location/Qualifiers

source 1..2283
/organism="unknown"
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ORIGIN

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Query Match          72.6%; Score 2283; DB 6; Length 2283;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2283; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      105 ATGGCCCTCCCAGCCCTGGGCCTGGACCCCTGGAGCCTCCTGGGCCTTTTCCTCTTCCAA 164
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Db      1 ATGGCCCTCCCAGCCCTGGGCCTGGACCCCTGGAGCCTCCTGGGCCTTTTCCTCTTCCAA 60

Qy      165 CTGCTTCAGCTGCTGCTGCCGACGACGACCGCGGGGGAGGCGGGCAGGGGCCCCATGCCC 224
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Db      61 CTGCTTCAGCTGCTGCTGCCGACGACGACCGCGGGGGAGGCGGGCAGGGGCCCCATGCCC 120

Qy      225 AGGGTCAGATACTATGCAGGGGATGAACGTAGGGCACTTAGCTTCTTCCACCAGAAGGGC 284
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Db      121 AGGGTCAGATACTATGCAGGGGATGAACGTAGGGCACTTAGCTTCTTCCACCAGAAGGGC 180

Qy      285 CTCCAGGATTTTGACACTCTGCTCCTGAGTGGTGATGGAAATACTCTCTACGTGGGGGCT 344
                |||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181 CTCCAGGATTTTGACACTCTGCTCCTGAGTGGTGATGGAAATACTCTCTACGTGGGGGCT 240

Qy      345 CGAGAAGCCATTCTGGCCTTGGATATCCAGGATCCAGGGGTCCCAGGCTAAAGAACATG 404

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Db	241	 CGAGAAGCCATTCTGGCCTTGGATATCCAGGATCCAGGGGTCCCCAGGCTAAAGAACATG	300
Qy	405	ATACCGTGGCCAGCCAGTGACAGAAAAAAGAGTGAATGTGCCTTTAAGAAGAAGAGCAAT	464
Db	301	 ATACCGTGGCCAGCCAGTGACAGAAAAAAGAGTGAATGTGCCTTTAAGAAGAAGAGCAAT	360
Qy	465	GAGACACAGTGTTCAACTTCATCCGTGTCCTGGTTTCTTACAATGTCACCCATCTCTAC	524
Db	361	 GAGACACAGTGTTCAACTTCATCCGTGTCCTGGTTTCTTACAATGTCACCCATCTCTAC	420
Qy	525	ACCTGCGGCACCTTCGCCTTCAGCCCTGCTTGTACCTTCATTGAACTTCAAGATTCTTAC	584
Db	421	 ACCTGCGGCACCTTCGCCTTCAGCCCTGCTTGTACCTTCATTGAACTTCAAGATTCTTAC	480
Qy	585	CTGTTGCCCATCTCGGAGGACAAGGTCATGGAGGGAAAAGGCCAAAGCCCCTTTGACCCC	644
Db	481	 CTGTTGCCCATCTCGGAGGACAAGGTCATGGAGGGAAAAGGCCAAAGCCCCTTTGACCCC	540
Qy	645	GCTCACAAGCATACGGCTGTCTTGGTGGATGGGATGCTCTATTCTGGTACTATGAACAAC	704
Db	541	 GCTCACAAGCATACGGCTGTCTTGGTGGATGGGATGCTCTATTCTGGTACTATGAACAAC	600
Qy	705	TTCCTGGGCAGTGAGCCCATCCTGATGCGCACACTGGGATCCCAGCCTGTCCTCAAGACC	764
Db	601	 TTCCTGGGCAGTGAGCCCATCCTGATGCGCACACTGGGATCCCAGCCTGTCCTCAAGACC	660
Qy	765	GACAACTTCCTCCGCTGGCTGCATCATGACGCCTCCTTTGTGGCAGCCATCCCTTCGACC	824
Db	661	 GACAACTTCCTCCGCTGGCTGCATCATGACGCCTCCTTTGTGGCAGCCATCCCTTCGACC	720
Qy	825	CAGGTCGTCTACTTCTTCTTCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAGAGGCTC	884
Db	721	 CAGGTCGTCTACTTCTTCTTCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAGAGGCTC	780
Qy	885	CACACATCGCGGGTGGCTAGAGTCTGCAAGAATGACGTGGGCGGCGAAAAGCTGCTGCAG	944
Db	781	 CACACATCGCGGGTGGCTAGAGTCTGCAAGAATGACGTGGGCGGCGAAAAGCTGCTGCAG	840
Qy	945	AAGAAGTGGACCACCTTCCTGAAGGCCAGCTGCTCTGCACCCAGCCGGGGCAGCTGCCC	1004
Db	841	 AAGAAGTGGACCACCTTCCTGAAGGCCAGCTGCTCTGCACCCAGCCGGGGCAGCTGCCC	900
Qy	1005	TTCAACGTCATCCGCCACGCGGTCTGCTCCCCGCCGATTCTCCCACAGCTCCCCACATC	1064
Db	901	 TTCAACGTCATCCGCCACGCGGTCTGCTCCCCGCCGATTCTCCCACAGCTCCCCACATC	960
Qy	1065	TACGCAGTCTTCACCTCCCAGTGGCAGGTTGGCGGGACCAGGAGCTCTGCGGTTTGTGCC	1124
Db	961	 TACGCAGTCTTCACCTCCCAGTGGCAGGTTGGCGGGACCAGGAGCTCTGCGGTTTGTGCC	1020
Qy	1125	TTCTCTCTCTTGGACATTGAACGTGTCTTTAAGGGGAAATACAAAGAGTTGAACAAAGAA	1184
Db	1021	 TTCTCTCTCTTGGACATTGAACGTGTCTTTAAGGGGAAATACAAAGAGTTGAACAAAGAA	1080
Qy	1185	ACTTCACGCTGGACTACTTATAGGGGCCCTGAGACCAACCCCCGGCCAGGCAGTTGCTCA	1244

Db	1081	ACTTCACGCTGGACTACTTATAGGGGCCCTGAGACCAACCCCCGGCCAGGCAGTTGCTCA	1140
Qy	1245	GTGGGCCCCCTCCTCTGATAAGGCCCTGACCTTCATGAAGGACCATTTCTGATGGATGAG	1304
Db	1141	GTGGGCCCCCTCCTCTGATAAGGCCCTGACCTTCATGAAGGACCATTTCTGATGGATGAG	1200
Qy	1305	CAAGTGGTGGGGACGCCCCTGCTGGTGAAATCTGGCGTGGAGTATACACGGCTTGCAAGTG	1364
Db	1201	CAAGTGGTGGGGACGCCCCTGCTGGTGAAATCTGGCGTGGAGTATACACGGCTTGCAAGTG	1260
Qy	1365	GAGACAGCCCAGGGCCTTGATGGGCACAGCCATCTTGTTCATGTACCTGGGAACCACCACA	1424
Db	1261	GAGACAGCCCAGGGCCTTGATGGGCACAGCCATCTTGTTCATGTACCTGGGAACCACCACA	1320
Qy	1425	GGGTCGCTCCACAAGGCTGTGGTAAGTGGGGACAGCAGTGCTCATCTGGTGGAAGAGATT	1484
Db	1321	GGGTCGCTCCACAAGGCTGTGGTAAGTGGGGACAGCAGTGCTCATCTGGTGGAAGAGATT	1380
Qy	1485	CAGCTGTTCCCTGACCCTGAACCTGTTTCGCAACCTGCAGCTGGCCCCCACCAGGGTGCA	1544
Db	1381	CAGCTGTTCCCTGACCCTGAACCTGTTTCGCAACCTGCAGCTGGCCCCCACCAGGGTGCA	1440
Qy	1545	GTGTTTGTAGGCTTCTCAGGAGGTGTCTGGAGGGTGCCCCGAGCCAACCTGTAGTGTCTAT	1604
Db	1441	GTGTTTGTAGGCTTCTCAGGAGGTGTCTGGAGGGTGCCCCGAGCCAACCTGTAGTGTCTAT	1500
Qy	1605	GAGAGCTGTGTGGACTGTGTCCTTGCCCGGGACCCCCACTGTGCCTGGGACCCTGAGTCC	1664
Db	1501	GAGAGCTGTGTGGACTGTGTCCTTGCCCGGGACCCCCACTGTGCCTGGGACCCTGAGTCC	1560
Qy	1665	CGAACCTGTTGCCTCCTGTCTGCCCCAACCTGAACCTCCTGGAAGCAGGACATGGAGCGG	1724
Db	1561	CGAACCTGTTGCCTCCTGTCTGCCCCAACCTGAACCTCCTGGAAGCAGGACATGGAGCGG	1620
Qy	1725	GGGAACCCAGAGTGGGCATGTGCCAGTGGCCCCATGAGCAGGAGCCTTCGGCCTCAGAGC	1784
Db	1621	GGGAACCCAGAGTGGGCATGTGCCAGTGGCCCCATGAGCAGGAGCCTTCGGCCTCAGAGC	1680
Qy	1785	CGCCCGCAAATCATTAAGAAGTCCTGGCTGTCCCCAACTCCATCCTGGAGCTCCCCTGC	1844
Db	1681	CGCCCGCAAATCATTAAGAAGTCCTGGCTGTCCCCAACTCCATCCTGGAGCTCCCCTGC	1740
Qy	1845	CCCCACCTGTCAGCCTTGGCCTCTTATTATTGGAGTCATGGCCCAGCAGCAGTCCCAGAA	1904
Db	1741	CCCCACCTGTCAGCCTTGGCCTCTTATTATTGGAGTCATGGCCCAGCAGCAGTCCCAGAA	1800
Qy	1905	GCCTCTTCCACTGTCTACAATGGCTCCCTCTTGCTGATAGTGCAGGATGGAGTTGGGGGT	1964
Db	1801	GCCTCTTCCACTGTCTACAATGGCTCCCTCTTGCTGATAGTGCAGGATGGAGTTGGGGGT	1860
Qy	1965	CTCTACCAAGTGCTGGGCAACTGAGAATGGCTTTTCATACCCTGTGATCTCCTACTGGGTG	2024
Db	1861	CTCTACCAAGTGCTGGGCAACTGAGAATGGCTTTTCATACCCTGTGATCTCCTACTGGGTG	1920
Qy	2025	GACAGCCAGGACCAGACCCTGGCCCTGGATCCTGAACTGGCAGGCATCCCCGGGAGCAT	2084
Db	1921	GACAGCCAGGACCAGACCCTGGCCCTGGATCCTGAACTGGCAGGCATCCCCGGGAGCAT	1980

Qy	2085	GTGAAGGTCCCGTTGACCAGGGTCAGTGGTGGGGCCGCCCTGGCTGCCCAGCAGTCCTAC	2144
Db	1981	GTGAAGGTCCCGTTGACCAGGGTCAGTGGTGGGGCCGCCCTGGCTGCCCAGCAGTCCTAC	2040
Qy	2145	TGGCCCCACTTTGTCACTGTCACTGTCCTCTTTGCCTTAGTGCTTTCAGGAGCCCTCATC	2204
Db	2041	TGGCCCCACTTTGTCACTGTCACTGTCCTCTTTGCCTTAGTGCTTTCAGGAGCCCTCATC	2100
Qy	2205	ATCCTCGTGGCCTCCCCATTGAGAGCACTCCGGGCTCGGGGCAAGGTTTCAGGGCTGTGAG	2264
Db	2101	ATCCTCGTGGCCTCCCCATTGAGAGCACTCCGGGCTCGGGGCAAGGTTTCAGGGCTGTGAG	2160
Qy	2265	ACCCTGCGCCCTGGGGAGAAGGCCCCGTTAAGCAGAGAGCAACACCTCCAGTCTCCCAAG	2324
Db	2161	ACCCTGCGCCCTGGGGAGAAGGCCCCGTTAAGCAGAGAGCAACACCTCCAGTCTCCCAAG	2220
Qy	2325	GAATGCAGGACCTCTGCCAGTGATGTGGACGCTGACAACAACCTGCCTAGGCACTGAGGTA	2384
Db	2221	GAATGCAGGACCTCTGCCAGTGATGTGGACGCTGACAACAACCTGCCTAGGCACTGAGGTA	2280
Qy	2385	GCT	2387
Db	2281	GCT	2283

RESULT 12

AX528271/c

LOCUS AX528271 2281 bp DNA linear PAT 21-NOV-2002

DEFINITION Sequence 9 from Patent WO0206339.

ACCESSION AX528271

VERSION AX528271.1 GI:25172573

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Spaderna,S.K., Tchernev,V., Liu,X., Shenoy,S., Spytek,K., Zerhusen,B., Patturajan,M., Taupier,R.J., Rastelli,L., Grosse,W.M., Szekeres,E.S., Alsobrook,J.I., Lepley,D.M., Shen,L., Burgess,C.E., Shimkets,R.A. and Padigar,M.

TITLE Proteins and nucleic acids encoding same

JOURNAL Patent: WO 0206339-A 9 24-JAN-2002;

Curagen Corporation (US)

FEATURES

Location/Qualifiers

source

1. .2281

/organism="Homo sapiens"

/mol_type="unassigned DNA"

/db_xref="taxon:9606"

ORIGIN

Query Match 72.6%; Score 2281; DB 6; Length 2281;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	125	CCTGGACCCCTGGAGCCTCCTGGGCCTTTTCCTCTTCCAACCTGCTTCAGCTGCTGCTGCC	184
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Db	2281	 CCTGGACCCCTGGAGCCTCCTGGGCCTTTTCCTCTTCCAAGTCTTCAGCTGCTGCTGCC	2222
Qy	185	GACGACGACCGCGGGGGGAGGCGGGCAGGGGCCCATGCCCAGGGTCAGATACTATGCAGG	244
Db	2221	 GACGACGACCGCGGGGGGAGGCGGGCAGGGGCCCATGCCCAGGGTCAGATACTATGCAGG	2162
Qy	245	GGATGAACGTAGGGCACTTAGCTTCTTCCACCAGAAGGGCCTCCAGGATTTTGACACTCT	304
Db	2161	 GGATGAACGTAGGGCACTTAGCTTCTTCCACCAGAAGGGCCTCCAGGATTTTGACACTCT	2102
Qy	305	GCTCCTGAGTGGTGATGGAAATACTCTCTACGTGGGGGCTCGAGAAGCCATTCTGGCCTT	364
Db	2101	 GCTCCTGAGTGGTGATGGAAATACTCTCTACGTGGGGGCTCGAGAAGCCATTCTGGCCTT	2042
Qy	365	GGATATCCAGGATCCAGGGGTCCCCAGGCTAAAGAACATGATACCGTGGCCAGCCAGTGA	424
Db	2041	 GGATATCCAGGATCCAGGGGTCCCCAGGCTAAAGAACATGATACCGTGGCCAGCCAGTGA	1982
Qy	425	CAGAAAAAAGAGTGAATGTGCCTTTAAGAAGAAGAGCAATGAGACACAGTGTTCACACTT	484
Db	1981	 CAGAAAAAAGAGTGAATGTGCCTTTAAGAAGAAGAGCAATGAGACACAGTGTTCACACTT	1922
Qy	485	CATCCGTGTCCTGGTTTCTTACAATGTCACCCATCTCTACACCTGCGGCACCTTCGCCTT	544
Db	1921	 CATCCGTGTCCTGGTTTCTTACAATGTCACCCATCTCTACACCTGCGGCACCTTCGCCTT	1862
Qy	545	CAGCCCTGCTTGTACCTTCATTGAACCTCAAGATTCCCTACCTGTTGCCCATCTCGGAGGA	604
Db	1861	 CAGCCCTGCTTGTACCTTCATTGAACCTCAAGATTCCCTACCTGTTGCCCATCTCGGAGGA	1802
Qy	605	CAAGGTCATGGAGGGAAGAGCCAAAGCCCCTTTGACCCCGCTCACAAGCATACGGCTGT	664
Db	1801	 CAAGGTCATGGAGGGAAGAGCCAAAGCCCCTTTGACCCCGCTCACAAGCATACGGCTGT	1742
Qy	665	CTTGGTGGATGGGATGCTCTATTCTGGTACTATGAACAACCTCCTGGGCAGTGAGCCCAT	724
Db	1741	 CTTGGTGGATGGGATGCTCTATTCTGGTACTATGAACAACCTCCTGGGCAGTGAGCCCAT	1682
Qy	725	CCTGATGCGCACACTGGGATCCCAGCCTGTCCTCAAGACCGACAACCTCCTCCGCTGGCT	784
Db	1681	 CCTGATGCGCACACTGGGATCCCAGCCTGTCCTCAAGACCGACAACCTCCTCCGCTGGCT	1622
Qy	785	GCATCATGACGCCTCCTTTGTGGCAGCCATCCCTTCGACCCAGGTCGTCTACTTCTTCTT	844
Db	1621	 GCATCATGACGCCTCCTTTGTGGCAGCCATCCCTTCGACCCAGGTCGTCTACTTCTTCTT	1562
Qy	845	CGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAGAGGCTCCACACATCGCGGTGGCTAG	904
Db	1561	 CGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAGAGGCTCCACACATCGCGGTGGCTAG	1502
Qy	905	AGTCTGCAAGAATGACGTGGGCGGCGAAAAGCTGCTGCAGAAGAAGTGGACCACCTTCCT	964
Db	1501	 AGTCTGCAAGAATGACGTGGGCGGCGAAAAGCTGCTGCAGAAGAAGTGGACCACCTTCCT	1442
Qy	965	GAAGGCCAGCTGCTCTGCACCCAGCCGGGGCAGCTGCCCTTCAACGTCATCCGCCACGC	1024

Db	1441	GAAGGCCAGCTGCTCTGCACCCAGCCGGGGCAGCTGCCCTTCAACGTCATCCGCCACGC	1382
Qy	1025	GGTCCTGCTCCCCGCCGATTCTCCCACAGCTCCCCACATCTACGCAGTCTTCACCTCCCA	1084
Db	1381	GGTCCTGCTCCCCGCCGATTCTCCCACAGCTCCCCACATCTACGCAGTCTTCACCTCCCA	1322
Qy	1085	GTGGCAGGTTGGCGGGACCAGGAGCTCTGCGGTTTGTGCCTTCTCTCTTGGACATTGA	1144
Db	1321	GTGGCAGGTTGGCGGGACCAGGAGCTCTGCGGTTTGTGCCTTCTCTCTTGGACATTGA	1262
Qy	1145	ACGTGTCTTTAAGGGGAAATACAAAGAGTTGAACAAAGAACTTCACGCTGGACTACTTA	1204
Db	1261	ACGTGTCTTTAAGGGGAAATACAAAGAGTTGAACAAAGAACTTCACGCTGGACTACTTA	1202
Qy	1205	TAGGGGCCCTGAGACCAACCCCGGCCAGGCAGTTGCTCAGTGGGGCCCTCCTCTGATAA	1264
Db	1201	TAGGGGCCCTGAGACCAACCCCGGCCAGGCAGTTGCTCAGTGGGGCCCTCCTCTGATAA	1142
Qy	1265	GGCCCTGACCTTCATGAAGGACCATTTCCTGATGGATGAGCAAGTGGTGGGGACGCCCCCT	1324
Db	1141	GGCCCTGACCTTCATGAAGGACCATTTCCTGATGGATGAGCAAGTGGTGGGGACGCCCCCT	1082
Qy	1325	GCTGGTGAAATCTGGCGTGGAGTATACACGGCTTGCAAGTGGAGACAGCCAGGGCCTTGA	1384
Db	1081	GCTGGTGAAATCTGGCGTGGAGTATACACGGCTTGCAAGTGGAGACAGCCAGGGCCTTGA	1022
Qy	1385	TGGGCACAGCCATCTTGTATGTACCTGGGAACCACCACAGGGTCGCTCCACAAGGCTGT	1444
Db	1021	TGGGCACAGCCATCTTGTATGTACCTGGGAACCACCACAGGGTCGCTCCACAAGGCTGT	962
Qy	1445	GGTAAGTGGGGACAGCAGTGCTCATCTGGTGGAAGAGATTAGCTGTTCCCTGACCCTGA	1504
Db	961	GGTAAGTGGGGACAGCAGTGCTCATCTGGTGGAAGAGATTAGCTGTTCCCTGACCCTGA	902
Qy	1505	ACCTGTTTCGCAACCTGCAGCTGGCCCCACCCAGGGTGCAGTGTTTGTAGGCTTCTCAGG	1564
Db	901	ACCTGTTTCGCAACCTGCAGCTGGCCCCACCCAGGGTGCAGTGTTTGTAGGCTTCTCAGG	842
Qy	1565	AGGTGTCTGGAGGGTGCCCCGAGCCAACCTGTAGTGTCTATGAGAGCTGTGTGGACTGTGT	1624
Db	841	AGGTGTCTGGAGGGTGCCCCGAGCCAACCTGTAGTGTCTATGAGAGCTGTGTGGACTGTGT	782
Qy	1625	CCTTGCCCGGGACCCCCACTGTGCCTGGGACCTGAGTCCCGAACCTGTTGCCTCCTGTC	1684
Db	781	CCTTGCCCGGGACCCCCACTGTGCCTGGGACCTGAGTCCCGAACCTGTTGCCTCCTGTC	722
Qy	1685	TGCCCCAACCTGAACCTCCTGGAAGCAGGACATGGAGCGGGGAACCCAGAGTGGGCATG	1744
Db	721	TGCCCCAACCTGAACCTCCTGGAAGCAGGACATGGAGCGGGGAACCCAGAGTGGGCATG	662
Qy	1745	TGCCAGTGGCCCCATGAGCAGGAGCCTTCGGCCTCAGAGCCGCCCGCAAATCATTAAGA	1804
Db	661	TGCCAGTGGCCCCATGAGCAGGAGCCTTCGGCCTCAGAGCCGCCCGCAAATCATTAAGA	602
Qy	1805	AGTCCTGGCTGTCCCCAACTCCATCCTGGAGCTCCCCTGCCCCACCTGTCAGCCTTGGC	1864
Db	601	AGTCCTGGCTGTCCCCAACTCCATCCTGGAGCTCCCCTGCCCCACCTGTCAGCCTTGGC	542

Qy	1865	CTCTTATTATTGGAGTCATGGCCCAGCAGCAGTCCCAGAAGCCTCTTCCACTGTCTACAA	1924
Db	541	CTCTTATTATTGGAGTCATGGCCCAGCAGCAGTCCCAGAAGCCTCTTCCACTGTCTACAA	482
Qy	1925	TGGCTCCCTCTTGCTGATAGTGCAGGATGGAGTTGGGGGTCTCTACCACTGCTGGGCAAC	1984
Db	481	TGGCTCCCTCTTGCTGATAGTGCAGGATGGAGTTGGGGGTCTCTACCACTGCTGGGCAAC	422
Qy	1985	TGAGAATGGCTTTTCATACCCTGTGATCTCCTACTGGGTGGACAGCCAGGACCAGACCCT	2044
Db	421	TGAGAATGGCTTTTCATACCCTGTGATCTCCTACTGGGTGGACAGCCAGGACCAGACCCT	362
Qy	2045	GGCCCTGGATCCTGAACTGGCAGGCATCCCCGGGAGCATGTGAAGGTCCCGTTGACCAG	2104
Db	361	GGCCCTGGATCCTGAACTGGCAGGCATCCCCGGGAGCATGTGAAGGTCCCGTTGACCAG	302
Qy	2105	GGTCAGTGGTGGGGCCGCCCTGGCTGCCAGCAGTCCCTACTGGCCCCACTTTGTCACTGT	2164
Db	301	GGTCAGTGGTGGGGCCGCCCTGGCTGCCAGCAGTCCCTACTGGCCCCACTTTGTCACTGT	242
Qy	2165	CACTGTCCTCTTTGCCTTAGTGCTTTCAGGAGCCCTCATCATCCTCGTGGCCTCCCCATT	2224
Db	241	CACTGTCCTCTTTGCCTTAGTGCTTTCAGGAGCCCTCATCATCCTCGTGGCCTCCCCATT	182
Qy	2225	GAGAGCACTCCGGGCTCGGGGCAAGGTTCAAGGCTGTGAGACCCTGCGCCCTGGGGAGAA	2284
Db	181	GAGAGCACTCCGGGCTCGGGGCAAGGTTCAAGGCTGTGAGACCCTGCGCCCTGGGGAGAA	122
Qy	2285	GGCCCCGTTAAGCAGAGAGCAACACCTCCAGTCTCCCAAGGAATGCAGGACCTCTGCCAG	2344
Db	121	GGCCCCGTTAAGCAGAGAGCAACACCTCCAGTCTCCCAAGGAATGCAGGACCTCTGCCAG	62
Qy	2345	TGATGTGGACGCTGACAACAACCTGCCTAGGCACTGAGGTAGCTTAAACTCTAGGCACAGG	2404
Db	61	TGATGTGGACGCTGACAACAACCTGCCTAGGCACTGAGGTAGCTTAAACTCTAGGCACAGG	2
Qy	2405	C	2405
Db	1	C	1

RESULT 13

AX528269

LOCUS AX528269 2271 bp DNA linear PAT 21-NOV-2002

DEFINITION Sequence 7 from Patent WO0206339.

ACCESSION AX528269

VERSION AX528269.1 GI:25172572

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Spaderna,S.K., Tchernev,V., Liu,X., Shenoy,S., Spytek,K., Zerhusen,B., Patturajan,M., Taupier,R.J., Rastelli,L., Grosse,W.M., Szekeres,E.S., Alsobrook,J.I., Lepley,D.M., Shen,L., Burgess,C.E.,

Shimkets,R.A. and Padigaru,M.
TITLE Proteins and nucleic acids encoding same
JOURNAL Patent: WO 0206339-A 7 24-JAN-2002;
Curagen Corporation (US)

FEATURES Location/Qualifiers
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ORIGIN

Query Match 70.9%; Score 2228.4; DB 6; Length 2271;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 2260; Conservative 0; Mismatches 11; Indels 15; Gaps 1;

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Qy      165 CTGCTTCAGCTGCTGCTGCCGACGACGACCGCGGGGGAGGCGGGCAGGGGCCCATGCCC 224
        |||
Db       61 CTGCTTCAGCTGCTGCTGCCGACGACGACCGCGGGGGAGGCGGGCAGGGGCCCATGCCC 120

Qy      225 AGGGTCAGATACTATGCAGGGGATGAACGTAGGGCACTTAGCTTCTTCCACCAGAAGGGC 284
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Db      121 AGGGTCAGATACTATGCAGGGGATGAACGTAGGGCACTTAGCTTCTTCCACCAGAAGGGC 180

Qy      285 CTCCAGGATTTTGACACTCTGCTCCTGAGTGGTGATGGAAATACTCTCTACGTGGGGGCT 344
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Db      181 CTCCAGGATTTTGACACTCTGCTCCTGAGTGGTGATGGAAATACTCTCTACGTGGGGGCT 240

Qy      345 CGAGAAGCCATTCTGGCCTTGGATATCCAGGATCCAGGGGTCCCCAGGCTAAAGAACATG 404
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Db      241 CGAGAAGCCATTCTGGCCTTGGATATCCAGGATCCAGGGGTCCCCAGGCTAAAGAACATG 300

Qy      405 ATACCGTGGCCAGCCAGTGACAGAAAAAGAGTGAATGTGCCTTTAAGAAGAAGAGCAAT 464
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Db      301 ATACCGTGGCCAGCCAGTGACAGAAAAAGAGTGAATGTGCCTTTAAGAAGAAGAGCAAT 360

Qy      465 GAGACACAGTGTTTCAACTTCATCCGTGTCCTGGTTTCTTACAATGTCACCCATCTCTAC 524
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Db      361 GAGACACAGTGTTTCAACTTCATCCGTGTCCTGGTTTCTTACAATGTCACCCATCTCTAC 420

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Db      421 ACCTGCGGCACCTTCGCCTTCAGCCCTGCTTGTACCTTCATTGAACTTCAAGATTCTTAC 480

Qy      585 CTGTTGCCCATCTCGGAGGACAAGGTCATGGAGGGAAAAGGCCAAAGCCCCTTTGACCCC 644
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Db      481 CTGTTGCCCATCTCGGAGGACAAGGTCATGGAGGGAAAAGGCCAAAGCCCCTTTGACCCC 540

Qy      645 GCTCACAAGCATACGGCTGTCTTGGTGGATGGGATGCTCTATTCTGGTACTATGAACAAC 704
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Db	661	GACAACTTCCTCCGCTGGCTGCATCATGACGCCTCCTTTGTGGCAGCCATCCCTTCGACC	720
Qy	825	CAGGTCGTCTACTTCTTCTTCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAGAGGCTC	884
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Qy	885	CACACATCGCGGGTGGCTAGAGTCTGCAAGAATGACGTGGGCGGCGAAAAGCTGCTGCAG	944
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Qy	945	AAGAAGTGGACCACCTTCCTGAAGGCCAGCTGCTCTGCACCCAGCCGGGGCAGCTGCCC	1004
Db	841	AAGAAGTGGACCACCTTCCTGAAGGCCAGCTGCTCTGCACCCAGCCGGGGCAGCTGCCC	900
Qy	1005	TTCAACGTCATCCGCCACGCGGTCTGCTCCCCGCCGATTCTCCACAGCTCCCCACATC	1064
Db	901	TTCAACGTCATCCGCCACGCGGTCTGCTCCCCGCCGATTCTCCACAGCTCCCCACATC	960
Qy	1065	TACGCAGTCTTCACCTCCCAGTGGCAGGTTGGCGGGACCAGGAGCTCTGCGGTTTGTGCC	1124
Db	961	TACGCAGTCTTCACCTCCCAGTGGCAGGTTGGCGGGACCAGGAGCTCTGCGGTTTGTGCC	1020
Qy	1125	TTCTCTCTCTTGGACATTGAACGTGTCTTTAAGGGGAAATACAAAGAGTTGAACAAAGAA	1184
Db	1021	TTCTCTCTCTTGGACATTGAACGTGTCTTTAAGGGGAAATACAAAGAGTTGAACAAAGAA	1080
Qy	1185	ACTTCACGCTGGACTACTTATAGGGGCCCTGAGACCAACCCCCGGCCAGGCAGTTGCTCA	1244
Db	1081	ACTTCACGCTGGACTACTTATAGGGGCCCTGAGACCAACCCCCGGCCAGGCAGTTGCTCA	1140
Qy	1245	GTGGGCCCCCTCCTCTGATAAGGCCCTGACCTTCATGAAGGACCATTTCCTGATGGATGAG	1304
Db	1141	GTGGGCCCCCTCCTCTGATAAGGCCCTGACCTTCATGAAGGACCATTTCCTGATGGATGAG	1200
Qy	1305	CAAGTGGTGGGGACGCCCCTGCTGGTGAAATCTGGCGTGGAGTATACACGGCTTGCAGTG	1364
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Qy	1365	GAGACAGCCCAGGGCCTTGATGGGCACAGCCATCTTGTCATGTACCTGGGAACCACCACA	1424
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Qy	1425	GGGTCGCTCCACAAGGCTGTGGTAAGTGGGGACAGCAGTGCTCATCTGGTGGAAGAGATT	1484
Db	1321	GGGTCGCTCCACAAGGCTGTGGTAAGTGGGGACAGCAGTGCTCATCTGGTGGAAGAGATT	1380
Qy	1485	CAGCTGTTCCCTGACCCTGAACCTGTTGCAACCTGCAGCTGGCCCCACCCAGGGTGCA	1544
Db	1381	CAGCTGTTCCCTGACCCTGAACCTGTTGCAACCTGCAGCTGGCCCCACCCAGGGTGCA	1440
Qy	1545	GTGTTTGTAGGCTTCTCAGGAGGTGTCTGGAGGGTGCCCCGAGCCAACCTGTAGTGTCTAT	1604
Db	1441	GTGTTTGTAGGCTTCTCAGGAGGTGTCTGGAGGGTGCCCCGAGCCAACCTGTAGTGTCTAT	1500

Qy	1605	GAGAGCTGTGTGGACTGTGTCCTTGCCCCGGGACCCCCACTGTGCCTGGGACCCTGAGTCC	1664
Db	1501	GAGAGCTGTGTGGACTGTGTCCTTGCCCCGGGACCCCCACTGTGCCTGGGACCCTGAGTCC	1560
Qy	1665	CGAACCTGTTGCCTCCTGTCTGCCCCAACCTGAACTCCTGGAAGCAGGACATGGAGCGG	1724
Db	1561	CGACTCTGCTCTCT-----TAGGAACTCCTGGAAGCAGGACATGGAGCGG	1605
Qy	1725	GGGAACCCAGAGTGGGCATGTGCCAGTGGCCCCATGAGCAGGAGCCTTCGGCCTCAGAGC	1784
Db	1606	GGGAACCCAGAGTGGGCATGTGCCAGTGGCCCCATGAGCAGGAGCCTTCGGCCTCAGAGC	1665
Qy	1785	CGCCCGCAAATCATTAAGAAGTCCTGGCTGTCCCCAACTCCATCCTGGAGCTCCCCTGC	1844
Db	1666	CGCCCGCAAATCGTTAAAGAAGTCCTGGCTGTCCCCAACTCCATCCTGGAGCTCCCCTGC	1725
Qy	1845	CCCCACCTGTCAGCCTTGGCCTCTTATTATTGGAGTCATGGCCCAGCAGCAGTCCCAGAA	1904
Db	1726	CCCCACCTGTCAGCCTTGGCCTCTTATTATTGGAGTCATGGCCCAGCAGCAGTCCCAGAA	1785
Qy	1905	GCCTCTTCCACTGTCTACAATGGCTCCCTCTTGCTGATAGTGCAGGATGGAGTTGGGGGT	1964
Db	1786	GCCTCTTCCACTGTCTACAATGGCTCCCTCTTGCTGATAGTGCAGGATGGAGTTGGGGGT	1845
Qy	1965	CTCTACCAGTGCTGGGCAACTGAGAATGGCTTTTCATACCCTGTGATCTCCTACTGGGTG	2024
Db	1846	CTCTACCAGTGCTGGGCAACTGAGAATGGCTTTTCATACCCTGTGATCTCCTACTGGGTG	1905
Qy	2025	GACAGCCAGGACCAGACCTTGGCCCTGGATCCTGAACTGGCAGGCATCCCCGGGAGCAT	2084
Db	1906	GACAGCCAGGACCAGACCTTGGCCCTGGATCCTGAACTGGCAGGCATCCCCGGGAGCAT	1965
Qy	2085	GTGAAGGTCCCGTTGACCAGGGTCAGTGGTGGGGCCGCCCTGGCTGCCAGCAGTCTTAC	2144
Db	1966	GTGAAGGTCCCGTTGACCAGGGTCAGTGGTGGGGCCGCCCTGGCTGCCAGCAGTCTTAC	2025
Qy	2145	TGGCCCCACTTTGTCACTGTCACTGTCTCTTTGCCTTAGTGCTTTCAGGAGCCCTCATC	2204
Db	2026	TGGCCCCACTTTGTCACTGTCACTGTCTCTTTGCCTTAGTGCTTTCAGGAGCCCTCATC	2085
Qy	2205	ATCCTCGTGGCCTCCCCATTGAGAGCACTCCGGGCTCGGGGCAAGGTTTCAGGGCTGTGAG	2264
Db	2086	ATCCTCGTGGCCTCCCCATTGAGAGCACTCCGGGCTCGGGGCAAGGTTTCAGGGCTGTGAG	2145
Qy	2265	ACCCTGCGCCCTGGGGAGAAGGCCCCGTTAAGCAGAGAGCAACACCTCCAGTCTCCCAAG	2324
Db	2146	ACCCTGCGCCCTGGGGAGAAGGCCCCGTTAAGCAGAGAGCAACACCTCCAGTCTCCCAAG	2205
Qy	2325	GAATGCAGGACCTCTGCCAGTGATGTGGACGCTGACAACAACCTGCCTAGGCACTGAGGTA	2384
Db	2206	GAATGCAGGACCTCTGCCAGTGATGTGGACGCTGACAACAACCTGCCTAGGCACTGAGGTA	2265
Qy	2385	GCTTAA 2390	
Db	2266	GCTTAA 2271	

RESULT 14

BD157628

LOCUS BD157628 1838 bp DNA linear PAT 17-JAN-2003

DEFINITION Primer for synthesizing full-length cDNA and use thereof.

ACCESSION BD157628

VERSION BD157628.1 GI:27863386

KEYWORDS JP 2002191363-A/12471.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1838)

AUTHORS Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J., Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T.

TITLE Primer for synthesizing full-length cDNA and use thereof

JOURNAL Patent: JP 2002191363-A 12471 09-JUL-2002;

HELIX RESEARCH INSTITUTE

COMMENT OS Homo sapiens (human)

PN JP 2002191363-A/12471

PD 09-JUL-2002

PF 28-JUL-2000 JP 2000280990

PI TOSHIO OTA,TAKAO ISOGAI,TETSUO NISHIKAWA,KOJI HAYASHI,KAORU

PI SAITO,

PI JUNICHI YAMAMOTO,SHIZUKO ISHII,TOMOYASU SUGIYAMA,AI WAKAMATSU,

PI KEIICHI NAGAI,TETSUJI OTSUKI

PC

C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/ 10,

PC C12P21/02,C12Q1/68//C12P21/08,G06F17/30,C12N15/00,C12N5/00 CC Primer for synthesizing full-length cDNA and use thereof FH Key

Location/Qualifiers

FT CDS (106)..(1089).

FEATURES Location/Qualifiers

source 1..1838

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ORIGIN

Query Match 58.4%; Score 1834.8; DB 6; Length 1838;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 1836; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1299 GATGAGCAAGTGGTGGGGACGCCCCTGCTGGTGAAATCTGGCGTGGAGTATACACGGCTT 1358
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Db 61 GCAGTGGAGACAGCCAGGGCCTTGATGGGCACAGCCATCTTGTCATGTACCTGGGAACC 120

Qy 1419 ACCACAGGGTCGCTCCACAAGGCTGTGGTAAGTGGGGACAGCAGTGCTCATCTGGTGGAA 1478
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Db 121 ACCACAGGGTCGCTCCACAAGGCTGTGGTAAGTGGGGACAGCAGTGCTCATCTGGTGGAA 180

Qy 1479 GAGATTGAGCTGTTCCCTGACCCTGAACCTGTTGCAACCTGCAGCTGGCCCCCAG 1538

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Db	241	 GGTGCAGTGTGTTGTAGGCTTCTCAGGAGGTGTCTGGAGGGTGCCCCGAGCCAACTGTAGT	300
Qy	1599	GTCTATGAGAGCTGTGTGGACTGTGTCTTGCCCGGGACCCCCACTGTGCCTGGGACCCT	1658
Db	301	 GTCTATGAGAGCTGTGTGGACTGTGTCTTGCCCGGGACCCCCACTGTGCCTGGGACCCT	360
Qy	1659	GAGTCCCGAACCTGTTGCCTCCTGTCTGCCCCAACCTGAACTCCTGGAAGCAGGACATG	1718
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Qy	1719	GAGCGGGGGAACCCAGAGTGGGCATGTGCCAGTGGCCCCATGAGCAGGAGCCTTCGGCCT	1778
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Qy	2559	CAGTCTGCCTCCCCTATGGGACTCCCTTCTACCAAGCACATGAGCTCTCTAACAGGGTGG	2618
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LOCUS AX879068 1838 bp DNA linear PAT 17-DEC-2003
 DEFINITION Sequence 13973 from Patent EP1074617.
 ACCESSION AX879068
 VERSION AX879068.1 GI:40033804
 KEYWORDS .
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 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1
 AUTHORS Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J.,
 Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T.
 TITLE Primers for synthesising full-length cDNA and their use
 JOURNAL Patent: EP 1074617-A 13973 07-FEB-2001;
 Research Association for Biotechnology (JP)
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 /organism="Homo sapiens"
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ORIGIN

Query Match 58.4%; Score 1834.8; DB 6; Length 1838;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 1836; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy	1299	GATGAGCAAGTGGTGGGGACGCCCCTGCTGGTGAAATCTGGCGTGGAGTATACACGGCTT	1358
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Qy	1359	GCAGTGGAGACAGCCCAGGGCCTTGATGGGCACAGCCATCTTGTTCATGTACCTGGGAACC	1418
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Qy	1479	GAGATTTCAGCTGTTCCCTGACCCTGAACCTGTTTCGCAACCTGCAGCTGGCCCCACCCAG	1538
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Qy	1659	GAGTCCCGAACCTGTTGCCTCCTGTCTGCCCCAACCTGAACTCCTGGAAGCAGGACATG	1718
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Qy	1719	GAGCGGGGGAACCCAGAGTGGGCATGTGCCAGTGGCCCCATGAGCAGGAGCCTTCGGCCT	1778
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Qy	1779	CAGAGCCGCCCGCAAATCATTAAGAAGTCCTGGCTGTCCCCAACTCCATCCTGGAGCTC	1838
Db	481	CAGAGCCGCCCGCAAATCATTAAGAAGTCCTGGCTGTCCCTAACTCCATCCTGGAGCTC	540
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Db	661	GGGGTCTCTACCAGTGCTGGGCAACTGAGAATGGCTTTTCATACCCTGTGATCTCCTAC	720
Qy	2019	TGGGTGGACAGCCAGGACCAGACCCTGGCCCTGGATCCTGAACTGGCAGGCATCCCCGG	2078
Db	721	TGGGTGGACAGCCAGGACCAGACCCTGGCCCTGGATCCTGAACTGGCAGGCATCCCCGG	780
Qy	2079	GAGCATGTGAAGGTCCCGTTGACCAGGGTCAGTGGTGGGGCCGCCCTGGCTGCCCAGCAG	2138
Db	781	GAGCATGTGAAGGTCCCGTTGACCAGGGTCAGTGGTGGGGCCGCCCTGGCTGCCCAGCAG	840
Qy	2139	TCCTACTGGCCCCACTTTGTCACTGTCACTGTCCCTCTTGCCCTTAGTGCTTTCAGGAGCC	2198
Db	841	TCCTACTGGCCCCACTTTGTCACTGTCACTGTCCCTCTTGCCCTTAGTGCTTTCAGGAGCC	900
Qy	2199	CTCATCATCCTCGTGGCCTCCCCATTGAGAGCACTCCGGGCTCGGGGCAAGGTTTCAGGGC	2258
Db	901	CTCATCATCCTCGTGGCCTCCCCATTGAGAGCACTCCGGGCTCGGGGCAAGGTTTCAGGGC	960
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Qy	2379	GAGGTAGCTTAAACTCTAGGCACAGGCCGGGGCTGCGGTGCAGGCACCTGGCCATGCTGG	2438
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Db	1141	CTGGGCGGCCCAAGCACAGCCCTGACTAGGATGACAGCAGCACAAAAGACCACCTTTCTC	1200
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Qy	2619	GGGCTACCCCCAGACCTGCTCCTACACTGATATTGAAGAACCCTGGAGAGGATCCTTCAGT	2678
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Qy	2679	TCTGGCCATTCCAGGGACCCCTCCAGAAACACAGTGTTTCAAGAGACCCTAACCAACCTGC	2738
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Qy	2979	CCCTTCTGCCCTGGCAGAATGGCAGGGGTAATCTGAGCCTTCTTCACTCCTTTACCCTAG	3038
Db	1681	CCCTTCTGCCCTGGCAGAATGGCAGGGGTAATCTGAGCCTTCTTCACTCCTTTACCCTAG	1740
Qy	3039	CTGACCCCTTCACCTCTCCCCCTCCCTTTTCCTTTGTTTTGGGATTGAGAAAAGTCTTG	3098
Db	1741	CTGACCCCTTCACCTCTCCCCCTCCCTTTTCCTTTGTTTTGGGATTGAGAAAAGTCTTG	1800
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(without alignments)
11585.148 Million cell updates/sec

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Gapop 10.0 , Gapext 1.0
Searched: 4390206 seqs, 2959870667 residues
Total number of hits satisfying chosen parameters: 8780412
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
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Listing first 1500 summaries

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- 11: geneseqn2003ds:*
- 12: geneseqn2004as:*
- 13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ID	AAC58392 standard; cDNA; 3143 BP.					
DE	Human PRO1317 nucleotide sequence SEQ ID NO:70.					
PN	WO200053755-A2.					
PD	14-SEP-2000.					
PA	(GETH) GENENTECH INC.					
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	Best Local Similarity	100.0%;	Pred. No. 0;			
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ID	ACD68436 standard; cDNA; 3143 BP.					
DE	Novel human secreted and transmembrane protein PRO1317 cDNA.					
PN	US2003073130-A1.					
PD	17-APR-2003.					
PA	(GETH) GENENTECH INC.					
	Query Match	100.0%;	Score 3143;	DB 9;	Length 3143;	
	Best Local Similarity	100.0%;	Pred. No. 0;			
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ID	ACH04538 standard; cDNA; 3143 BP.					
DE	Human cDNA encoding secreted/transmembrane protein PRO1317.					
PN	US2003044841-A1.					
PD	06-MAR-2003.					
PA	(GETH) GENENTECH INC.					

Query Match 100.0%; Score 3143; DB 9; Length 3143;
 Best Local Similarity 100.0%; Pred. No. 0;

RESULT 4

ID ACD68082 standard; cDNA; 3143 BP.
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 PN US2003073129-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 3143; DB 9; Length 3143;
 Best Local Similarity 100.0%; Pred. No. 0;

RESULT 5

ID ADC18145 standard; cDNA; 3143 BP.
 DE Human PRO polynucleotide #79.
 PN US2003064925-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 3143; DB 10; Length 3143;
 Best Local Similarity 100.0%; Pred. No. 0;

RESULT 6

ID ADD70791 standard; cDNA; 3143 BP.
 DE Human cDNA encoding secreted/transmembrane protein PRO1317.
 PN US2003099625-A1.
 PD 29-MAY-2003.
 PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 3143; DB 10; Length 3143;
 Best Local Similarity 100.0%; Pred. No. 0;

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ID ADD39868 standard; cDNA; 3143 BP.
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 PN US2003083462-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 3143; DB 10; Length 3143;
 Best Local Similarity 100.0%; Pred. No. 0;

RESULT 8

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 DE Human cDNA encoding secreted/transmembrane protein PRO1317.
 PN US2003054406-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC.

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 Best Local Similarity 100.0%; Pred. No. 0;

RESULT 9

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 PN US2003096955-A1.
 PD 22-MAY-2003.
 PA (GETH) GENENTECH INC.

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 Best Local Similarity 100.0%; Pred. No. 0;

RESULT 10

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 DE Human cDNA encoding secreted/transmembrane protein PRO1317.
 PN US2003096954-A1.
 PD 22-MAY-2003.
 PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 3143; DB 10; Length 3143;

Best Local Similarity 100.0%; Pred. No. 0;

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ID ADD38914 standard; cDNA; 3143 BP.

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PN US2003092061-A1.

PD 15-MAY-2003.

PA (GETH) GENENTECH INC.

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Best Local Similarity 100.0%; Pred. No. 0;

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PN US2003082627-A1.

PD 01-MAY-2003.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 3143; DB 10; Length 3143;

Best Local Similarity 100.0%; Pred. No. 0;

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PN US2003069179-A1.

PD 10-APR-2003.

PA (GETH) GENENTECH INC.

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Best Local Similarity 100.0%; Pred. No. 0;

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PN US2003092883-A1.

PD 15-MAY-2003.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 3143; DB 10; Length 3143;

Best Local Similarity 100.0%; Pred. No. 0;

RESULT 15

ID ADE50089 standard; cDNA; 3143 BP.

DE Human cDNA encoding secreted/transmembrane protein PRO1317.

PN US2003082626-A1.

PD 01-MAY-2003.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 3143; DB 10; Length 3143;

Best Local Similarity 100.0%; Pred. No. 0;

RESULT 16

ID ADE21647 standard; cDNA; 3143 BP.

DE Human cDNA encoding secreted/transmembrane protein PRO1317.

PN US2003082628-A1.

PD 01-MAY-2003.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 3143; DB 10; Length 3143;

Best Local Similarity 100.0%; Pred. No. 0;

RESULT 17

ID ADF30072 standard; cDNA; 3143 BP.

DE Human cDNA encoding secreted/transmembrane protein PRO1317.

PN US2003204053-A1.

PD 30-OCT-2003.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 3143; DB 10; Length 3143;

Best Local Similarity 100.0%; Pred. No. 0;

RESULT 18

ID ADF55965 standard; cDNA; 3143 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1317.
PN US2003204054-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3143; DB 10; Length 3143;
Best Local Similarity 100.0%; Pred. No. 0;

RESULT 19

ID ADH99469 standard; cDNA; 3143 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1317.
PN US2003065142-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3143; DB 10; Length 3143;
Best Local Similarity 100.0%; Pred. No. 0;

RESULT 20

ID ADE96649 standard; cDNA; 3143 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1317.
PN US2003195347-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3143; DB 12; Length 3143;
Best Local Similarity 100.0%; Pred. No. 0;

RESULT 21

ID ADF25960 standard; cDNA; 3143 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1317.
PN US2003199675-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3143; DB 12; Length 3143;
Best Local Similarity 100.0%; Pred. No. 0;

RESULT 22

ID ADF24859 standard; cDNA; 3143 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1317.
PN US2003198993-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3143; DB 12; Length 3143;
Best Local Similarity 100.0%; Pred. No. 0;

RESULT 23

ID ADF29595 standard; cDNA; 3143 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1317.
PN US2003203401-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3143; DB 12; Length 3143;
Best Local Similarity 100.0%; Pred. No. 0;

RESULT 24

ID ADE97126 standard; cDNA; 3143 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1317.
PN US2003195334-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3143; DB 12; Length 3143;
Best Local Similarity 100.0%; Pred. No. 0;

RESULT 25

ID ADH03164 standard; cDNA; 3143 BP.
 DE Human cDNA encoding secreted/transmembrane protein PRO1317.
 PN US2003216562-A1.
 PD 20-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 3143; DB 12; Length 3143;
 Best Local Similarity 100.0%; Pred. No. 0;
 RESULT 26
 ID ADH04118 standard; cDNA; 3143 BP.
 DE Human cDNA encoding secreted/transmembrane protein PRO1317.
 PN US2003220471-A1.
 PD 27-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 3143; DB 12; Length 3143;
 Best Local Similarity 100.0%; Pred. No. 0;
 RESULT 27
 ID ADH03641 standard; cDNA; 3143 BP.
 DE Human cDNA encoding secreted/transmembrane protein PRO1317.
 PN US2003224478-A1.
 PD 04-DEC-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 3143; DB 12; Length 3143;
 Best Local Similarity 100.0%; Pred. No. 0;
 RESULT 28
 ID ADH04595 standard; cDNA; 3143 BP.
 DE Human cDNA encoding secreted/transmembrane protein PRO1317.
 PN US2004005626-A1.
 PD 08-JAN-2004.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 3143; DB 12; Length 3143;
 Best Local Similarity 100.0%; Pred. No. 0;
 RESULT 29
 ID ADH61596 standard; cDNA; 3143 BP.
 DE Human cDNA encoding secreted/transmembrane protein PRO1317.
 PN US2004014130-A1.
 PD 22-JAN-2004.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 3143; DB 12; Length 3143;
 Best Local Similarity 100.0%; Pred. No. 0;
 RESULT 30
 ID ADL94795 standard; cDNA; 3143 BP.
 DE Human cDNA encoding secreted/transmembrane protein PRO1317.
 PN US2004073015-A1.
 PD 15-APR-2004.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 3143; DB 12; Length 3143;
 Best Local Similarity 100.0%; Pred. No. 0;
 RESULT 31
 ID AAA37100 standard; cDNA; 3142 BP.
 DE Human PRO1317 (UNQ783) cDNA sequence SEQ ID NO:276.
 PN WO200012708-A2.
 PD 09-MAR-2000.
 PA (GETH) GENENTECH INC.
 Query Match 99.6%; Score 3131; DB 3; Length 3142;
 Best Local Similarity 100.0%; Pred. No. 0;
 RESULT 32
 ID AAF54397 standard; DNA; 3075 BP.

DE DNA encoding protein of the invention #77.
 PN WO200078961-A1.
 PD 28-DEC-2000.
 PA (GETH) GENENTECH INC.
 Query Match 97.8%; Score 3075; DB 4; Length 3075;
 Best Local Similarity 100.0%; Pred. No. 0;
 RESULT 33
 ID ADP25056 standard; cDNA; 3257 BP.
 DE PRO polypeptide encoding cDNA SEQ ID NO:2234.
 PN WO2004041170-A2.
 PD 21-MAY-2004.
 PA (GETH) GENENTECH INC.
 Query Match 97.6%; Score 3068.4; DB 13; Length 3257;
 Best Local Similarity 100.0%; Pred. No. 0;
 RESULT 34
 ID ADF60955 standard; cDNA; 3505 BP.
 DE DNA demethylating agent treated cell differentially expressed cDNA #13.
 PN US2003165864-A1.
 PD 04-SEP-2003.
 PA (LASE/) LASEK A W.
 PA (JONE/) JONES D A.
 Query Match 97.4%; Score 3060.8; DB 10; Length 3505;
 Best Local Similarity 99.9%; Pred. No. 0;
 RESULT 35
 ID ADD67570 standard; cDNA; 3252 BP.
 DE Human Ly667S encoding cDNA SEQ ID NO:47.
 PN WO2003062401-A2.
 PD 31-JUL-2003.
 PA (CORI-) CORIXA CORP.
 Query Match 96.8%; Score 3041.4; DB 10; Length 3252;
 Best Local Similarity 99.4%; Pred. No. 0;
 RESULT 36
 ID AAF45125 standard; cDNA; 3104 BP.
 DE Human TANGO 265 cDNA.
 PN WO200077239-A2.
 PD 21-DEC-2000.
 PA (MILL-) MILLENNIUM PHARM INC.
 Query Match 96.7%; Score 3040.8; DB 5; Length 3104;
 Best Local Similarity 99.9%; Pred. No. 0;
 RESULT 37
 ID ABX94103 standard; cDNA; 3104 BP.
 DE cDNA encoding human TANGO 265.
 PN US2002182675-A1.
 PD 05-DEC-2002.
 PA (MILL-) MILLENNIUM PHARM INC.
 Query Match 96.7%; Score 3040.8; DB 8; Length 3104;
 Best Local Similarity 99.9%; Pred. No. 0;
 RESULT 38
 ID ACD66780 standard; cDNA; 3104 BP.
 DE Secreted polypeptide-related cDNA #56.
 PN US2003022279-A1.
 PD 30-JAN-2003.
 PA (FRAS/) FRASER C C.
 PA (BARN/) BARNES T M.
 PA (SHAR/) SHARP J D.
 PA (KIRS/) KIRST S J.
 PA (MYER/) MYERS P S.

PA (LEIB/) LEIBY K R.
 PA (HOLT/) HOLTZMAN D A.
 PA (MCCA/) MCCARTHY S A.
 PA (WRIG/) WRIGHTON N.
 PA (MACK/) MACKAY C R.
 PA (GOOD/) GOODEARL A D J.
 Query Match 96.7%; Score 3040.8; DB 8; Length 3104;
 Best Local Similarity 99.9%; Pred. No. 0;
 RESULT 39
 ID ADQ10373 standard; cDNA; 3104 BP.
 DE Human polynucleotide #71.
 PN US2004121396-A1.
 PD 24-JUN-2004.
 PA (MILL-) MILLENNIUM PHARM INC.
 Query Match 96.7%; Score 3040.8; DB 12; Length 3104;
 Best Local Similarity 99.9%; Pred. No. 0;
 RESULT 40
 ID ADQ98237 standard; cDNA; 3104 BP.
 DE Human polynucleotide #5.
 PN US6764677-B1.
 PD 20-JUL-2004.
 PA (MILL-) MILLENNIUM PHARM INC.
 Query Match 96.7%; Score 3040.8; DB 12; Length 3104;
 Best Local Similarity 99.9%; Pred. No. 0;
 RESULT 41
 ID AAC69084 standard; DNA; 3191 BP.
 DE Human secreted protein gene 1 clone HTDAA93.
 PN WO200055371-A1.
 PD 21-SEP-2000.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 96.6%; Score 3035.8; DB 3; Length 3191;
 Best Local Similarity 99.7%; Pred. No. 0;
 RESULT 42
 ID AAK53428 standard; cDNA; 3042 BP.
 DE Human polynucleotide SEQ ID NO 3941.
 PN WO200157190-A2.
 PD 09-AUG-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match 96.4%; Score 3029.8; DB 4; Length 3042;
 Best Local Similarity 99.9%; Pred. No. 0;
 RESULT 43
 ID ABX13628 standard; cDNA; 3042 BP.
 DE Human cytokine or cell proliferation/differentiation protein cDNA #5.
 PN US2002137044-A1.
 PD 26-SEP-2002.
 PA (TANG/) TANG Y T.
 PA (ZHOU/) ZHOU P.
 PA (GOOD/) GOODRICH R.
 PA (LIUC/) LIU C.
 PA (ASUN/) ASUNDI V.
 PA (WEHR/) WEHRMAN T.
 PA (YANG/) YANG Y.
 PA (DRMA/) DRMANAC R T.
 Query Match 96.3%; Score 3028.2; DB 8; Length 3042;
 Best Local Similarity 99.9%; Pred. No. 0;
 RESULT 44
 ID ACC69002 standard; cDNA; 3146 BP.

DE Human neurotransmission-associated protein NTRAN-24 cDNA SEQ ID NO:49.
PN WO2003025129-A2.
PD 27-MAR-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 91.0%; Score 2860.4; DB 10; Length 3146;
Best Local Similarity 96.7%; Pred. No. 0;

RESULT 45
ID ADB62165 standard; cDNA; 2981 BP.
DE Human cDNA encoding clone CTONG20017490.
PN EP1308459-A2.
PD 07-MAY-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 85.3%; Score 2682.2; DB 10; Length 2981;
Best Local Similarity 96.5%; Pred. No. 0;

RESULT 46
ID ACN42096 standard; cDNA; 3033 BP.
DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:971.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 78.9%; Score 2479.6; DB 13; Length 3033;
Best Local Similarity 90.9%; Pred. No. 0;

RESULT 47
ID ABS64946 standard; cDNA; 2768 BP.
DE Human cDNA for SECP11, Incyte ID No. 7487507CB1.
PN WO200262841-A2.
PD 15-AUG-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 78.8%; Score 2476.4; DB 6; Length 2768;
Best Local Similarity 96.5%; Pred. No. 0;

RESULT 48
ID ACN43554 standard; cDNA; 3188 BP.
DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:2429.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 78.4%; Score 2464.6; DB 13; Length 3188;
Best Local Similarity 87.1%; Pred. No. 0;

RESULT 49
ID ACC68985 standard; cDNA; 2745 BP.
DE Human neurotransmission-associated protein NTRAN-7 cDNA SEQ ID NO:32.
PN WO2003025129-A2.
PD 27-MAR-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 77.5%; Score 2437; DB 10; Length 2745;
Best Local Similarity 96.1%; Pred. No. 0;

RESULT 50
ID ACN43555 standard; cDNA; 3165 BP.
DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:2430.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 76.1%; Score 2392.8; DB 13; Length 3165;
Best Local Similarity 86.8%; Pred. No. 0;

RESULT 51
ID ACN43551 standard; cDNA; 3342 BP.

DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:2426.
 PN WO2004023973-A2.
 PD 25-MAR-2004.
 PA (INCY-) INCYTE CORP.
 Query Match 76.1%; Score 2391.6; DB 13; Length 3342;
 Best Local Similarity 86.9%; Pred. No. 0;
 RESULT 52
 ID ACN43552 standard; cDNA; 3333 BP.
 DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:2427.
 PN WO2004023973-A2.
 PD 25-MAR-2004.
 PA (INCY-) INCYTE CORP.
 Query Match 76.1%; Score 2390.6; DB 13; Length 3333;
 Best Local Similarity 86.9%; Pred. No. 0;
 RESULT 53
 ID ACN43553 standard; cDNA; 3316 BP.
 DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:2428.
 PN WO2004023973-A2.
 PD 25-MAR-2004.
 PA (INCY-) INCYTE CORP.
 Query Match 74.4%; Score 2339.6; DB 13; Length 3316;
 Best Local Similarity 86.1%; Pred. No. 0;
 RESULT 54
 ID AAF45126 standard; cDNA; 2283 BP.
 DE Human TANGO 265 ORF.
 PN WO200077239-A2.
 PD 21-DEC-2000.
 PA (MILL-) MILLENNIUM PHARM INC.
 Query Match 72.6%; Score 2283; DB 5; Length 2283;
 Best Local Similarity 100.0%; Pred. No. 0;
 RESULT 55
 ID ACD66781 standard; cDNA; 2283 BP.
 DE Secreted polypeptide-related cDNA #57.
 PN US2003022279-A1.
 PD 30-JAN-2003.
 PA (FRAS/) FRASER C C.
 PA (BARN/) BARNES T M.
 PA (SHAR/) SHARP J D.
 PA (KIRS/) KIRST S J.
 PA (MYER/) MYERS P S.
 PA (LEIB/) LEIBY K R.
 PA (HOLT/) HOLTZMAN D A.
 PA (MCCA/) MCCARTHY S A.
 PA (WRIG/) WRIGHTON N.
 PA (MACK/) MACKAY C R.
 PA (GOOD/) GOODEARL A D J.
 Query Match 72.6%; Score 2283; DB 8; Length 2283;
 Best Local Similarity 100.0%; Pred. No. 0;
 RESULT 56
 ID ADQ10374 standard; cDNA; 2283 BP.
 DE Human polynucleotide #72.
 PN US2004121396-A1.
 PD 24-JUN-2004.
 PA (MILL-) MILLENNIUM PHARM INC.
 Query Match 72.6%; Score 2283; DB 12; Length 2283;
 Best Local Similarity 100.0%; Pred. No. 0;
 RESULT 57

ID ADQ98238 standard; cDNA; 2283 BP.
 DE Human polynucleotide #6.
 PN US6764677-B1.
 PD 20-JUL-2004.
 PA (MILL-) MILLENNIUM PHARM INC.
 Query Match 72.6%; Score 2283; DB 12; Length 2283;
 Best Local Similarity 100.0%; Pred. No. 0;
 RESULT 58
 ID AAD28945 standard; cDNA; 2281 BP.
 DE Human MOL3b cDNA.
 PN WO200206339-A2.
 PD 24-JAN-2002.
 PA (CURA-) CURAGEN CORP.
 Query Match 72.6%; Score 2281; DB 6; Length 2281;
 Best Local Similarity 100.0%; Pred. No. 0;
 RESULT 59
 ID ADD18199 standard; DNA; 2281 BP.
 DE Human molecule (MOL) protein MOL3b DNA sequence.
 PN WO2003003984-A2.
 PD 16-JAN-2003.
 PA (CURA-) CURAGEN CORP.
 Query Match 72.6%; Score 2281; DB 10; Length 2281;
 Best Local Similarity 100.0%; Pred. No. 0;
 RESULT 60
 ID AAD28944 standard; cDNA; 2271 BP.
 DE Human MOL3a cDNA.
 PN WO200206339-A2.
 PD 24-JAN-2002.
 PA (CURA-) CURAGEN CORP.
 Query Match 70.9%; Score 2228.4; DB 6; Length 2271;
 Best Local Similarity 98.9%; Pred. No. 0;
 RESULT 61
 ID ADD18197 standard; DNA; 2271 BP.
 DE Human molecule (MOL) protein MOL3a DNA sequence.
 PN WO2003003984-A2.
 PD 16-JAN-2003.
 PA (CURA-) CURAGEN CORP.
 Query Match 70.9%; Score 2228.4; DB 10; Length 2271;
 Best Local Similarity 98.9%; Pred. No. 0;
 RESULT 62
 ID ACC69003 standard; cDNA; 2238 BP.
 DE Human neurotransmission-associated protein NTRAN-25 cDNA SEQ ID NO:50.
 PN WO2003025129-A2.
 PD 27-MAR-2003.
 PA (INCY-) INCYTE GENOMICS INC.
 Query Match 67.0%; Score 2104.8; DB 10; Length 2238;
 Best Local Similarity 95.5%; Pred. No. 0;
 RESULT 63
 ID ACN43550 standard; cDNA; 2670 BP.
 DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:2425.
 PN WO2004023973-A2.
 PD 25-MAR-2004.
 PA (INCY-) INCYTE CORP.
 Query Match 66.9%; Score 2104; DB 13; Length 2670;
 Best Local Similarity 84.7%; Pred. No. 0;
 RESULT 64
 ID ACN43547 standard; cDNA; 2838 BP.

DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:2422.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 66.9%; Score 2101.8; DB 13; Length 2838;
Best Local Similarity 84.8%; Pred. No. 0;
RESULT 65
ID ACN43548 standard; cDNA; 2830 BP.
DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:2423.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 66.4%; Score 2085.8; DB 13; Length 2830;
Best Local Similarity 84.5%; Pred. No. 0;
RESULT 66
ID ACN43549 standard; cDNA; 2759 BP.
DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:2424.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 61.8%; Score 1943.8; DB 13; Length 2759;
Best Local Similarity 82.2%; Pred. No. 0;
RESULT 67
ID ADQ86307 standard; cDNA; 1838 BP.
DE Human tumour-associated antigenic target (TAT) cDNA sequence #3179.
PN WO2004060270-A2.
PD 22-JUL-2004.
PA (GETH) GENENTECH INC.
PA (WUTD/) WU T D.
PA (ZHOU/) ZHOU Y.
Query Match 58.5%; Score 1838; DB 12; Length 1838;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 68
ID ADQ83210 standard; cDNA; 1838 BP.
DE Human tumour-associated antigenic target (TAT) cDNA sequence #24.
PN WO2004060270-A2.
PD 22-JUL-2004.
PA (GETH) GENENTECH INC.
PA (WUTD/) WU T D.
PA (ZHOU/) ZHOU Y.
Query Match 58.5%; Score 1838; DB 12; Length 1838;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 69
ID ADQ83890 standard; cDNA; 1838 BP.
DE Human tumour-associated antigenic target (TAT) cDNA sequence #704.
PN WO2004060270-A2.
PD 22-JUL-2004.
PA (GETH) GENENTECH INC.
PA (WUTD/) WU T D.
PA (ZHOU/) ZHOU Y.
Query Match 58.5%; Score 1838; DB 12; Length 1838;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 70
ID ADQ85119 standard; cDNA; 1838 BP.
DE Human tumour-associated antigenic target (TAT) cDNA sequence #1933.
PN WO2004060270-A2.
PD 22-JUL-2004.

PA (GETH) GENENTECH INC.
PA (WUTD/) WU T D.
PA (ZHOU/) ZHOU Y.
Query Match 58.5%; Score 1838; DB 13; Length 1838;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 71
ID AAH15636 standard; cDNA; 1838 BP.
DE Human cDNA sequence SEQ ID NO:13973.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 58.4%; Score 1834.8; DB 4; Length 1838;
Best Local Similarity 99.9%; Pred. No. 0;
RESULT 72
ID AAF45137 standard; cDNA; 3046 BP.
DE Murine semaphorin B cDNA.
PN WO200077239-A2.
PD 21-DEC-2000.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 55.0%; Score 1727.6; DB 5; Length 3046;
Best Local Similarity 76.0%; Pred. No. 0;
RESULT 73
ID AAF45140 standard; cDNA; 3046 BP.
DE Murine DNA: SEQ ID 77.
PN WO200077239-A2.
PD 21-DEC-2000.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 55.0%; Score 1727.6; DB 5; Length 3046;
Best Local Similarity 76.0%; Pred. No. 0;
RESULT 74
ID ACD26369 standard; cDNA; 3046 BP.
DE Secreted polypeptide-related cDNA #80.
PN US2003022279-A1.
PD 30-JAN-2003.
PA (FRAS/) FRASER C C.
PA (BARN/) BARNES T M.
PA (SHAR/) SHARP J D.
PA (KIRS/) KIRST S J.
PA (MYER/) MYERS P S.
PA (LEIB/) LEIBY K R.
PA (HOLT/) HOLTZMAN D A.
PA (MCCA/) MCCARTHY S A.
PA (WRIG/) WRIGHTON N.
PA (MACK/) MACKAY C R.
PA (GOOD/) GOODEARL A D J.
Query Match 55.0%; Score 1727.6; DB 8; Length 3046;
Best Local Similarity 76.0%; Pred. No. 0;
RESULT 75
ID ACD26370 standard; cDNA; 3046 BP.
DE Secreted polypeptide-related cDNA #81.
PN US2003022279-A1.
PD 30-JAN-2003.
PA (FRAS/) FRASER C C.
PA (BARN/) BARNES T M.
PA (SHAR/) SHARP J D.
PA (KIRS/) KIRST S J.
PA (MYER/) MYERS P S.

PA (LEIB/) LEIBY K R.
 PA (HOLT/) HOLTZMAN D A.
 PA (MCCA/) MCCARTHY S A.
 PA (WRIG/) WRIGHTON N.
 PA (MACK/) MACKAY C R.
 PA (GOOD/) GOODEARL A D J.
 Query Match 55.0%; Score 1727.6; DB 8; Length 3046;
 Best Local Similarity 76.0%; Pred. No. 0;
 RESULT 76
 ID ADQ10422 standard; cDNA; 3046 BP.
 DE Human polynucleotide #81.
 PN US2004121396-A1.
 PD 24-JUN-2004.
 PA (MILL-) MILLENNIUM PHARM INC.
 Query Match 55.0%; Score 1727.6; DB 12; Length 3046;
 Best Local Similarity 76.0%; Pred. No. 0;
 RESULT 77
 ID ADQ98291 standard; cDNA; 3046 BP.
 DE Murine polynucleotide #3.
 PN US6764677-B1.
 PD 20-JUL-2004.
 PA (MILL-) MILLENNIUM PHARM INC.
 Query Match 55.0%; Score 1727.6; DB 12; Length 3046;
 Best Local Similarity 76.0%; Pred. No. 0;
 RESULT 78
 ID ADQ98297 standard; cDNA; 3046 BP.
 DE Murine polynucleotide #6.
 PN US6764677-B1.
 PD 20-JUL-2004.
 PA (MILL-) MILLENNIUM PHARM INC.
 Query Match 55.0%; Score 1727.6; DB 12; Length 3046;
 Best Local Similarity 76.0%; Pred. No. 0;
 RESULT 79
 ID AAK53434 standard; cDNA; 1901 BP.
 DE Human polynucleotide SEQ ID NO 3953.
 PN WO200157190-A2.
 PD 09-AUG-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match 54.6%; Score 1714.8; DB 4; Length 1901;
 Best Local Similarity 98.5%; Pred. No. 0;
 RESULT 80
 ID ADL13501 standard; DNA; 167932 BP.
 DE Osteoarthritis-associated polymorphic nucleotide #33.
 PN WO2003054166-A2.
 PD 03-JUL-2003.
 PA (INCY-) INCYTE GENOMICS INC.
 Query Match 42.6%; Score 1340; DB 10; Length 167932;
 Best Local Similarity 100.0%; Pred. No. 0;
 RESULT 81
 ID ABK94920 standard; cDNA; 1674 BP.
 DE Human novel polynucleotide #31.
 PN WO200244340-A2.
 PD 06-JUN-2002.
 PA (HYSE-) HYSEQ INC.
 Query Match 32.3%; Score 1015.8; DB 6; Length 1674;
 Best Local Similarity 99.3%; Pred. No. 1.1e-259;
 RESULT 82

ID ABS54021 standard; cDNA; 1730 BP.
 DE cDNA encoding semaphorin protein B28.71.
 PN CN1342663-A.
 PD 03-APR-2002.
 PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.
 Query Match 29.5%; Score 925.8; DB 6; Length 1730;
 Best Local Similarity 99.3%; Pred. No. 1e-235;
 RESULT 83
 ID AAH04875 standard; cDNA; 775 BP.
 DE Human cDNA clone (5'-primer) SEQ ID NO:1710.
 PN EP1074617-A2.
 PD 07-FEB-2001.
 PA (HELI-) HELIX RES INST.
 Query Match 22.2%; Score 696.6; DB 4; Length 775;
 Best Local Similarity 96.9%; Pred. No. 8.7e-175;
 RESULT 84
 ID ACH92749 standard; DNA; 576 BP.
 DE Human genome derived single exon probe #25944.
 PN US2003194704-A1.
 PD 16-OCT-2003.
 PA (PENN/) PENN S G.
 PA (RANK/) RANK D R.
 PA (HANZ/) HANZEL D K.
 Query Match 18.3%; Score 576; DB 12; Length 576;
 Best Local Similarity 100.0%; Pred. No. 1e-142;
 RESULT 85
 ID ADD67569 standard; cDNA; 551 BP.
 DE Human Ly667S partial cDNA SEQ ID NO:46.
 PN WO2003062401-A2.
 PD 31-JUL-2003.
 PA (CORI-) CORIXA CORP.
 Query Match 17.5%; Score 551; DB 10; Length 551;
 Best Local Similarity 100.0%; Pred. No. 4.7e-136;
 RESULT 86
 ID ACH79049 standard; DNA; 515 BP.
 DE Human genome derived single exon probe #12244.
 PN US2003194704-A1.
 PD 16-OCT-2003.
 PA (PENN/) PENN S G.
 PA (RANK/) RANK D R.
 PA (HANZ/) HANZEL D K.
 Query Match 16.4%; Score 515; DB 12; Length 515;
 Best Local Similarity 100.0%; Pred. No. 1.8e-126;
 RESULT 87
 ID AAH10375 standard; cDNA; 567 BP.
 DE Human cDNA clone (3'-primer) SEQ ID NO:7210.
 PN EP1074617-A2.
 PD 07-FEB-2001.
 PA (HELI-) HELIX RES INST.
 Query Match 15.8%; Score 498; DB 4; Length 567;
 Best Local Similarity 95.7%; Pred. No. 6.4e-122;
 RESULT 88
 ID ADI28054 standard; cDNA; 1223 BP.
 DE ECMCAD gene clone 1672338CB1.
 PN WO200202634-A2.
 PD 10-JAN-2002.
 PA (INCY-) INCYTE GENOMICS INC.

Query Match 15.7%; Score 494; DB 6; Length 1223;
 Best Local Similarity 100.0%; Pred. No. 1.1e-120;
 RESULT 89
 ID ABQ72561 standard; cDNA; 988 BP.
 DE Human MDDT encoding cDNA SEQ ID NO 113.
 PN WO200240715-A2.
 PD 23-MAY-2002.
 PA (INCY-) INCYTE GENOMICS INC.
 Query Match 15.0%; Score 470; DB 6; Length 988;
 Best Local Similarity 99.8%; Pred. No. 2.5e-114;
 RESULT 90
 ID AAH15658 standard; cDNA; 2405 BP.
 DE Human cDNA sequence SEQ ID NO:14006.
 PN EP1074617-A2.
 PD 07-FEB-2001.
 PA (HELI-) HELIX RES INST.
 Query Match 10.4%; Score 327; DB 4; Length 2405;
 Best Local Similarity 100.0%; Pred. No. 5e-76;
 RESULT 91
 ID AAI84263 standard; cDNA; 408 BP.
 DE Human polynucleotide SEQ ID NO 4323.
 PN WO200164835-A2.
 PD 07-SEP-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match 9.6%; Score 303.2; DB 4; Length 408;
 Best Local Similarity 97.5%; Pred. No. 4.6e-70;
 RESULT 92
 ID ABN83984 standard; DNA; 3766 BP.
 DE Human gene sequence #31.
 PN WO200252005-A1.
 PD 04-JUL-2002.
 PA (KAZU-) KAZUSA DNA RES INST FOUND.
 PA (CELE-) CELESTAR LEXICO-SCI LTD.
 Query Match 8.4%; Score 263.6; DB 6; Length 3766;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 93
 ID ABV77918 standard; DNA; 3766 BP.
 DE Hypoxia-induced protein coding sequence #32.
 PN WO200246465-A2.
 PD 13-JUN-2002.
 PA (OXFO-) OXFORD BIOMEDICA UK LTD.
 Query Match 8.4%; Score 263.6; DB 6; Length 3766;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 94
 ID ACC51059 standard; cDNA; 3766 BP.
 DE Human bladder cancer associated cDNA sequence SEQ ID NO:205.
 PN WO2003003906-A2.
 PD 16-JAN-2003.
 PA (EOSB-) EOS BIOTECHNOLOGY INC.
 Query Match 8.4%; Score 263.6; DB 8; Length 3766;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 95
 ID ABX76369 standard; DNA; 3766 BP.
 DE Lung cancer-associated polynucleotide #233.
 PN WO200286443-A2.
 PD 31-OCT-2002.
 PA (EOSB-) EOS BIOTECHNOLOGY INC.

Query Match 8.4%; Score 263.6; DB 8; Length 3766;
 Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 96

ID ADN38874 standard; cDNA; 3766 BP.
 DE Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO:192.
 PN WO2003042661-A2.
 PD 22-MAY-2003.
 PA (EOSB-) EOS BIOTECHNOLOGY INC.

Query Match 8.4%; Score 263.6; DB 11; Length 3766;
 Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 97

ID ADN39676 standard; cDNA; 3766 BP.
 DE Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO:C48.
 PN WO2003042661-A2.
 PD 22-MAY-2003.
 PA (EOSB-) EOS BIOTECHNOLOGY INC.

Query Match 8.4%; Score 263.6; DB 11; Length 3766;
 Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 98

ID AAA37092 standard; cDNA; 3781 BP.
 DE Human PRO1480 (UNQ749) cDNA sequence SEQ ID NO:252.
 PN WO200012708-A2.
 PD 09-MAR-2000.
 PA (GETH) GENENTECH INC.

Query Match 8.4%; Score 263.6; DB 3; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 99

ID AAF54381 standard; DNA; 3781 BP.
 DE Primer #75 used in the identification of proteins.
 PN WO200078961-A1.
 PD 28-DEC-2000.
 PA (GETH) GENENTECH INC.

Query Match 8.4%; Score 263.6; DB 4; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 100

ID AAS46151 standard; cDNA; 3781 BP.
 DE Human DNA encoding PRO polypeptide sequence #227.
 PN WO200168848-A2.
 PD 20-SEP-2001.
 PA (GETH) GENENTECH INC.

Query Match 8.4%; Score 263.6; DB 4; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 101

ID ACA89601 standard; cDNA; 3781 BP.
 DE cDNA encoding human PRO polypeptide #227.
 PN US2003036141-A1.
 PD 20-FEB-2003.

Query Match 8.4%; Score 263.6; DB 8; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 102

ID ACA73611 standard; cDNA; 3781 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #227.
 PN US2003036146-A1.
 PD 20-FEB-2003.
 PA (GETH) GENENTECH INC.

Query Match 8.4%; Score 263.6; DB 8; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 103

ID ACA05926 standard; cDNA; 3781 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #227.
PN US2003036162-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 8.4%; Score 263.6; DB 8; Length 3781;
Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 104

ID ACA66760 standard; cDNA; 3781 BP.
DE cDNA encoding human PRO protein #227.
PN US2003036137-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 8.4%; Score 263.6; DB 8; Length 3781;
Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 105

ID ACF20335 standard; cDNA; 3781 BP.
DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.
PN US2003040063-A1.
PD 27-FEB-2003.
Query Match 8.4%; Score 263.6; DB 8; Length 3781;
Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 106

ID ACF19721 standard; cDNA; 3781 BP.
DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.
PN US2003040064-A1.
PD 27-FEB-2003.
Query Match 8.4%; Score 263.6; DB 8; Length 3781;
Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 107

ID ACD22009 standard; cDNA; 3781 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #227.
PN US2003027267-A1.
PD 06-FEB-2003.
Query Match 8.4%; Score 263.6; DB 8; Length 3781;
Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 108

ID ACF13174 standard; cDNA; 3781 BP.
DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.
PN US2003036160-A1.
PD 20-FEB-2003.
Query Match 8.4%; Score 263.6; DB 8; Length 3781;
Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 109

ID ACD25277 standard; cDNA; 3781 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #227.
PN US2003044925-A1.
PD 06-MAR-2003.
Query Match 8.4%; Score 263.6; DB 8; Length 3781;
Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 110

ID ACF00326 standard; cDNA; 3781 BP.
DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.
PN US2003054474-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.

Query Match 8.4%; Score 263.6; DB 8; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 111
 ID ACA72383 standard; cDNA; 3781 BP.
 DE Novel human secreted and transmembrane protein PRO1480 cDNA.
 PN US2003032114-A1.
 PD 13-FEB-2003.
 Query Match 8.4%; Score 263.6; DB 8; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 112
 ID ACD04907 standard; cDNA; 3781 BP.
 DE Novel human secreted and transmembrane protein PRO1480 cDNA.
 PN US2003032101-A1.
 PD 13-FEB-2003.
 Query Match 8.4%; Score 263.6; DB 8; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 113
 ID ACC49493 standard; cDNA; 3781 BP.
 DE Tumour-associated antigenic target protein TAT207 cDNA SEQ ID NO:1.
 PN WO2003024392-A2.
 PD 27-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 8.4%; Score 263.6; DB 8; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 114
 ID ACD18368 standard; cDNA; 3781 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #227.
 PN US2003036124-A1.
 PD 20-FEB-2003.
 Query Match 8.4%; Score 263.6; DB 8; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 115
 ID ACD08375 standard; cDNA; 3781 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #227.
 PN US2003040054-A1.
 PD 27-FEB-2003.
 Query Match 8.4%; Score 263.6; DB 8; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 116
 ID ACA88809 standard; cDNA; 3781 BP.
 DE Novel human secreted and transmembrane protein PRO1480 cDNA.
 PN US2003036133-A1.
 PD 20-FEB-2003.
 Query Match 8.4%; Score 263.6; DB 8; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 117
 ID ACA70251 standard; cDNA; 3781 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #227.
 PN US2003036134-A1.
 PD 20-FEB-2003.
 Query Match 8.4%; Score 263.6; DB 8; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 118
 ID ACD12473 standard; cDNA; 3781 BP.
 DE Novel human secreted and transmembrane protein PRO1480 cDNA.
 PN US2003022294-A1.
 PD 30-JAN-2003.

Query Match 8.4%; Score 263.6; DB 8; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 119
 ID ACC74388 standard; cDNA; 3781 BP.
 DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.
 PN US2003027275-A1.
 PD 06-FEB-2003.
 Query Match 8.4%; Score 263.6; DB 8; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 120
 ID ACD16016 standard; cDNA; 3781 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #227.
 PN US2003027324-A1.
 PD 06-FEB-2003.
 Query Match 8.4%; Score 263.6; DB 8; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 121
 ID ACD25584 standard; cDNA; 3781 BP.
 DE Novel human secreted and transmembrane protein PRO1480 cDNA.
 PN US2003036118-A1.
 PD 20-FEB-2003.
 PA (GETH) GENENTECH INC.
 Query Match 8.4%; Score 263.6; DB 8; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 122
 ID ACD18061 standard; cDNA; 3781 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #227.
 PN US2003036123-A1.
 PD 20-FEB-2003.
 Query Match 8.4%; Score 263.6; DB 8; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 123
 ID ACC88348 standard; cDNA; 3781 BP.
 DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.
 PN US2003036148-A1.
 PD 20-FEB-2003.
 Query Match 8.4%; Score 263.6; DB 8; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 124
 ID ACD21702 standard; cDNA; 3781 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #227.
 PN US2003040060-A1.
 PD 27-FEB-2003.
 Query Match 8.4%; Score 263.6; DB 8; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 125
 ID ACD18769 standard; cDNA; 3781 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #227.
 PN US2003044916-A1.
 PD 06-MAR-2003.
 Query Match 8.4%; Score 263.6; DB 8; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 126
 ID ABX98379 standard; cDNA; 3781 BP.
 DE Human cDNA encoding a secreted/transmembrane protein, SEQ ID 453.
 PN US2003036156-A1.
 PD 20-FEB-2003.

Query Match 8.4%; Score 263.6; DB 8; Length 3781;
Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 127

ID ACD14130 standard; cDNA; 3781 BP.

DE Human PRO polynucleotide #227.

PN US2003032117-A1.

PD 13-FEB-2003.

Query Match 8.4%; Score 263.6; DB 8; Length 3781;

Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 128

ID ACD09910 standard; cDNA; 3781 BP.

DE Human secreted/transmembrane protein (PRO) cDNA #227.

PN US2003036128-A1.

PD 20-FEB-2003.

Query Match 8.4%; Score 263.6; DB 8; Length 3781;

Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 129

ID ACC88655 standard; cDNA; 3781 BP.

DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.

PN US2003027266-A1.

PD 06-FEB-2003.

Query Match 8.4%; Score 263.6; DB 8; Length 3781;

Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 130

ID ACD21395 standard; cDNA; 3781 BP.

DE Human secreted/transmembrane protein (PRO) cDNA #227.

PN US2003054483-A1.

PD 20-MAR-2003.

PA (GETH) GENENTECH INC.

Query Match 8.4%; Score 263.6; DB 8; Length 3781;

Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 131

ID ABX75767 standard; cDNA; 3781 BP.

DE Human cDNA encoding secreted/transmembrane protein, PRO1480.

PN US2003022298-A1.

PD 30-JAN-2003.

Query Match 8.4%; Score 263.6; DB 8; Length 3781;

Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 132

ID ABX97970 standard; cDNA; 3781 BP.

DE Human PRO polynucleotide #227.

PN US2003032102-A1.

PD 13-FEB-2003.

Query Match 8.4%; Score 263.6; DB 8; Length 3781;

Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 133

ID ACA97446 standard; cDNA; 3781 BP.

DE Novel human secreted and transmembrane protein PRO1480 cDNA.

PN US2003036117-A1.

PD 20-FEB-2003.

Query Match 8.4%; Score 263.6; DB 8; Length 3781;

Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 134

ID ACA57909 standard; cDNA; 3781 BP.

DE Human PRO1480 cDNA.

PN US2003036143-A1.

PD 20-FEB-2003.

Query Match 8.4%; Score 263.6; DB 8; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 135
 ID ACD14437 standard; cDNA; 3781 BP.
 DE Human PRO polynucleotide #227.
 PN US2003032130-A1.
 PD 13-FEB-2003.
 Query Match 8.4%; Score 263.6; DB 8; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 136
 ID ACC91220 standard; cDNA; 3781 BP.
 DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.
 PN US2003032138-A1.
 PD 13-FEB-2003.
 PA (GETH) GENENTECH INC.
 Query Match 8.4%; Score 263.6; DB 8; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 137
 ID ACC88962 standard; cDNA; 3781 BP.
 DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.
 PN US2003036132-A1.
 PD 20-FEB-2003.
 Query Match 8.4%; Score 263.6; DB 8; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 138
 ID ACD07159 standard; cDNA; 3781 BP.
 DE Human PRO polynucleotide #227.
 PN US2003008353-A1.
 PD 09-JAN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 8.4%; Score 263.6; DB 8; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 139
 ID ACA67610 standard; cDNA; 3781 BP.
 DE Human PRO polynucleotide #227.
 PN US2003017542-A1.
 PD 23-JAN-2003.
 Query Match 8.4%; Score 263.6; DB 8; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 140
 ID ACC81665 standard; cDNA; 3781 BP.
 DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.
 PN US2003032137-A1.
 PD 13-FEB-2003.
 Query Match 8.4%; Score 263.6; DB 8; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 141
 ID ACC89269 standard; cDNA; 3781 BP.
 DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.
 PN US2003027269-A1.
 PD 06-FEB-2003.
 Query Match 8.4%; Score 263.6; DB 8; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 142
 ID ACC86625 standard; cDNA; 3781 BP.
 DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.
 PN US2003027268-A1.

PD 06-FEB-2003.

Query Match 8.4%; Score 263.6; DB 8; Length 3781;
Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 143

ID ACC89883 standard; cDNA; 3781 BP.

DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.

PN US2003027274-A1.

PD 06-FEB-2003.

Query Match 8.4%; Score 263.6; DB 8; Length 3781;
Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 144

ID ACC93062 standard; cDNA; 3781 BP.

DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.

PN US2003032135-A1.

PD 13-FEB-2003.

PA (GETH) GENENTECH INC.

Query Match 8.4%; Score 263.6; DB 8; Length 3781;
Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 145

ID ACA72690 standard; cDNA; 3781 BP.

DE Human PRO polynucleotide #227.

PN US2003022295-A1.

PD 30-JAN-2003.

Query Match 8.4%; Score 263.6; DB 8; Length 3781;
Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 146

ID ACA89208 standard; cDNA; 3781 BP.

DE Human secreted/transmembrane protein (PRO) cDNA #227.

PN US2003022297-A1.

PD 30-JAN-2003.

Query Match 8.4%; Score 263.6; DB 8; Length 3781;
Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 147

ID ACA69944 standard; cDNA; 3781 BP.

DE Human secreted/transmembrane protein (PRO) cDNA #227.

PN US2003032105-A1.

PD 13-FEB-2003.

Query Match 8.4%; Score 263.6; DB 8; Length 3781;
Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 148

ID ACA97087 standard; cDNA; 3781 BP.

DE Novel human secreted and transmembrane protein PRO1480 cDNA.

PN US2003032123-A1.

PD 13-FEB-2003.

Query Match 8.4%; Score 263.6; DB 8; Length 3781;
Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 149

ID ACA91083 standard; cDNA; 3781 BP.

DE Novel human secreted and transmembrane protein PRO1480 cDNA.

PN US2003032108-A1.

PD 13-FEB-2003.

Query Match 8.4%; Score 263.6; DB 8; Length 3781;
Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 150

ID ACA70865 standard; cDNA; 3781 BP.

DE Human secreted/transmembrane protein (PRO) cDNA #227.

PN US2003032111-A1.

PD 13-FEB-2003.

Query Match 8.4%; Score 263.6; DB 8; Length 3781;
Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 151

ID ACA95375 standard; cDNA; 3781 BP.

DE Novel human secreted and transmembrane protein PRO1480 cDNA.

PN US2003032119-A1.

PD 13-FEB-2003.

PA (GETH) GENENTECH INC.

Query Match 8.4%; Score 263.6; DB 8; Length 3781;
Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 152

ID ACC86318 standard; cDNA; 3781 BP.

DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.

PN US2003027263-A1.

PD 06-FEB-2003.

Query Match 8.4%; Score 263.6; DB 8; Length 3781;
Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 153

ID ACC90190 standard; cDNA; 3781 BP.

DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.

PN US2003027271-A1.

PD 06-FEB-2003.

Query Match 8.4%; Score 263.6; DB 8; Length 3781;
Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 154

ID ACD12798 standard; cDNA; 3781 BP.

DE Human secreted/transmembrane protein (PRO) cDNA #227.

PN US2003036125-A1.

PD 20-FEB-2003.

Query Match 8.4%; Score 263.6; DB 8; Length 3781;
Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 155

ID ACF20028 standard; cDNA; 3781 BP.

DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.

PN US2003040068-A1.

PD 27-FEB-2003.

Query Match 8.4%; Score 263.6; DB 8; Length 3781;
Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 156

ID ABX76972 standard; cDNA; 3781 BP.

DE Human PRO polynucleotide #227.

PN US2003027280-A1.

PD 06-FEB-2003.

Query Match 8.4%; Score 263.6; DB 8; Length 3781;
Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 157

ID ACA73304 standard; cDNA; 3781 BP.

DE Novel human secreted and transmembrane protein PRO1480 cDNA.

PN US2003022300-A1.

PD 30-JAN-2003.

Query Match 8.4%; Score 263.6; DB 8; Length 3781;
Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 158

ID ACA68847 standard; cDNA; 3781 BP.

DE Novel human secreted and transmembrane protein PRO1480 cDNA.

PN US2003036136-A1.

PD 20-FEB-2003.

Query Match 8.4%; Score 263.6; DB 8; Length 3781;
Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 159

ID ACA74691 standard; cDNA; 3781 BP.

DE cDNA encoding human PRO polypeptide #227.

PN US2003036138-A1.

PD 20-FEB-2003.

Query Match 8.4%; Score 263.6; DB 8; Length 3781;
Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 160

ID ACA70558 standard; cDNA; 3781 BP.

DE Human secreted/transmembrane protein (PRO) cDNA #227.

PN US2003032109-A1.

PD 13-FEB-2003.

Query Match 8.4%; Score 263.6; DB 8; Length 3781;
Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 161

ID ACD14744 standard; cDNA; 3781 BP.

DE Human PRO polynucleotide #227.

PN US2003040066-A1.

PD 27-FEB-2003.

Query Match 8.4%; Score 263.6; DB 8; Length 3781;
Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 162

ID ACA68416 standard; cDNA; 3781 BP.

DE Novel human secreted and transmembrane protein PRO1480 cDNA.

PN US2003032104-A1.

PD 13-FEB-2003.

Query Match 8.4%; Score 263.6; DB 8; Length 3781;
Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 163

ID ABX98881 standard; cDNA; 3781 BP.

DE Novel human secreted and transmembrane protein PRO1480 cDNA.

PN US2003036157-A1.

PD 20-FEB-2003.

Query Match 8.4%; Score 263.6; DB 8; Length 3781;
Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 164

ID ACC81358 standard; cDNA; 3781 BP.

DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.

PN US2003032120-A1.

PD 13-FEB-2003.

Query Match 8.4%; Score 263.6; DB 8; Length 3781;
Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 165

ID ACA95682 standard; cDNA; 3781 BP.

DE Novel human secreted and transmembrane protein PRO1480 cDNA.

PN US2003036155-A1.

PD 20-FEB-2003.

Query Match 8.4%; Score 263.6; DB 8; Length 3781;
Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 166

ID ACD04600 standard; cDNA; 3781 BP.

DE Novel human secreted and transmembrane protein PRO1480 cDNA.

PN US2003022296-A1.

PD 30-JAN-2003.

Query Match 8.4%; Score 263.6; DB 8; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 167
 ID ACC88041 standard; cDNA; 3781 BP.
 DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.
 PN US2003027281-A1.
 PD 06-FEB-2003.
 PA (GETH) GENENTECH INC.
 Query Match 8.4%; Score 263.6; DB 8; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 168
 ID ACF12703 standard; cDNA; 3781 BP.
 DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.
 PN US2003040058-A1.
 PD 27-FEB-2003.
 Query Match 8.4%; Score 263.6; DB 8; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 169
 ID ACA96418 standard; cDNA; 3781 BP.
 DE Human PRO polynucleotide #227.
 PN US2003017540-A1.
 PD 23-JAN-2003.
 Query Match 8.4%; Score 263.6; DB 8; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 170
 ID ACA65192 standard; cDNA; 3781 BP.
 DE Human PRO polynucleotide #227.
 PN US2003032106-A1.
 PD 13-FEB-2003.
 Query Match 8.4%; Score 263.6; DB 8; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 171
 ID ACA73918 standard; cDNA; 3781 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #227.
 PN US2003032129-A1.
 PD 13-FEB-2003.
 Query Match 8.4%; Score 263.6; DB 8; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 172
 ID ACA74330 standard; cDNA; 3781 BP.
 DE Novel human secreted and transmembrane protein PRO1480 cDNA.
 PN US2003032131-A1.
 PD 13-FEB-2003.
 Query Match 8.4%; Score 263.6; DB 8; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 173
 ID ACA96725 standard; cDNA; 3781 BP.
 DE Human PRO polynucleotide #227.
 PN US2003032103-A1.
 PD 13-FEB-2003.
 Query Match 8.4%; Score 263.6; DB 8; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 174
 ID ACD10831 standard; cDNA; 3781 BP.
 DE cDNA encoding human PRO polypeptide #227.
 PN US2003032107-A1.
 PD 13-FEB-2003.

Query Match 8.4%; Score 263.6; DB 8; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 175
 ID ACC91527 standard; cDNA; 3781 BP.
 DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.
 PN US2003032139-A1.
 PD 13-FEB-2003.
 Query Match 8.4%; Score 263.6; DB 8; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 176
 ID ACD02862 standard; cDNA; 3781 BP.
 DE cDNA encoding human PRO polypeptide #227.
 PN US2003022301-A1.
 PD 30-JAN-2003.
 Query Match 8.4%; Score 263.6; DB 8; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 177
 ID ACC87427 standard; cDNA; 3781 BP.
 DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.
 PN US2003036165-A1.
 PD 20-FEB-2003.
 PA (GETH) GENENTECH INC.
 Query Match 8.4%; Score 263.6; DB 8; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 178
 ID ACC86011 standard; cDNA; 3781 BP.
 DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.
 PN US2003027262-A1.
 PD 06-FEB-2003.
 Query Match 8.4%; Score 263.6; DB 8; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 179
 ID ACA65499 standard; cDNA; 3781 BP.
 DE Human PRO polynucleotide #227.
 PN US2003032110-A1.
 PD 13-FEB-2003.
 Query Match 8.4%; Score 263.6; DB 8; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 180
 ID ACA94316 standard; cDNA; 3781 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #227.
 PN US2003036142-A1.
 PD 20-FEB-2003.
 Query Match 8.4%; Score 263.6; DB 8; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 181
 ID ACA98060 standard; cDNA; 3781 BP.
 DE Human PRO polynucleotide #227.
 PN US2003036145-A1.
 PD 20-FEB-2003.
 Query Match 8.4%; Score 263.6; DB 8; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 182
 ID ACA91562 standard; cDNA; 3781 BP.
 DE Novel human secreted and transmembrane protein PRO1480 cDNA.
 PN US2003036154-A1.
 PD 20-FEB-2003.

Query Match 8.4%; Score 263.6; DB 8; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 183
 ID ACA90776 standard; cDNA; 3781 BP.
 DE Novel human secreted and transmembrane protein PRO1480 cDNA.
 PN US2003036153-A1.
 PD 20-FEB-2003.
 Query Match 8.4%; Score 263.6; DB 8; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 184
 ID ACD16323 standard; cDNA; 3781 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #227.
 PN US2003044931-A1.
 PD 06-MAR-2003.
 Query Match 8.4%; Score 263.6; DB 8; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 185
 ID ACD17484 standard; cDNA; 3781 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #227.
 PN US2003036150-A1.
 PD 20-FEB-2003.
 Query Match 8.4%; Score 263.6; DB 8; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 186
 ID ACC92141 standard; cDNA; 3781 BP.
 DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.
 PN US2003040069-A1.
 PD 27-FEB-2003.
 Query Match 8.4%; Score 263.6; DB 8; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 187
 ID ACA74998 standard; cDNA; 3781 BP.
 DE cDNA encoding human PRO polypeptide #227.
 PN US2003022293-A1.
 PD 30-JAN-2003.
 Query Match 8.4%; Score 263.6; DB 8; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 188
 ID ACA91869 standard; cDNA; 3781 BP.
 DE Human PRO polynucleotide #227.
 PN US2003032128-A1.
 PD 13-FEB-2003.
 Query Match 8.4%; Score 263.6; DB 8; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 189
 ID ACA71513 standard; cDNA; 3781 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #227.
 PN US2003032116-A1.
 PD 13-FEB-2003.
 Query Match 8.4%; Score 263.6; DB 8; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 190
 ID ACC90913 standard; cDNA; 3781 BP.
 DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.
 PN US2003032122-A1.
 PD 13-FEB-2003.
 Query Match 8.4%; Score 263.6; DB 8; Length 3781;

Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 191

ID ACA65923 standard; cDNA; 3781 BP.

DE cDNA encoding human PRO protein #227.

PN US2003036139-A1.

PD 20-FEB-2003.

Query Match 8.4%; Score 263.6; DB 8; Length 3781;

Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 192

ID ACA95068 standard; cDNA; 3781 BP.

DE cDNA encoding human PRO polypeptide #227.

PN US2003017541-A1.

PD 23-JAN-2003.

Query Match 8.4%; Score 263.6; DB 8; Length 3781;

Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 193

ID ACD16630 standard; cDNA; 3781 BP.

DE Human secreted/transmembrane protein (PRO) cDNA #227.

PN US2003017543-A1.

PD 23-JAN-2003.

Query Match 8.4%; Score 263.6; DB 8; Length 3781;

Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 194

ID ACD15709 standard; cDNA; 3781 BP.

DE Human secreted/transmembrane protein (PRO) cDNA #227.

PN US2003036152-A1.

PD 20-FEB-2003.

Query Match 8.4%; Score 263.6; DB 8; Length 3781;

Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 195

ID ABX16812 standard; cDNA; 3781 BP.

DE Human cDNA encoding secreted/transmembrane protein #227.

PN US2002127584-A1.

PD 12-SEP-2002.

PA (GETH) GENENTECH INC.

Query Match 8.4%; Score 263.6; DB 8; Length 3781;

Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 196

ID ACA97753 standard; cDNA; 3781 BP.

DE Human PRO polynucleotide #227.

PN US2003032115-A1.

PD 13-FEB-2003.

Query Match 8.4%; Score 263.6; DB 9; Length 3781;

Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 197

ID ACA99202 standard; cDNA; 3781 BP.

DE Novel human secreted and transmembrane protein PRO1480 cDNA.

PN US2003032140-A1.

PD 13-FEB-2003.

Query Match 8.4%; Score 263.6; DB 9; Length 3781;

Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 198

ID ACC91834 standard; cDNA; 3781 BP.

DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.

PN US2003040076-A1.

PD 27-FEB-2003.

PA (GETH) GENENTECH INC.

Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 199
 ID ACD11245 standard; cDNA; 3781 BP.
 DE Novel human secreted and transmembrane protein PRO1480 cDNA.
 PN US2003008352-A1.
 PD 09-JAN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 200
 ID ACD15095 standard; cDNA; 3781 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #227.
 PN US2003044922-A1.
 PD 06-MAR-2003.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 201
 ID ACD11859 standard; cDNA; 3781 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #227.
 PN US2003032118-A1.
 PD 13-FEB-2003.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 202
 ID ACC95988 standard; cDNA; 3781 BP.
 DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.
 PN US2003036135-A1.
 PD 20-FEB-2003.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 203
 ID ACF16551 standard; cDNA; 3781 BP.
 DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.
 PN US2003054455-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 204
 ID ACF02669 standard; cDNA; 3781 BP.
 DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.
 PN US2003049741-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 205
 ID ACF02976 standard; cDNA; 3781 BP.
 DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.
 PN US2003049743-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 206
 ID ACF21563 standard; cDNA; 3781 BP.

DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.
 PN US2003049769-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 207
 ID ACF10247 standard; cDNA; 3781 BP.
 DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.
 PN US2003068743-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 208
 ID ACF78140 standard; cDNA; 3781 BP.
 DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.
 PN US2003054479-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 209
 ID ACD46845 standard; cDNA; 3781 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #227.
 PN US2003068685-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 210
 ID ACD49608 standard; cDNA; 3781 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #227.
 PN US2003068725-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 211
 ID ACF28375 standard; cDNA; 3781 BP.
 DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.
 PN US2003068752-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 212
 ID ACD89065 standard; cDNA; 3781 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #227.
 PN US2003068682-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 213
 ID ACD84460 standard; cDNA; 3781 BP.
 DE Human PRO polynucleotide #227.

PN US2003068701-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 214
 ID ACD99234 standard; cDNA; 3781 BP.
 DE cDNA encoding human PRO polypeptide #227.
 PN US2003068755-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 215
 ID ADA78205 standard; cDNA; 3781 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #227.
 PN US2003073180-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 216
 ID ACF48976 standard; cDNA; 3781 BP.
 DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.
 PN US2003104539-A1.
 PD 05-JUN-2003.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 217
 ID ACD09296 standard; cDNA; 3781 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #227.
 PN US2003036131-A1.
 PD 20-FEB-2003.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 218
 ID ACF12089 standard; cDNA; 3781 BP.
 DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.
 PN US2003040075-A1.
 PD 27-FEB-2003.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 219
 ID ACF41323 standard; cDNA; 3781 BP.
 DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.
 PN US2003054459-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 220
 ID ACF15937 standard; cDNA; 3781 BP.
 DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.
 PN US2003044930-A1.
 PD 06-MAR-2003.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 221

ID ACF16244 standard; cDNA; 3781 BP.
DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.
PN US2003040071-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.

Query Match 8.4%; Score 263.6; DB 9; Length 3781;
Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 222

ID ACD32071 standard; cDNA; 3781 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #227.
PN US2003054471-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.

Query Match 8.4%; Score 263.6; DB 9; Length 3781;
Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 223

ID ACF18879 standard; cDNA; 3781 BP.
DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.
PN US2003064452-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 8.4%; Score 263.6; DB 9; Length 3781;
Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 224

ID ACF09326 standard; cDNA; 3781 BP.
DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.
PN US2003068705-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 8.4%; Score 263.6; DB 9; Length 3781;
Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 225

ID ACF78447 standard; cDNA; 3781 BP.
DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.
PN US2003054473-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.

Query Match 8.4%; Score 263.6; DB 9; Length 3781;
Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 226

ID ACF52046 standard; cDNA; 3781 BP.
DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.
PN US2003064440-A1.
PD 03-APR-2003.

Query Match 8.4%; Score 263.6; DB 9; Length 3781;
Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 227

ID ACF26533 standard; cDNA; 3781 BP.
DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.
PN US2003068704-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 8.4%; Score 263.6; DB 9; Length 3781;
Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 228

ID ACF24326 standard; cDNA; 3781 BP.

DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.
PN US2003068722-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.4%; Score 263.6; DB 9; Length 3781;
Best Local Similarity 50.7%; Pred. No. 5e-59;
RESULT 229
ID ACF63637 standard; cDNA; 3781 BP.
DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.
PN US2003073183-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.4%; Score 263.6; DB 9; Length 3781;
Best Local Similarity 50.7%; Pred. No. 5e-59;
RESULT 230
ID ACF50511 standard; cDNA; 3781 BP.
DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.
PN US2003104549-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 8.4%; Score 263.6; DB 9; Length 3781;
Best Local Similarity 50.7%; Pred. No. 5e-59;
RESULT 231
ID ACH07982 standard; cDNA; 3781 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #227.
PN US2003049749-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.4%; Score 263.6; DB 9; Length 3781;
Best Local Similarity 50.7%; Pred. No. 5e-59;
RESULT 232
ID ACF13788 standard; cDNA; 3781 BP.
DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.
PN US2003064462-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.4%; Score 263.6; DB 9; Length 3781;
Best Local Similarity 50.7%; Pred. No. 5e-59;
RESULT 233
ID ACD41714 standard; cDNA; 3781 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #227.
PN US2003065159-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.4%; Score 263.6; DB 9; Length 3781;
Best Local Similarity 50.7%; Pred. No. 5e-59;
RESULT 234
ID ACF32127 standard; cDNA; 3781 BP.
DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.
PN US2003064447-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.4%; Score 263.6; DB 9; Length 3781;
Best Local Similarity 50.7%; Pred. No. 5e-59;
RESULT 235
ID ACF23405 standard; cDNA; 3781 BP.
DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.

PN US2003073184-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 236
 ID ACF40095 standard; cDNA; 3781 BP.
 DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.
 PN US2003064463-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 237
 ID ACD45617 standard; cDNA; 3781 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #227.
 PN US2003064451-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 238
 ID ACF53274 standard; cDNA; 3781 BP.
 DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.
 PN US2003068721-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 239
 ID ACF27454 standard; cDNA; 3781 BP.
 DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.
 PN US2003068699-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 240
 ID ACF45292 standard; cDNA; 3781 BP.
 DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.
 PN US2003068707-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 241
 ID ACF29910 standard; cDNA; 3781 BP.
 DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.
 PN US2003073175-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 242
 ID ACD89986 standard; cDNA; 3781 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #227.
 PN US2003068695-A1.

PD 10-APR-2003.

PA (GETH) GENENTECH INC.

Query Match 8.4%; Score 263.6; DB 9; Length 3781;

Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 243

ID ACD84767 standard; cDNA; 3781 BP.

DE Human PRO polynucleotide #227.

PN US2003068703-A1.

PD 10-APR-2003.

PA (GETH) GENENTECH INC.

Query Match 8.4%; Score 263.6; DB 9; Length 3781;

Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 244

ID ACD98927 standard; cDNA; 3781 BP.

DE cDNA encoding human PRO polypeptide #227.

PN US2003068732-A1.

PD 10-APR-2003.

PA (GETH) GENENTECH INC.

Query Match 8.4%; Score 263.6; DB 9; Length 3781;

Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 245

ID ACF77219 standard; cDNA; 3781 BP.

DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.

PN US2003082717-A1.

PD 01-MAY-2003.

Query Match 8.4%; Score 263.6; DB 9; Length 3781;

Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 246

ID ACF76912 standard; cDNA; 3781 BP.

DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.

PN US2003104548-A1.

PD 05-JUN-2003.

PA (GETH) GENENTECH INC.

Query Match 8.4%; Score 263.6; DB 9; Length 3781;

Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 247

ID ACF49897 standard; cDNA; 3781 BP.

DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.

PN US2003104542-A1.

PD 05-JUN-2003.

Query Match 8.4%; Score 263.6; DB 9; Length 3781;

Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 248

ID ACF50204 standard; cDNA; 3781 BP.

DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.

PN US2003104543-A1.

PD 05-JUN-2003.

Query Match 8.4%; Score 263.6; DB 9; Length 3781;

Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 249

ID ACD09603 standard; cDNA; 3781 BP.

DE Human secreted/transmembrane protein (PRO) cDNA #227.

PN US2003036127-A1.

PD 20-FEB-2003.

Query Match 8.4%; Score 263.6; DB 9; Length 3781;

Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 250

ID ACD08682 standard; cDNA; 3781 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #227.
 PN US2003040061-A1.
 PD 27-FEB-2003.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 251
 ID ACF12396 standard; cDNA; 3781 BP.
 DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.
 PN US2003036130-A1.
 PD 20-FEB-2003.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 252
 ID ACC94904 standard; cDNA; 3781 BP.
 DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.
 PN US2003054468-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 253
 ID ACD22623 standard; cDNA; 3781 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #227.
 PN US2003054470-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 254
 ID ACF15323 standard; cDNA; 3781 BP.
 DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.
 PN US2003044917-A1.
 PD 06-MAR-2003.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 255
 ID ACC97418 standard; cDNA; 3781 BP.
 DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.
 PN US2003044929-A1.
 PD 06-MAR-2003.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 256
 ID ACC92448 standard; cDNA; 3781 BP.
 DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.
 PN US2003059880-A1.
 PD 27-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 257
 ID ACF14095 standard; cDNA; 3781 BP.
 DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.
 PN US2003064465-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC.

Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 258
 ID ACF14402 standard; cDNA; 3781 BP.
 DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.
 PN US2003054478-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 259
 ID ACF09633 standard; cDNA; 3781 BP.
 DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.
 PN US2003068718-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 260
 ID ACD68420 standard; cDNA; 3781 BP.
 DE Novel human secreted and transmembrane protein PRO1480 cDNA.
 PN US2003073130-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 261
 ID ACD45924 standard; cDNA; 3781 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #227.
 PN US2003064454-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 262
 ID ACD48073 standard; cDNA; 3781 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #227.
 PN US2003064461-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 263
 ID ACD67804 standard; cDNA; 3781 BP.
 DE cDNA encoding human PRO polypeptide #227.
 PN US2003068724-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 264
 ID ACF25612 standard; cDNA; 3781 BP.
 DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.
 PN US2003068727-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;

Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 265
 ID ACF29296 standard; cDNA; 3781 BP.
 DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.
 PN US2003068772-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 266
 ID ACD85074 standard; cDNA; 3781 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #227.
 PN US2003068714-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 267
 ID ACD84153 standard; cDNA; 3781 BP.
 DE Human PRO polynucleotide #227.
 PN US2003068758-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 268
 ID ACD88144 standard; cDNA; 3781 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #227.
 PN US2003068776-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 269
 ID ACF30831 standard; cDNA; 3781 BP.
 DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.
 PN US2003069407-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 270
 ID ACF32434 standard; cDNA; 3781 BP.
 DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.
 PN US2003104555-A1.
 PD 05-JUN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 271
 ID ACH12094 standard; cDNA; 3781 BP.
 DE cDNA encoding human PRO polypeptide #227.
 PN US2003049768-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 272

ID ACH12401 standard; cDNA; 3781 BP.
DE cDNA encoding human PRO polypeptide #227.
PN US2003049771-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.

Query Match 8.4%; Score 263.6; DB 9; Length 3781;
Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 273

ID ACD40793 standard; cDNA; 3781 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #227.
PN US2003032134-A1.
PD 13-FEB-2003.

Query Match 8.4%; Score 263.6; DB 9; Length 3781;
Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 274

ID ACF18265 standard; cDNA; 3781 BP.
DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.
PN US2003054481-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.

Query Match 8.4%; Score 263.6; DB 9; Length 3781;
Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 275

ID ACF08712 standard; cDNA; 3781 BP.
DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.
PN US2003049778-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.

Query Match 8.4%; Score 263.6; DB 9; Length 3781;
Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 276

ID ACF31513 standard; cDNA; 3781 BP.
DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.
PN US2003049782-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.

Query Match 8.4%; Score 263.6; DB 9; Length 3781;
Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 277

ID ACF52353 standard; cDNA; 3781 BP.
DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.
PN US2003054476-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.

Query Match 8.4%; Score 263.6; DB 9; Length 3781;
Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 278

ID ACD50222 standard; cDNA; 3781 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #227.
PN US2003068733-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 8.4%; Score 263.6; DB 9; Length 3781;
Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 279

ID ACF38925 standard; cDNA; 3781 BP.

DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.
 PN US2003068692-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 280
 ID ACF26840 standard; cDNA; 3781 BP.
 DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.
 PN US2003068709-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 281
 ID ACF24940 standard; cDNA; 3781 BP.
 DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.
 PN US2003068716-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 282
 ID ACF46520 standard; cDNA; 3781 BP.
 DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.
 PN US2003068740-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 283
 ID ACF28068 standard; cDNA; 3781 BP.
 DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.
 PN US2003068751-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 284
 ID ACD89372 standard; cDNA; 3781 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #227.
 PN US2003068684-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 285
 ID ACF63944 standard; cDNA; 3781 BP.
 DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.
 PN US2003073179-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 286
 ID ACF60584 standard; cDNA; 3781 BP.
 DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.

PN US2003087374-A1.
 PD 08-MAY-2003.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 287
 ID ACH12708 standard; cDNA; 3781 BP.
 DE cDNA encoding human PRO polypeptide #227.
 PN US2003049773-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 288
 ID ACH10131 standard; cDNA; 3781 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #227.
 PN US2003049777-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 289
 ID ACD03986 standard; cDNA; 3781 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #227.
 PN US2003040055-A1.
 PD 27-FEB-2003.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 290
 ID ACD10524 standard; cDNA; 3781 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #227.
 PN US2003036164-A1.
 PD 20-FEB-2003.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 291
 ID ACD12166 standard; cDNA; 3781 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #227.
 PN US2003040074-A1.
 PD 27-FEB-2003.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 292
 ID ACF42551 standard; cDNA; 3781 BP.
 DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.
 PN US2003054480-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 293
 ID ACF18572 standard; cDNA; 3781 BP.
 DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.
 PN US2003059885-A1.
 PD 27-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 294

ID ACF02362 standard; cDNA; 3781 BP.
DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.
PN US2003049740-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.

Query Match 8.4%; Score 263.6; DB 9; Length 3781;
Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 295

ID ACF21870 standard; cDNA; 3781 BP.
DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.
PN US2003049770-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.

Query Match 8.4%; Score 263.6; DB 9; Length 3781;
Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 296

ID ACF10554 standard; cDNA; 3781 BP.
DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.
PN US2003073169-A1.
PD 17-APR-2003.

Query Match 8.4%; Score 263.6; DB 9; Length 3781;
Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 297

ID ACF34006 standard; cDNA; 3781 BP.
DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.
PN US2003064457-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 8.4%; Score 263.6; DB 9; Length 3781;
Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 298

ID ACF44968 standard; cDNA; 3781 BP.
DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.
PN US2003068711-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 8.4%; Score 263.6; DB 9; Length 3781;
Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 299

ID ACD90600 standard; cDNA; 3781 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #227.
PN US2003049745-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.

Query Match 8.4%; Score 263.6; DB 9; Length 3781;
Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 300

ID ACD91213 standard; cDNA; 3781 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #227.
PN US2003049751-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.

Query Match 8.4%; Score 263.6; DB 9; Length 3781;
Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 301

ID ACF30524 standard; cDNA; 3781 BP.

DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.
PN US2003067478-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.4%; Score 263.6; DB 9; Length 3781;
Best Local Similarity 50.7%; Pred. No. 5e-59;
RESULT 302
ID ACD87223 standard; cDNA; 3781 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #227.
PN US2003068773-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.4%; Score 263.6; DB 9; Length 3781;
Best Local Similarity 50.7%; Pred. No. 5e-59;
RESULT 303
ID ACF60277 standard; cDNA; 3781 BP.
DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.
PN US2003073185-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.4%; Score 263.6; DB 9; Length 3781;
Best Local Similarity 50.7%; Pred. No. 5e-59;
RESULT 304
ID ACF46827 standard; cDNA; 3781 BP.
DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.
PN US2003087373-A1.
PD 08-MAY-2003.
Query Match 8.4%; Score 263.6; DB 9; Length 3781;
Best Local Similarity 50.7%; Pred. No. 5e-59;
RESULT 305
ID ACF75684 standard; cDNA; 3781 BP.
DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.
PN US2003096353-A1.
PD 22-MAY-2003.
Query Match 8.4%; Score 263.6; DB 9; Length 3781;
Best Local Similarity 50.7%; Pred. No. 5e-59;
RESULT 306
ID ADA79997 standard; cDNA; 3781 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #227.
PN US2003073173-A1.
PD 17-APR-2003.
Query Match 8.4%; Score 263.6; DB 9; Length 3781;
Best Local Similarity 50.7%; Pred. No. 5e-59;
RESULT 307
ID ACF17344 standard; cDNA; 3781 BP.
DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.
PN US2003054458-A1.
PD 20-MAR-2003.
Query Match 8.4%; Score 263.6; DB 9; Length 3781;
Best Local Similarity 50.7%; Pred. No. 5e-59;
RESULT 308
ID ACF23098 standard; cDNA; 3781 BP.
DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.
PN US2003059886-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.4%; Score 263.6; DB 9; Length 3781;

Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 309
 ID ACF08098 standard; cDNA; 3781 BP.
 DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.
 PN US2003049758-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 310
 ID ACF08405 standard; cDNA; 3781 BP.
 DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.
 PN US2003049772-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 311
 ID ACF40709 standard; cDNA; 3781 BP.
 DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.
 PN US2003064448-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 312
 ID ACF53888 standard; cDNA; 3781 BP.
 DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.
 PN US2003064456-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 313
 ID ACD47152 standard; cDNA; 3781 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #227.
 PN US2003068693-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 314
 ID ACF48055 standard; cDNA; 3781 BP.
 DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.
 PN US2003068735-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 315
 ID ACF47441 standard; cDNA; 3781 BP.
 DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.
 PN US2003068753-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 316

ID ACF46213 standard; cDNA; 3781 BP.
DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.
PN US2003068742-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 8.4%; Score 263.6; DB 9; Length 3781;
Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 317

ID ACD86302 standard; cDNA; 3781 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #227.
PN US2003068756-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 8.4%; Score 263.6; DB 9; Length 3781;
Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 318

ID ACF52660 standard; cDNA; 3781 BP.
DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.
PN US2003082715-A1.
PD 01-MAY-2003.

Query Match 8.4%; Score 263.6; DB 9; Length 3781;
Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 319

ID ACF52967 standard; cDNA; 3781 BP.
DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.
PN US2003082716-A1.
PD 01-MAY-2003.

Query Match 8.4%; Score 263.6; DB 9; Length 3781;
Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 320

ID ACF64960 standard; cDNA; 3781 BP.
DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.
PN US2003068737-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 8.4%; Score 263.6; DB 9; Length 3781;
Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 321

ID ACF76605 standard; cDNA; 3781 BP.
DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.
PN US2003104547-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.

Query Match 8.4%; Score 263.6; DB 9; Length 3781;
Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 322

ID ACF61505 standard; cDNA; 3781 BP.
DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.
PN US2003096359-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.

Query Match 8.4%; Score 263.6; DB 9; Length 3781;
Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 323

ID ACF61812 standard; cDNA; 3781 BP.
DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.

PN US2003100061-A1.
 PD 29-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 324
 ID ACD30843 standard; cDNA; 3781 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #227.
 PN US2003032125-A1.
 PD 13-FEB-2003.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 325
 ID ACD31764 standard; cDNA; 3781 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #227.
 PN US2003054454-A1.
 PD 20-MAR-2003.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 326
 ID ACD32685 standard; cDNA; 3781 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #227.
 PN US2003054477-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 327
 ID ACF17651 standard; cDNA; 3781 BP.
 DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.
 PN US2003054460-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 328
 ID ACF07484 standard; cDNA; 3781 BP.
 DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.
 PN US2003049753-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 329
 ID ACF20642 standard; cDNA; 3781 BP.
 DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.
 PN US2003049763-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 330
 ID ACF20949 standard; cDNA; 3781 BP.
 DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.
 PN US2003073172-A1.
 PD 17-APR-2003.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;

Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 331

ID ACF21256 standard; cDNA; 3781 BP.

DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.

PN US2003073172-A1.

PD 17-APR-2003.

Query Match 8.4%; Score 263.6; DB 9; Length 3781;

Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 332

ID ACD47766 standard; cDNA; 3781 BP.

DE Human secreted/transmembrane protein (PRO) cDNA #227.

PN US2003068700-A1.

PD 10-APR-2003.

PA (GETH) GENENTECH INC.

Query Match 8.4%; Score 263.6; DB 9; Length 3781;

Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 333

ID ACF47748 standard; cDNA; 3781 BP.

DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.

PN US2003068736-A1.

PD 10-APR-2003.

PA (GETH) GENENTECH INC.

Query Match 8.4%; Score 263.6; DB 9; Length 3781;

Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 334

ID ACF53581 standard; cDNA; 3781 BP.

DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.

PN US2003068679-A1.

PD 10-APR-2003.

PA (GETH) GENENTECH INC.

Query Match 8.4%; Score 263.6; DB 9; Length 3781;

Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 335

ID ACD86916 standard; cDNA; 3781 BP.

DE Human secreted/transmembrane protein (PRO) cDNA #227.

PN US2003068767-A1.

PD 10-APR-2003.

PA (GETH) GENENTECH INC.

Query Match 8.4%; Score 263.6; DB 9; Length 3781;

Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 336

ID ACH05164 standard; cDNA; 3781 BP.

DE cDNA encoding human PRO polypeptide #227.

PN US2003073182-A1.

PD 17-APR-2003.

PA (GETH) GENENTECH INC.

Query Match 8.4%; Score 263.6; DB 9; Length 3781;

Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 337

ID ACF44661 standard; cDNA; 3781 BP.

DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.

PN US2003104557-A1.

PD 05-JUN-2003.

PA (GETH) GENENTECH INC.

Query Match 8.4%; Score 263.6; DB 9; Length 3781;

Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 338

ID ADA81724 standard; cDNA; 3781 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #227.
 PN US2003092121-A1.
 PD 15-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 339
 ID ACD22316 standard; cDNA; 3781 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #227.
 PN US2003027276-A1.
 PD 06-FEB-2003.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 340
 ID ACD24663 standard; cDNA; 3781 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #227.
 PN US2003044920-A1.
 PD 06-MAR-2003.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 341
 ID ACD39866 standard; cDNA; 3781 BP.
 DE cDNA encoding human PRO polypeptide #227.
 PN US2003027265-A1.
 PD 06-FEB-2003.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 342
 ID ACD40173 standard; cDNA; 3781 BP.
 DE cDNA encoding human PRO polypeptide #227.
 PN US2003054461-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 343
 ID ACF13481 standard; cDNA; 3781 BP.
 DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.
 PN US2003064446-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 344
 ID ACF03283 standard; cDNA; 3781 BP.
 DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.
 PN US2003049744-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 345
 ID ACF78754 standard; cDNA; 3781 BP.
 DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.
 PN US2003049783-A1.
 PD 13-MAR-2003.

PA (GETH) GENENTECH INC.

Query Match 8.4%; Score 263.6; DB 9; Length 3781;
Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 346

ID ACF11475 standard; cDNA; 3781 BP.

DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.

PN US2003073171-A1.

PD 17-APR-2003.

Query Match 8.4%; Score 263.6; DB 9; Length 3781;
Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 347

ID ACF50818 standard; cDNA; 3781 BP.

DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.

PN US2003032121-A1.

PD 13-FEB-2003.

Query Match 8.4%; Score 263.6; DB 9; Length 3781;
Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 348

ID ACF34313 standard; cDNA; 3781 BP.

DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.

PN US2003064458-A1.

PD 03-APR-2003.

PA (GETH) GENENTECH INC.

Query Match 8.4%; Score 263.6; DB 9; Length 3781;
Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 349

ID ACD46538 standard; cDNA; 3781 BP.

DE Human secreted/transmembrane protein (PRO) cDNA #227.

PN US2003064460-A1.

PD 03-APR-2003.

PA (GETH) GENENTECH INC.

Query Match 8.4%; Score 263.6; DB 9; Length 3781;
Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 350

ID ACD48380 standard; cDNA; 3781 BP.

DE Human secreted/transmembrane protein (PRO) cDNA #227.

PN US2003064464-A1.

PD 03-APR-2003.

PA (GETH) GENENTECH INC.

Query Match 8.4%; Score 263.6; DB 9; Length 3781;
Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 351

ID ACF27761 standard; cDNA; 3781 BP.

DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.

PN US2003068702-A1.

PD 10-APR-2003.

PA (GETH) GENENTECH INC.

Query Match 8.4%; Score 263.6; DB 9; Length 3781;
Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 352

ID ACF24633 standard; cDNA; 3781 BP.

DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.

PN US2003068734-A1.

PD 10-APR-2003.

PA (GETH) GENENTECH INC.

Query Match 8.4%; Score 263.6; DB 9; Length 3781;
Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 353

ID ACD85688 standard; cDNA; 3781 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #227.
PN US2003068719-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.4%; Score 263.6; DB 9; Length 3781;
Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 354

ID ACD90293 standard; cDNA; 3781 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #227.
PN US2003068729-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.4%; Score 263.6; DB 9; Length 3781;
Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 355

ID ACD83846 standard; cDNA; 3781 BP.
DE Human PRO polynucleotide #227.
PN US2003068738-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.4%; Score 263.6; DB 9; Length 3781;
Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 356

ID ACF49283 standard; cDNA; 3781 BP.
DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.
PN US2003104540-A1.
PD 05-JUN-2003.
Query Match 8.4%; Score 263.6; DB 9; Length 3781;
Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 357

ID ACH07368 standard; cDNA; 3781 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #227.
PN US2003049742-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.4%; Score 263.6; DB 9; Length 3781;
Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 358

ID ACH07675 standard; cDNA; 3781 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #227.
PN US2003049747-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.4%; Score 263.6; DB 9; Length 3781;
Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 359

ID ACH08289 standard; cDNA; 3781 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #227.
PN US2003049750-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.4%; Score 263.6; DB 9; Length 3781;
Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 360

ID ACH11480 standard; cDNA; 3781 BP.

DE cDNA encoding human PRO polypeptide #227.
 PN US2003049766-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 361
 ID ACH11787 standard; cDNA; 3781 BP.
 DE cDNA encoding human PRO polypeptide #227.
 PN US2003049767-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 362
 ID ACH10438 standard; cDNA; 3781 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #227.
 PN US2003049779-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 363
 ID ACF01441 standard; cDNA; 3781 BP.
 DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.
 PN US2003040059-A1.
 PD 27-FEB-2003.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 364
 ID ACF41016 standard; cDNA; 3781 BP.
 DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.
 PN US2003040078-A1.
 PD 27-FEB-2003.
 PA (GETH) GENENTECH INC.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 365
 ID ACD24356 standard; cDNA; 3781 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #227.
 PN US2003044918-A1.
 PD 06-MAR-2003.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 366
 ID ACD31457 standard; cDNA; 3781 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #227.
 PN US2003032132-A1.
 PD 13-FEB-2003.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 367
 ID ACF17958 standard; cDNA; 3781 BP.
 DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.
 PN US2003054462-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC.

Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 368
 ID ACF32741 standard; cDNA; 3781 BP.
 DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.
 PN US2003064445-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 369
 ID ACF40402 standard; cDNA; 3781 BP.
 DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.
 PN US2003064449-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 370
 ID ACF48362 standard; cDNA; 3781 BP.
 DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.
 PN US2003064441-A1.
 PD 03-APR-2003.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 371
 ID ACF38311 standard; cDNA; 3781 BP.
 DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.
 PN US2003068696-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 372
 ID ACF25247 standard; cDNA; 3781 BP.
 DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.
 PN US2003068712-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 373
 ID ACF27147 standard; cDNA; 3781 BP.
 DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.
 PN US2003068730-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 374
 ID ACF29603 standard; cDNA; 3781 BP.
 DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.
 PN US2003073174-A1.
 PD 17-APR-2003.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 375

ID ACD87837 standard; cDNA; 3781 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #227.
 PN US2003068775-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 376
 ID ACF76298 standard; cDNA; 3781 BP.
 DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.
 PN US2003104545-A1.
 PD 05-JUN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 377
 ID ACF49590 standard; cDNA; 3781 BP.
 DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.
 PN US2003104541-A1.
 PD 05-JUN-2003.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 378
 ID ACF44047 standard; cDNA; 3781 BP.
 DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.
 PN US2003104554-A1.
 PD 05-JUN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 379
 ID ACH06392 standard; cDNA; 3781 BP.
 DE cDNA encoding human PRO polypeptide #227.
 PN US2003049762-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 380
 ID ACH06699 standard; cDNA; 3781 BP.
 DE cDNA encoding human PRO polypeptide #227.
 PN US2003049765-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 381
 ID ADA83522 standard; cDNA; 3781 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #227.
 PN US2003049752-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 382
 ID ACC92755 standard; cDNA; 3781 BP.
 DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.

PN US2003032133-A1.

PD 13-FEB-2003.

Query Match 8.4%; Score 263.6; DB 9; Length 3781;
Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 383

ID ACC93369 standard; cDNA; 3781 BP.

DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.

PN US2003032136-A1.

PD 13-FEB-2003.

Query Match 8.4%; Score 263.6; DB 9; Length 3781;
Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 384

ID ACF19414 standard; cDNA; 3781 BP.

DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.

PN US2003036129-A1.

PD 20-FEB-2003.

Query Match 8.4%; Score 263.6; DB 9; Length 3781;
Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 385

ID ACD13105 standard; cDNA; 3781 BP.

DE Human secreted/transmembrane protein (PRO) cDNA #227.

PN US2003040053-A1.

PD 27-FEB-2003.

Query Match 8.4%; Score 263.6; DB 9; Length 3781;
Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 386

ID ACF06563 standard; cDNA; 3781 BP.

DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.

PN US2003040057-A1.

PD 27-FEB-2003.

Query Match 8.4%; Score 263.6; DB 9; Length 3781;
Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 387

ID ACC94597 standard; cDNA; 3781 BP.

DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.

PN US2003054467-A1.

PD 20-MAR-2003.

PA (GETH) GENENTECH INC.

Query Match 8.4%; Score 263.6; DB 9; Length 3781;
Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 388

ID ACC98025 standard; cDNA; 3781 BP.

DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.

PN US2003044932-A1.

PD 06-MAR-2003.

Query Match 8.4%; Score 263.6; DB 9; Length 3781;
Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 389

ID ACC94290 standard; cDNA; 3781 BP.

DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.

PN US2003027270-A1.

PD 06-FEB-2003.

Query Match 8.4%; Score 263.6; DB 9; Length 3781;
Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 390

ID ACF42244 standard; cDNA; 3781 BP.

DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.

PN US2003054469-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 391
 ID ACD31150 standard; cDNA; 3781 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #227.
 PN US2003032126-A1.
 PD 13-FEB-2003.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 392
 ID ACD43179 standard; cDNA; 3781 BP.
 DE cDNA encoding human PRO polypeptide #227.
 PN US2003054463-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 393
 ID ACD43486 standard; cDNA; 3781 BP.
 DE cDNA encoding human PRO polypeptide #227.
 PN US2003054466-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 394
 ID ACF15016 standard; cDNA; 3781 BP.
 DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.
 PN US2003059879-A1.
 PD 27-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 395
 ID ACF01748 standard; cDNA; 3781 BP.
 DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.
 PN US2003049738-A1.
 PD 13-MAR-2003.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 396
 ID ACF31820 standard; cDNA; 3781 BP.
 DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.
 PN US2003064469-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 397
 ID ACD67497 standard; cDNA; 3781 BP.
 DE cDNA encoding human PRO polypeptide #227.
 PN US2003064453-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC.

Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 398
 ID ACD48687 standard; cDNA; 3781 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #227.
 PN US2003064466-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 399
 ID ACD48994 standard; cDNA; 3781 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #227.
 PN US2003064468-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 400
 ID ACF51432 standard; cDNA; 3781 BP.
 DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.
 PN US2003068760-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 401
 ID ACF54195 standard; cDNA; 3781 BP.
 DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.
 PN US2003068769-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 402
 ID ACF25919 standard; cDNA; 3781 BP.
 DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.
 PN US2003045700-A1.
 PD 06-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 403
 ID ACF39232 standard; cDNA; 3781 BP.
 DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.
 PN US2003068698-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 404
 ID ACF28989 standard; cDNA; 3781 BP.
 DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.
 PN US2003068759-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;

Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 405

ID ACD90906 standard; cDNA; 3781 BP.

DE Human secreted/transmembrane protein (PRO) cDNA #227.

PN US2003049748-A1.

PD 13-MAR-2003.

PA (GETH) GENENTECH INC.

Query Match 8.4%; Score 263.6; DB 9; Length 3781;

Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 406

ID ACD86609 standard; cDNA; 3781 BP.

DE Human secreted/transmembrane protein (PRO) cDNA #227.

PN US2003068765-A1.

PD 10-APR-2003.

PA (GETH) GENENTECH INC.

Query Match 8.4%; Score 263.6; DB 9; Length 3781;

Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 407

ID ACH05471 standard; cDNA; 3781 BP.

DE cDNA encoding human PRO polypeptide #227.

PN US2003049754-A1.

PD 13-MAR-2003.

PA (GETH) GENENTECH INC.

Query Match 8.4%; Score 263.6; DB 9; Length 3781;

Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 408

ID ACF65267 standard; cDNA; 3781 BP.

DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.

PN US2003068688-A1.

PD 10-APR-2003.

PA (GETH) GENENTECH INC.

Query Match 8.4%; Score 263.6; DB 9; Length 3781;

Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 409

ID ADB20565 standard; cDNA; 3781 BP.

DE Human secreted/transmembrane protein (PRO) cDNA #227.

PN US2003082767-A1.

PD 01-MAY-2003.

Query Match 8.4%; Score 263.6; DB 9; Length 3781;

Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 410

ID ACF43740 standard; cDNA; 3781 BP.

DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.

PN US2003104552-A1.

PD 05-JUN-2003.

PA (GETH) GENENTECH INC.

Query Match 8.4%; Score 263.6; DB 9; Length 3781;

Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 411

ID ACH09210 standard; cDNA; 3781 BP.

DE Human secreted/transmembrane protein (PRO) cDNA #227.

PN US2003049774-A1.

PD 13-MAR-2003.

PA (GETH) GENENTECH INC.

Query Match 8.4%; Score 263.6; DB 9; Length 3781;

Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 412

ID ACH09517 standard; cDNA; 3781 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #227.
 PN US2003049775-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 413
 ID ADA78817 standard; cDNA; 3781 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #227.
 PN US2003073181-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 414
 ID ACF09940 standard; cDNA; 3781 BP.
 DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.
 PN US2003068720-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 415
 ID ACF51125 standard; cDNA; 3781 BP.
 DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.
 PN US2003068739-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 416
 ID ACF24019 standard; cDNA; 3781 BP.
 DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.
 PN US2003068763-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 417
 ID ACD88451 standard; cDNA; 3781 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #227.
 PN US2003068689-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 418
 ID ACH09824 standard; cDNA; 3781 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #227.
 PN US2003049776-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 419
 ID ACH10745 standard; cDNA; 3781 BP.

DE Human secreted/transmembrane protein (PRO) cDNA #227.
PN US2003049780-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.4%; Score 263.6; DB 9; Length 3781;
Best Local Similarity 50.7%; Pred. No. 5e-59;
RESULT 420
ID ACD11552 standard; cDNA; 3781 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #227.
PN US2003036126-A1.
PD 20-FEB-2003.
Query Match 8.4%; Score 263.6; DB 9; Length 3781;
Best Local Similarity 50.7%; Pred. No. 5e-59;
RESULT 421
ID ACC96602 standard; cDNA; 3781 BP.
DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.
PN US2003044924-A1.
PD 06-MAR-2003.
Query Match 8.4%; Score 263.6; DB 9; Length 3781;
Best Local Similarity 50.7%; Pred. No. 5e-59;
RESULT 422
ID ACH04522 standard; cDNA; 3781 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1480.
PN US2003044841-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.4%; Score 263.6; DB 9; Length 3781;
Best Local Similarity 50.7%; Pred. No. 5e-59;
RESULT 423
ID ACC98632 standard; cDNA; 3781 BP.
DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.
PN US2003044927-A1.
PD 06-MAR-2003.
Query Match 8.4%; Score 263.6; DB 9; Length 3781;
Best Local Similarity 50.7%; Pred. No. 5e-59;
RESULT 424
ID ACF41937 standard; cDNA; 3781 BP.
DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.
PN US2003040072-A1.
PD 27-FEB-2003.
Query Match 8.4%; Score 263.6; DB 9; Length 3781;
Best Local Similarity 50.7%; Pred. No. 5e-59;
RESULT 425
ID ACF16858 standard; cDNA; 3781 BP.
DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.
PN US2003040073-A1.
PD 27-FEB-2003.
Query Match 8.4%; Score 263.6; DB 9; Length 3781;
Best Local Similarity 50.7%; Pred. No. 5e-59;
RESULT 426
ID ACD32378 standard; cDNA; 3781 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #227.
PN US2003054475-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.4%; Score 263.6; DB 9; Length 3781;
Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 427

ID ACD30536 standard; cDNA; 3781 BP.

DE Human secreted/transmembrane protein (PRO) cDNA #227.

PN US2003032124-A1.

PD 13-FEB-2003.

Query Match 8.4%; Score 263.6; DB 9; Length 3781;

Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 428

ID ACD41407 standard; cDNA; 3781 BP.

DE Human secreted/transmembrane protein (PRO) cDNA #227.

PN US2003064467-A1.

PD 03-APR-2003.

PA (GETH) GENENTECH INC.

Query Match 8.4%; Score 263.6; DB 9; Length 3781;

Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 429

ID ACF07791 standard; cDNA; 3781 BP.

DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.

PN US2003049759-A1.

PD 13-MAR-2003.

PA (GETH) GENENTECH INC.

Query Match 8.4%; Score 263.6; DB 9; Length 3781;

Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 430

ID ACF31206 standard; cDNA; 3781 BP.

DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.

PN US2003064455-A1.

PD 03-APR-2003.

PA (GETH) GENENTECH INC.

Query Match 8.4%; Score 263.6; DB 9; Length 3781;

Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 431

ID ACF77526 standard; cDNA; 3781 BP.

DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.

PN US2003054465-A1.

PD 20-MAR-2003.

PA (GETH) GENENTECH INC.

Query Match 8.4%; Score 263.6; DB 9; Length 3781;

Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 432

ID ACF11168 standard; cDNA; 3781 BP.

DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.

PN US2003073170-A1.

PD 17-APR-2003.

Query Match 8.4%; Score 263.6; DB 9; Length 3781;

Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 433

ID ACF33048 standard; cDNA; 3781 BP.

DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.

PN US2003073176-A1.

PD 17-APR-2003.

PA (GETH) GENENTECH INC.

Query Match 8.4%; Score 263.6; DB 9; Length 3781;

Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 434

ID ACF26226 standard; cDNA; 3781 BP.

DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.

PN US2003068717-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 435
 ID ACD83539 standard; cDNA; 3781 BP.
 DE Human PRO polynucleotide #227.
 PN US2003068728-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 436
 ID ACF23712 standard; cDNA; 3781 BP.
 DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.
 PN US2003068764-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 437
 ID ACF43126 standard; cDNA; 3781 BP.
 DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.
 PN US2003104550-A1.
 PD 05-JUN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 438
 ID ACF43433 standard; cDNA; 3781 BP.
 DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.
 PN US2003104551-A1.
 PD 05-JUN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 439
 ID ACH06085 standard; cDNA; 3781 BP.
 DE cDNA encoding human PRO polypeptide #227.
 PN US2003049761-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 440
 ID ACH08903 standard; cDNA; 3781 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #227.
 PN US2003049757-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 441
 ID ACC90497 standard; cDNA; 3781 BP.
 DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.
 PN US2003027273-A1.

PD 06-FEB-2003.

Query Match 8.4%; Score 263.6; DB 9; Length 3781;
Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 442

ID ACF10861 standard; cDNA; 3781 BP.

DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.

PN US2003036119-A1.

PD 20-FEB-2003.

Query Match 8.4%; Score 263.6; DB 9; Length 3781;
Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 443

ID ACC93676 standard; cDNA; 3781 BP.

DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.

PN US2003036120-A1.

PD 20-FEB-2003.

Query Match 8.4%; Score 263.6; DB 9; Length 3781;
Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 444

ID ACC96295 standard; cDNA; 3781 BP.

DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.

PN US2003036161-A1.

PD 20-FEB-2003.

PA (GETH) GENENTECH INC.

Query Match 8.4%; Score 263.6; DB 9; Length 3781;
Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 445

ID ACD24970 standard; cDNA; 3781 BP.

DE Human secreted/transmembrane protein (PRO) cDNA #227.

PN US2003044921-A1.

PD 06-MAR-2003.

Query Match 8.4%; Score 263.6; DB 9; Length 3781;
Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 446

ID ACF02055 standard; cDNA; 3781 BP.

DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.

PN US2003049739-A1.

PD 13-MAR-2003.

PA (GETH) GENENTECH INC.

Query Match 8.4%; Score 263.6; DB 9; Length 3781;
Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 447

ID ACF22177 standard; cDNA; 3781 BP.

DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.

PN US2003059882-A1.

PD 27-MAR-2003.

PA (GETH) GENENTECH INC.

Query Match 8.4%; Score 263.6; DB 9; Length 3781;
Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 448

ID ACF22791 standard; cDNA; 3781 BP.

DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.

PN US2003059884-A1.

PD 27-MAR-2003.

PA (GETH) GENENTECH INC.

Query Match 8.4%; Score 263.6; DB 9; Length 3781;
Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 449

ID ACF09019 standard; cDNA; 3781 BP.
 DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.
 PN US2003068687-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 450
 ID ACF33355 standard; cDNA; 3781 BP.
 DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.
 PN US2003073186-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 451
 ID ACF54809 standard; cDNA; 3781 BP.
 DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.
 PN US2003064443-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 452
 ID ACF48669 standard; cDNA; 3781 BP.
 DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.
 PN US2003064444-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 453
 ID ACD47459 standard; cDNA; 3781 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #227.
 PN US2003068697-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 454
 ID ACD49301 standard; cDNA; 3781 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #227.
 PN US2003068710-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 455
 ID ACF38004 standard; cDNA; 3781 BP.
 DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.
 PN US2003068686-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 456
 ID ACF30217 standard; cDNA; 3781 BP.

DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.
 PN US2003073178-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 457
 ID ACD87530 standard; cDNA; 3781 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #227.
 PN US2003068774-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 458
 ID ACF62119 standard; cDNA; 3781 BP.
 DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.
 PN US2003104538-A1.
 PD 05-JUN-2003.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 459
 ID ACH11052 standard; cDNA; 3781 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #227.
 PN US2003049781-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 460
 ID ACD10217 standard; cDNA; 3781 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #227.
 PN US2003036158-A1.
 PD 20-FEB-2003.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 461
 ID ACD16942 standard; cDNA; 3781 BP.
 DE cDNA encoding human PRO polypeptide #227.
 PN US2003036151-A1.
 PD 20-FEB-2003.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 462
 ID ACC99239 standard; cDNA; 3781 BP.
 DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.
 PN US2003040067-A1.
 PD 27-FEB-2003.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 463
 ID ACF00633 standard; cDNA; 3781 BP.
 DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.
 PN US2003054456-A1.
 PD 20-MAR-2003.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 464

ID ACD41100 standard; cDNA; 3781 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #227.
PN US2003054482-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.4%; Score 263.6; DB 9; Length 3781;
Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 465

ID ACF14709 standard; cDNA; 3781 BP.
DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.
PN US2003054457-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.4%; Score 263.6; DB 9; Length 3781;
Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 466

ID ACF22484 standard; cDNA; 3781 BP.
DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.
PN US2003059883-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.4%; Score 263.6; DB 9; Length 3781;
Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 467

ID ACF79061 standard; cDNA; 3781 BP.
DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.
PN US2003049764-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.4%; Score 263.6; DB 9; Length 3781;
Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 468

ID ACD68066 standard; cDNA; 3781 BP.
DE Novel human secreted and transmembrane protein PRO1480 cDNA.
PN US2003073129-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.4%; Score 263.6; DB 9; Length 3781;
Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 469

ID ACF11782 standard; cDNA; 3781 BP.
DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.
PN US2003073177-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.4%; Score 263.6; DB 9; Length 3781;
Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 470

ID ACF51739 standard; cDNA; 3781 BP.
DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.
PN US2003064442-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.4%; Score 263.6; DB 9; Length 3781;
Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 471

ID ACF33662 standard; cDNA; 3781 BP.
 DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.
 PN US2003064450-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 472
 ID ACD49915 standard; cDNA; 3781 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #227.
 PN US2003068731-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 473
 ID ACF37697 standard; cDNA; 3781 BP.
 DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.
 PN US2003068683-A1.
 PD 10-APR-2003.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 474
 ID ACF28682 standard; cDNA; 3781 BP.
 DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.
 PN US2003068754-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 475
 ID ACD88758 standard; cDNA; 3781 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #227.
 PN US2003068681-A1.
 PD 10-APR-2003.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 476
 ID ACF75377 standard; cDNA; 3781 BP.
 DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.
 PN US2003096351-A1.
 PD 22-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 477
 ID ACF61198 standard; cDNA; 3781 BP.
 DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.
 PN US2003096358-A1.
 PD 22-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 478
 ID ACF44354 standard; cDNA; 3781 BP.
 DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.
 PN US2003104556-A1.

PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 8.4%; Score 263.6; DB 9; Length 3781;
Best Local Similarity 50.7%; Pred. No. 5e-59;
RESULT 479
ID ACH08596 standard; cDNA; 3781 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #227.
PN US2003049756-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.4%; Score 263.6; DB 9; Length 3781;
Best Local Similarity 50.7%; Pred. No. 5e-59;
RESULT 480
ID ACC93983 standard; cDNA; 3781 BP.
DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.
PN US2003036122-A1.
PD 20-FEB-2003.
Query Match 8.4%; Score 263.6; DB 9; Length 3781;
Best Local Similarity 50.7%; Pred. No. 5e-59;
RESULT 481
ID ACD21088 standard; cDNA; 3781 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #227.
PN US2003036121-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 8.4%; Score 263.6; DB 9; Length 3781;
Best Local Similarity 50.7%; Pred. No. 5e-59;
RESULT 482
ID ACF06870 standard; cDNA; 3781 BP.
DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.
PN US2003040065-A1.
PD 27-FEB-2003.
Query Match 8.4%; Score 263.6; DB 9; Length 3781;
Best Local Similarity 50.7%; Pred. No. 5e-59;
RESULT 483
ID ACD20781 standard; cDNA; 3781 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #227.
PN US2003044919-A1.
PD 06-MAR-2003.
Query Match 8.4%; Score 263.6; DB 9; Length 3781;
Best Local Similarity 50.7%; Pred. No. 5e-59;
RESULT 484
ID ACD22930 standard; cDNA; 3781 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #227.
PN US2003040077-A1.
PD 27-FEB-2003.
Query Match 8.4%; Score 263.6; DB 9; Length 3781;
Best Local Similarity 50.7%; Pred. No. 5e-59;
RESULT 485
ID ACF41630 standard; cDNA; 3781 BP.
DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.
PN US2003044928-A1.
PD 06-MAR-2003.
Query Match 8.4%; Score 263.6; DB 9; Length 3781;
Best Local Similarity 50.7%; Pred. No. 5e-59;
RESULT 486
ID ACF07177 standard; cDNA; 3781 BP.

DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.
 PN US2003049746-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 487
 ID ACF77833 standard; cDNA; 3781 BP.
 DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.
 PN US2003054464-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 488
 ID ACD46231 standard; cDNA; 3781 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #227.
 PN US2003064459-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 489
 ID ACF47134 standard; cDNA; 3781 BP.
 DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.
 PN US2003068757-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 490
 ID ACF54502 standard; cDNA; 3781 BP.
 DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.
 PN US2003068723-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 491
 ID ACF45906 standard; cDNA; 3781 BP.
 DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.
 PN US2003068741-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 492
 ID ACF45599 standard; cDNA; 3781 BP.
 DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.
 PN US2003068744-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 493
 ID ACF38618 standard; cDNA; 3781 BP.
 DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.

PN US2003068766-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 494
 ID ACD89679 standard; cDNA; 3781 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #227.
 PN US2003068694-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 495
 ID ACD85381 standard; cDNA; 3781 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #227.
 PN US2003068715-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 496
 ID ACD85995 standard; cDNA; 3781 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #227.
 PN US2003068726-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 497
 ID ACF75991 standard; cDNA; 3781 BP.
 DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.
 PN US2003104544-A1.
 PD 05-JUN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 498
 ID ACF60891 standard; cDNA; 3781 BP.
 DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.
 PN US2003096357-A1.
 PD 22-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 499
 ID ACH05778 standard; cDNA; 3781 BP.
 DE cDNA encoding human PRO polypeptide #227.
 PN US2003049760-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 8.4%; Score 263.6; DB 9; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 500
 ID ADA82888 standard; cDNA; 3781 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #227.
 PN US2003049755-A1.

PD 13-MAR-2003.

PA (GETH) GENENTECH INC.

Query Match 8.4%; Score 263.6; DB 9; Length 3781;

Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 501

ID ACF56037 standard; cDNA; 3781 BP.

DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.

PN US2003068680-A1.

PD 10-APR-2003.

Query Match 8.4%; Score 263.6; DB 9; Length 3781;

Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 502

ID ACF55423 standard; cDNA; 3781 BP.

DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.

PN US2003068762-A1.

PD 10-APR-2003.

PA (GETH) GENENTECH INC.

Query Match 8.4%; Score 263.6; DB 10; Length 3781;

Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 503

ID ADB86196 standard; cDNA; 3781 BP.

DE Human secreted/transmembrane protein (PRO) cDNA #227.

PN US2003054472-A1.

PD 20-MAR-2003.

PA (GETH) GENENTECH INC.

Query Match 8.4%; Score 263.6; DB 10; Length 3781;

Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 504

ID ACF56344 standard; cDNA; 3781 BP.

DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.

PN US2003068708-A1.

PD 10-APR-2003.

PA (GETH) GENENTECH INC.

Query Match 8.4%; Score 263.6; DB 10; Length 3781;

Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 505

ID ACF56651 standard; cDNA; 3781 BP.

DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.

PN US2003068713-A1.

PD 10-APR-2003.

PA (GETH) GENENTECH INC.

Query Match 8.4%; Score 263.6; DB 10; Length 3781;

Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 506

ID ACF55730 standard; cDNA; 3781 BP.

DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.

PN US2003068761-A1.

PD 10-APR-2003.

PA (GETH) GENENTECH INC.

Query Match 8.4%; Score 263.6; DB 10; Length 3781;

Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 507

ID ACF55116 standard; cDNA; 3781 BP.

DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.

PN US2003068771-A1.

PD 10-APR-2003.

PA (GETH) GENENTECH INC.

Query Match 8.4%; Score 263.6; DB 10; Length 3781;
Best Local Similarity 50.7%; Pred. No. 5e-59;
RESULT 508

ID ADC18121 standard; cDNA; 3781 BP.
DE Human PRO polynucleotide #71.
PN US2003064925-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 8.4%; Score 263.6; DB 10; Length 3781;
Best Local Similarity 50.7%; Pred. No. 5e-59;
RESULT 509

ID ADD05926 standard; cDNA; 3781 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #227.
PN US2003087376-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.

Query Match 8.4%; Score 263.6; DB 10; Length 3781;
Best Local Similarity 50.7%; Pred. No. 5e-59;
RESULT 510

ID ADD70767 standard; cDNA; 3781 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1480.
PN US2003099625-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.

Query Match 8.4%; Score 263.6; DB 10; Length 3781;
Best Local Similarity 50.7%; Pred. No. 5e-59;
RESULT 511

ID ADD39844 standard; cDNA; 3781 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1480.
PN US2003083462-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.

Query Match 8.4%; Score 263.6; DB 10; Length 3781;
Best Local Similarity 50.7%; Pred. No. 5e-59;
RESULT 512

ID ADD70290 standard; cDNA; 3781 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1480.
PN US2003054406-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.

Query Match 8.4%; Score 263.6; DB 10; Length 3781;
Best Local Similarity 50.7%; Pred. No. 5e-59;
RESULT 513

ID ADD38411 standard; cDNA; 3781 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1480.
PN US2003096955-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.

Query Match 8.4%; Score 263.6; DB 10; Length 3781;
Best Local Similarity 50.7%; Pred. No. 5e-59;
RESULT 514

ID ADD39367 standard; cDNA; 3781 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1480.
PN US2003096954-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.

Query Match 8.4%; Score 263.6; DB 10; Length 3781;

Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 515

ID ADD38890 standard; cDNA; 3781 BP.

DE Human cDNA encoding secreted/transmembrane protein PRO1480.

PN US2003092061-A1.

PD 15-MAY-2003.

PA (GETH) GENENTECH INC.

Query Match 8.4%; Score 263.6; DB 10; Length 3781;

Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 516

ID ADD40321 standard; cDNA; 3781 BP.

DE Human cDNA encoding secreted/transmembrane protein PRO1480.

PN US2003082627-A1.

PD 01-MAY-2003.

PA (GETH) GENENTECH INC.

Query Match 8.4%; Score 263.6; DB 10; Length 3781;

Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 517

ID ADE50542 standard; cDNA; 3781 BP.

DE Human cDNA encoding secreted/transmembrane protein PRO1480.

PN US2003069179-A1.

PD 10-APR-2003.

PA (GETH) GENENTECH INC.

Query Match 8.4%; Score 263.6; DB 10; Length 3781;

Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 518

ID ADE20154 standard; cDNA; 3781 BP.

DE Human cDNA encoding secreted/transmembrane protein PRO1480.

PN US2003092883-A1.

PD 15-MAY-2003.

PA (GETH) GENENTECH INC.

Query Match 8.4%; Score 263.6; DB 10; Length 3781;

Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 519

ID ADE50065 standard; cDNA; 3781 BP.

DE Human cDNA encoding secreted/transmembrane protein PRO1480.

PN US2003082626-A1.

PD 01-MAY-2003.

PA (GETH) GENENTECH INC.

Query Match 8.4%; Score 263.6; DB 10; Length 3781;

Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 520

ID ADE21623 standard; cDNA; 3781 BP.

DE Human cDNA encoding secreted/transmembrane protein PRO1480.

PN US2003082628-A1.

PD 01-MAY-2003.

PA (GETH) GENENTECH INC.

Query Match 8.4%; Score 263.6; DB 10; Length 3781;

Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 521

ID ADF30048 standard; cDNA; 3781 BP.

DE Human cDNA encoding secreted/transmembrane protein PRO1480.

PN US2003204053-A1.

PD 30-OCT-2003.

PA (GETH) GENENTECH INC.

Query Match 8.4%; Score 263.6; DB 10; Length 3781;

Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 522

ID ADF55941 standard; cDNA; 3781 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1480.
PN US2003204054-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 8.4%; Score 263.6; DB 10; Length 3781;
Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 523

ID ADG02921 standard; cDNA; 3781 BP.
DE Novel human secreted and transmembrane protein PRO1480 cDNA.
PN US2003207397-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.4%; Score 263.6; DB 10; Length 3781;
Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 524

ID ADG01628 standard; cDNA; 3781 BP.
DE Novel human secreted and transmembrane protein PRO1480 cDNA.
PN US2003207399-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.4%; Score 263.6; DB 10; Length 3781;
Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 525

ID ADF95803 standard; cDNA; 3781 BP.
DE Novel human secreted and transmembrane protein PRO1480 cDNA.
PN US2003207398-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.4%; Score 263.6; DB 10; Length 3781;
Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 526

ID ADG12618 standard; cDNA; 3781 BP.
DE Novel human secreted and transmembrane protein PRO1480 cDNA.
PN US2003207392-A1.
PD 06-NOV-2003.
Query Match 8.4%; Score 263.6; DB 10; Length 3781;
Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 527

ID ADH09278 standard; cDNA; 3781 BP.
DE Human PRO polynucleotide #227.
PN US2003207395-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.4%; Score 263.6; DB 10; Length 3781;
Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 528

ID ADH99445 standard; cDNA; 3781 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1480.
PN US2003065142-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.4%; Score 263.6; DB 10; Length 3781;
Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 529

ID ABX78754 standard; cDNA; 3781 BP.

DE Human PRO polynucleotide #227.
PN US2003027272-A1.
PD 06-FEB-2003.
Query Match 8.4%; Score 263.6; DB 10; Length 3781;
Best Local Similarity 50.7%; Pred. No. 5e-59;
RESULT 530
ID ACA75726 standard; cDNA; 3781 BP.
DE Novel human secreted and transmembrane protein PRO1480 cDNA.
PN US2003032127-A1.
PD 13-FEB-2003.
Query Match 8.4%; Score 263.6; DB 10; Length 3781;
Best Local Similarity 50.7%; Pred. No. 5e-59;
RESULT 531
ID ACA71206 standard; cDNA; 3781 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #227.
PN US2003032112-A1.
PD 13-FEB-2003.
Query Match 8.4%; Score 263.6; DB 10; Length 3781;
Best Local Similarity 50.7%; Pred. No. 5e-59;
RESULT 532
ID ACC87734 standard; cDNA; 3781 BP.
DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.
PN US2003027278-A1.
PD 06-FEB-2003.
Query Match 8.4%; Score 263.6; DB 10; Length 3781;
Best Local Similarity 50.7%; Pred. No. 5e-59;
RESULT 533
ID ACC87120 standard; cDNA; 3781 BP.
DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.
PN US2003036159-A1.
PD 20-FEB-2003.
Query Match 8.4%; Score 263.6; DB 10; Length 3781;
Best Local Similarity 50.7%; Pred. No. 5e-59;
RESULT 534
ID ACD04293 standard; cDNA; 3781 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #227.
PN US2003040070-A1.
PD 27-FEB-2003.
Query Match 8.4%; Score 263.6; DB 10; Length 3781;
Best Local Similarity 50.7%; Pred. No. 5e-59;
RESULT 535
ID ACA69624 standard; cDNA; 3781 BP.
DE cDNA encoding human PRO polypeptide #227.
PN US2003032113-A1.
PD 13-FEB-2003.
Query Match 8.4%; Score 263.6; DB 10; Length 3781;
Best Local Similarity 50.7%; Pred. No. 5e-59;
RESULT 536
ID ACA90469 standard; cDNA; 3781 BP.
DE Novel human secreted and transmembrane protein PRO1480 cDNA.
PN US2003036147-A1.
PD 20-FEB-2003.
Query Match 8.4%; Score 263.6; DB 10; Length 3781;
Best Local Similarity 50.7%; Pred. No. 5e-59;
RESULT 537
ID ACC89576 standard; cDNA; 3781 BP.
DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.

PN US2003027264-A1.

PD 06-FEB-2003.

Query Match 8.4%; Score 263.6; DB 10; Length 3781;
Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 538

ID ACA98367 standard; cDNA; 3781 BP.

DE Novel human secreted and transmembrane protein PRO1480 cDNA.

PN US2003036144-A1.

PD 20-FEB-2003.

Query Match 8.4%; Score 263.6; DB 10; Length 3781;
Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 539

ID ACA94009 standard; cDNA; 3781 BP.

DE Human secreted/transmembrane protein (PRO) cDNA #227.

PN US2003036149-A1.

PD 20-FEB-2003.

Query Match 8.4%; Score 263.6; DB 10; Length 3781;
Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 540

ID ACD15402 standard; cDNA; 3781 BP.

DE Human secreted/transmembrane protein (PRO) cDNA #227.

PN US2003044923-A1.

PD 06-MAR-2003.

Query Match 8.4%; Score 263.6; DB 10; Length 3781;
Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 541

ID ACD08989 standard; cDNA; 3781 BP.

DE Human secreted/transmembrane protein (PRO) cDNA #227.

PN US2003040062-A1.

PD 27-FEB-2003.

Query Match 8.4%; Score 263.6; DB 10; Length 3781;
Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 542

ID ACC96909 standard; cDNA; 3781 BP.

DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.

PN US2003040056-A1.

PD 27-FEB-2003.

Query Match 8.4%; Score 263.6; DB 10; Length 3781;
Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 543

ID ACF15630 standard; cDNA; 3781 BP.

DE Human secreted polypeptide PRO1480-encoding cDNA, SEQ ID NO:453.

PN US2003044926-A1.

PD 06-MAR-2003.

Query Match 8.4%; Score 263.6; DB 10; Length 3781;
Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 544

ID ACA72997 standard; cDNA; 3781 BP.

DE Human PRO polynucleotide #227.

PN US2003036140-A1.

PD 20-FEB-2003.

PA (GETH) GENENTECH INC.

Query Match 8.4%; Score 263.6; DB 10; Length 3781;
Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 545

ID ACD03169 standard; cDNA; 3781 BP.

DE Novel human secreted and transmembrane protein PRO1480 cDNA.

PN US2003013153-A1.
 PD 16-JAN-2003.
 Query Match 8.4%; Score 263.6; DB 10; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 546
 ID ACD01984 standard; cDNA; 3781 BP.
 DE Novel human secreted and transmembrane protein PRO1480 cDNA.
 PN US2003017544-A1.
 PD 23-JAN-2003.
 Query Match 8.4%; Score 263.6; DB 10; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 547
 ID ACA92176 standard; cDNA; 3781 BP.
 DE Novel human secreted and transmembrane protein PRO1480 cDNA.
 PN US2003027277-A1.
 PD 06-FEB-2003.
 Query Match 8.4%; Score 263.6; DB 10; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 548
 ID ADL33057 standard; cDNA; 3781 BP.
 DE Novel human secreted and transmembrane protein PRO1480 cDNA.
 PN US2003207396-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 8.4%; Score 263.6; DB 11; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 549
 ID ADM30593 standard; cDNA; 3781 BP.
 DE Novel human secreted and transmembrane protein PRO1480 cDNA.
 PN US2003073813-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 8.4%; Score 263.6; DB 11; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 550
 ID ADE74590 standard; cDNA; 3781 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #227.
 PN US2003211572-A1.
 PD 13-NOV-2003.
 Query Match 8.4%; Score 263.6; DB 12; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 551
 ID ADE75202 standard; cDNA; 3781 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #227.
 PN US2003211574-A1.
 PD 13-NOV-2003.
 Query Match 8.4%; Score 263.6; DB 12; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 552
 ID ADE96625 standard; cDNA; 3781 BP.
 DE Human cDNA encoding secreted/transmembrane protein PRO1480.
 PN US2003195347-A1.
 PD 16-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 8.4%; Score 263.6; DB 12; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 553

ID ADF25936 standard; cDNA; 3781 BP.
 DE Human cDNA encoding secreted/transmembrane protein PRO1480.
 PN US2003199675-A1.
 PD 23-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 8.4%; Score 263.6; DB 12; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 554
 ID ADF24835 standard; cDNA; 3781 BP.
 DE Human cDNA encoding secreted/transmembrane protein PRO1480.
 PN US2003198993-A1.
 PD 23-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 8.4%; Score 263.6; DB 12; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 555
 ID ADF29571 standard; cDNA; 3781 BP.
 DE Human cDNA encoding secreted/transmembrane protein PRO1480.
 PN US2003203401-A1.
 PD 30-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 8.4%; Score 263.6; DB 12; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 556
 ID ADE97102 standard; cDNA; 3781 BP.
 DE Human cDNA encoding secreted/transmembrane protein PRO1480.
 PN US2003195334-A1.
 PD 16-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 8.4%; Score 263.6; DB 12; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 557
 ID ADF96415 standard; cDNA; 3781 BP.
 DE Novel human secreted and transmembrane protein PRO1480 cDNA.
 PN US2003215909-A1.
 PD 20-NOV-2003.
 Query Match 8.4%; Score 263.6; DB 12; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 558
 ID ADG04686 standard; cDNA; 3781 BP.
 DE Novel human secreted and transmembrane protein PRO1480 cDNA.
 PN US2003215912-A1.
 PD 20-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 8.4%; Score 263.6; DB 12; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 559
 ID ADG00846 standard; cDNA; 3781 BP.
 DE Novel human secreted and transmembrane protein PRO1480 cDNA.
 PN US2003215911-A1.
 PD 20-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 8.4%; Score 263.6; DB 12; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 560
 ID ADG83102 standard; cDNA; 3781 BP.
 DE Human PRO polynucleotide #227.

PN US2003215910-A1.
 PD 20-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 8.4%; Score 263.6; DB 12; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 561
 ID ADH03140 standard; cDNA; 3781 BP.
 DE Human cDNA encoding secreted/transmembrane protein PRO1480.
 PN US2003216562-A1.
 PD 20-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 8.4%; Score 263.6; DB 12; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 562
 ID ADH04094 standard; cDNA; 3781 BP.
 DE Human cDNA encoding secreted/transmembrane protein PRO1480.
 PN US2003220471-A1.
 PD 27-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 8.4%; Score 263.6; DB 12; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 563
 ID ADH03617 standard; cDNA; 3781 BP.
 DE Human cDNA encoding secreted/transmembrane protein PRO1480.
 PN US2003224478-A1.
 PD 04-DEC-2003.
 PA (GETH) GENENTECH INC.
 Query Match 8.4%; Score 263.6; DB 12; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 564
 ID ADH26383 standard; cDNA; 3781 BP.
 DE Novel human secreted and transmembrane protein PRO1480 cDNA.
 PN US2003068770-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 8.4%; Score 263.6; DB 12; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 565
 ID ADH33352 standard; cDNA; 3781 BP.
 DE Human PRO polynucleotide #227.
 PN US2003068768-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 8.4%; Score 263.6; DB 12; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 566
 ID ADH04571 standard; cDNA; 3781 BP.
 DE Human cDNA encoding secreted/transmembrane protein PRO1480.
 PN US2004005626-A1.
 PD 08-JAN-2004.
 PA (GETH) GENENTECH INC.
 Query Match 8.4%; Score 263.6; DB 12; Length 3781;
 Best Local Similarity 50.7%; Pred. No. 5e-59;
 RESULT 567
 ID ADH61572 standard; cDNA; 3781 BP.
 DE Human cDNA encoding secreted/transmembrane protein PRO1480.
 PN US2004014130-A1.

PD 22-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 8.4%; Score 263.6; DB 12; Length 3781;
Best Local Similarity 50.7%; Pred. No. 5e-59;
RESULT 568
ID ADJ55091 standard; cDNA; 3781 BP.
DE Human PRO polynucleotide #227.
PN US2004023321-A1.
PD 05-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 8.4%; Score 263.6; DB 12; Length 3781;
Best Local Similarity 50.7%; Pred. No. 5e-59;
RESULT 569
ID ADJ64862 standard; cDNA; 3781 BP.
DE Human PRO polynucleotide #227.
PN US2004038337-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 8.4%; Score 263.6; DB 12; Length 3781;
Best Local Similarity 50.7%; Pred. No. 5e-59;
RESULT 570
ID ADM31758 standard; cDNA; 3781 BP.
DE Novel human secreted and transmembrane protein PRO1480 cDNA.
PN US2004048334-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 8.4%; Score 263.6; DB 12; Length 3781;
Best Local Similarity 50.7%; Pred. No. 5e-59;
RESULT 571
ID ADM36805 standard; cDNA; 3781 BP.
DE Novel human secreted and transmembrane protein PRO1480 cDNA.
PN US2004053358-A1.
PD 18-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 8.4%; Score 263.6; DB 12; Length 3781;
Best Local Similarity 50.7%; Pred. No. 5e-59;
RESULT 572
ID ADM40610 standard; cDNA; 3781 BP.
DE Novel human secreted and transmembrane protein PRO1480 cDNA.
PN US2004048335-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 8.4%; Score 263.6; DB 12; Length 3781;
Best Local Similarity 50.7%; Pred. No. 5e-59;
RESULT 573
ID ADL94771 standard; cDNA; 3781 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1480.
PN US2004073015-A1.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 8.4%; Score 263.6; DB 12; Length 3781;
Best Local Similarity 50.7%; Pred. No. 5e-59;
RESULT 574
ID ADN38218 standard; cDNA; 3781 BP.
DE Novel human secreted and transmembrane protein PRO1480 cDNA.
PN US2004091959-A1.
PD 13-MAY-2004.

PA (GETH) GENENTECH INC.

Query Match 8.4%; Score 263.6; DB 12; Length 3781;

Best Local Similarity 50.7%; Pred. No. 5e-59;

RESULT 575

ID AAD08283 standard; cDNA; 3556 BP.

DE Human secreted protein-encoding gene 1 cDNA clone HKAHL26, SEQ ID NO: 11.

PN WO200136440-A1.

PD 25-MAY-2001.

PA (HUMA-) HUMAN GENOME SCI INC.

Query Match 8.3%; Score 262; DB 4; Length 3556;

Best Local Similarity 50.7%; Pred. No. 1.3e-58;

RESULT 576

ID ADQ86529 standard; cDNA; 3766 BP.

DE Human tumour-associated antigenic target (TAT) cDNA sequence #3402.

PN WO2004060270-A2.

PD 22-JUL-2004.

PA (GETH) GENENTECH INC.

PA (WUTD/) WU T D.

PA (ZHOU/) ZHOU Y.

Query Match 8.1%; Score 255.6; DB 13; Length 3766;

Best Local Similarity 50.5%; Pred. No. 6.8e-57;

RESULT 577

ID ACN39884 standard; cDNA; 3766 BP.

DE Tumour-associated antigenic target (TAT) cDNA DNA326060, SEQ ID NO:4307.

PN WO2004030615-A2.

PD 15-APR-2004.

PA (GETH) GENENTECH INC.

Query Match 8.1%; Score 255.6; DB 13; Length 3766;

Best Local Similarity 50.5%; Pred. No. 6.8e-57;

RESULT 578

ID ADQ37655 standard; cDNA; 2511 BP.

DE Human SEMA4B-M2 encoding cDNA SEQ ID NO:8.

PN WO2004058817-A1.

PD 15-JUL-2004.

PA (TAKE) TAKEDA CHEM IND LTD.

Query Match 8.1%; Score 254; DB 13; Length 2511;

Best Local Similarity 50.4%; Pred. No. 1.5e-56;

RESULT 579

ID ADQ37649 standard; cDNA; 2511 BP.

DE Human SEMA4B encoding cDNA SEQ ID NO:2.

PN WO2004058817-A1.

PD 15-JUL-2004.

PA (TAKE) TAKEDA CHEM IND LTD.

Query Match 8.1%; Score 254; DB 13; Length 2511;

Best Local Similarity 50.4%; Pred. No. 1.5e-56;

RESULT 580

ID ADQ37656 standard; cDNA; 3766 BP.

DE Human SEMA4B-M2 encoding cDNA SEQ ID NO:9.

PN WO2004058817-A1.

PD 15-JUL-2004.

PA (TAKE) TAKEDA CHEM IND LTD.

Query Match 8.1%; Score 254; DB 13; Length 3766;

Best Local Similarity 50.4%; Pred. No. 1.8e-56;

RESULT 581

ID ADQ37650 standard; cDNA; 3766 BP.

DE Human SEMA4B encoding cDNA SEQ ID NO:3.

PN WO2004058817-A1.

PD 15-JUL-2004.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 8.1%; Score 254; DB 13; Length 3766;
Best Local Similarity 50.4%; Pred. No. 1.8e-56;
RESULT 582
ID ADQ37658 standard; cDNA; 2511 BP.
DE Human SEMA4B-M3 encoding cDNA SEQ ID NO:11.
PN WO2004058817-A1.
PD 15-JUL-2004.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 8.0%; Score 252.4; DB 13; Length 2511;
Best Local Similarity 50.4%; Pred. No. 4e-56;
RESULT 583
ID ADQ37659 standard; cDNA; 3766 BP.
DE Human SEMA4B-M3 encoding cDNA SEQ ID NO:12.
PN WO2004058817-A1.
PD 15-JUL-2004.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 8.0%; Score 252.4; DB 13; Length 3766;
Best Local Similarity 50.4%; Pred. No. 4.8e-56;
RESULT 584
ID ADQ37652 standard; cDNA; 2511 BP.
DE Human SEMA4B-M1 encoding cDNA SEQ ID NO:5.
PN WO2004058817-A1.
PD 15-JUL-2004.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 8.0%; Score 250.8; DB 13; Length 2511;
Best Local Similarity 50.3%; Pred. No. 1.1e-55;
RESULT 585
ID ADQ37653 standard; cDNA; 3766 BP.
DE Human SEMA4B-M1 encoding cDNA SEQ ID NO:6.
PN WO2004058817-A1.
PD 15-JUL-2004.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 8.0%; Score 250.8; DB 13; Length 3766;
Best Local Similarity 50.3%; Pred. No. 1.3e-55;
RESULT 586
ID AAA47437 standard; DNA; 2703 BP.
DE Sequence encoding human neuron-associated protein.
PN WO200034477-A2.
PD 15-JUN-2000.
PA (INCY-) INCYTE PHARM INC.
Query Match 7.9%; Score 247.4; DB 3; Length 2703;
Best Local Similarity 50.7%; Pred. No. 8.8e-55;
RESULT 587
ID ABK11109 standard; DNA; 2390 BP.
DE DNA encoding human NOV7 protein, homologue of semaphorin proteins.
PN WO200206329-A2.
PD 24-JAN-2002.
PA (CURA-) CURAGEN CORP.
Query Match 7.8%; Score 246.6; DB 6; Length 2390;
Best Local Similarity 50.7%; Pred. No. 1.4e-54;
RESULT 588
ID AAD08048 standard; cDNA; 3293 BP.
DE Human extracellular matrix and cell adhesion molecule-4 (XMAD-4) cDNA.
PN WO200142285-A2.
PD 14-JUN-2001.

PA (INCY-) INCYTE GENOMICS INC.

Query Match 7.6%; Score 237.8; DB 4; Length 3293;

Best Local Similarity 52.8%; Pred. No. 3.5e-52;

RESULT 589

ID AAC84887 standard; cDNA; 2155 BP.

DE Human SEC6 nucleic acid sequence (clone ID 20422974.0.132).

PN WO200078802-A2.

PD 28-DEC-2000.

PA (CURA-) CURAGEN CORP.

Query Match 7.5%; Score 236.6; DB 4; Length 2155;

Best Local Similarity 52.3%; Pred. No. 6e-52;

RESULT 590

ID AAC84892 standard; cDNA; 2156 BP.

DE Human SEC11 nucleic acid sequence (clone ID 20422974.0.132-ext2).

PN WO200078802-A2.

PD 28-DEC-2000.

PA (CURA-) CURAGEN CORP.

Query Match 7.5%; Score 236.6; DB 4; Length 2156;

Best Local Similarity 52.3%; Pred. No. 6e-52;

RESULT 591

ID AAC84888 standard; cDNA; 2284 BP.

DE Human SEC7 nucleic acid sequence (clone ID 20422974.2).

PN WO200078802-A2.

PD 28-DEC-2000.

PA (CURA-) CURAGEN CORP.

Query Match 7.5%; Score 236.6; DB 4; Length 2284;

Best Local Similarity 52.3%; Pred. No. 6.1e-52;

RESULT 592

ID ADI28075 standard; cDNA; 2646 BP.

DE ECMCAD gene clone 7950094CB1.

PN WO200202634-A2.

PD 10-JAN-2002.

PA (INCY-) INCYTE GENOMICS INC.

Query Match 7.5%; Score 236.6; DB 6; Length 2646;

Best Local Similarity 52.3%; Pred. No. 6.6e-52;

RESULT 593

ID ADR67099 standard; cDNA; 3579 BP.

DE Human cancer associated gene cDNA sequence SEQ ID NO:145.

PN WO2004074321-A2.

PD 02-SEP-2004.

PA (SAGR-) SAGRES DISCOVERY INC.

Query Match 7.5%; Score 236.6; DB 13; Length 3579;

Best Local Similarity 52.3%; Pred. No. 7.7e-52;

RESULT 594

ID ADD18233 standard; DNA; 1914 BP.

DE Human molecule (MOL) protein MOL5d DNA sequence.

PN WO2003003984-A2.

PD 16-JAN-2003.

PA (CURA-) CURAGEN CORP.

Query Match 7.5%; Score 235; DB 10; Length 1914;

Best Local Similarity 52.2%; Pred. No. 1.5e-51;

RESULT 595

ID ADD18236 standard; DNA; 1914 BP.

DE Human molecule (MOL) protein MOL5e reverse DNA sequence.

PN WO2003003984-A2.

PD 16-JAN-2003.

PA (CURA-) CURAGEN CORP.

Query Match 7.5%; Score 235; DB 10; Length 1914;
 Best Local Similarity 52.2%; Pred. No. 1.5e-51;
 RESULT 596
 ID ADD18238 standard; DNA; 1914 BP.
 DE Human molecule (MOL) protein MOL5f DNA sequence.
 PN WO2003003984-A2.
 PD 16-JAN-2003.
 PA (CURA-) CURAGEN CORP.
 Query Match 7.5%; Score 235; DB 10; Length 1914;
 Best Local Similarity 52.2%; Pred. No. 1.5e-51;
 RESULT 597
 ID ADD18235 standard; DNA; 1914 BP.
 DE Human molecule (MOL) protein MOL5e DNA sequence.
 PN WO2003003984-A2.
 PD 16-JAN-2003.
 PA (CURA-) CURAGEN CORP.
 Query Match 7.5%; Score 235; DB 10; Length 1914;
 Best Local Similarity 52.2%; Pred. No. 1.5e-51;
 RESULT 598
 ID ADG76096 standard; cDNA; 1914 BP.
 DE Human NOVX cDNA to treat human pathological conditions (SeqID 9).
 PN WO2003085096-A2.
 PD 16-OCT-2003.
 PA (CURA-) CURAGEN CORP.
 Query Match 7.5%; Score 235; DB 10; Length 1914;
 Best Local Similarity 52.2%; Pred. No. 1.5e-51;
 RESULT 599
 ID ADG76094 standard; cDNA; 1914 BP.
 DE Human NOVX cDNA to treat human pathological conditions (SeqID 7).
 PN WO2003085096-A2.
 PD 16-OCT-2003.
 PA (CURA-) CURAGEN CORP.
 Query Match 7.5%; Score 235; DB 10; Length 1914;
 Best Local Similarity 52.2%; Pred. No. 1.5e-51;
 RESULT 600
 ID ADG76088 standard; cDNA; 1914 BP.
 DE Human NOVX cDNA to treat human pathological conditions (SeqID 1).
 PN WO2003085096-A2.
 PD 16-OCT-2003.
 PA (CURA-) CURAGEN CORP.
 Query Match 7.5%; Score 235; DB 10; Length 1914;
 Best Local Similarity 52.2%; Pred. No. 1.5e-51;
 RESULT 601
 ID AAF29461 standard; cDNA; 3503 BP.
 DE Murine M-Sema-F cDNA.
 PN WO200100638-A2.
 PD 04-JAN-2001.
 PA (MILL-) MILLENNIUM PHARM INC.
 Query Match 7.5%; Score 235; DB 4; Length 3503;
 Best Local Similarity 52.0%; Pred. No. 2e-51;
 RESULT 602
 ID ACD66768 standard; cDNA; 3503 BP.
 DE Secreted polypeptide-related cDNA #75.
 PN US2003022279-A1.
 PD 30-JAN-2003.
 PA (FRAS/) FRASER C C.
 PA (BARN/) BARNES T M.

PA (SHAR/) SHARP J D.
 PA (KIRS/) KIRST S J.
 PA (MYER/) MYERS P S.
 PA (LEIB/) LEIBY K R.
 PA (HOLT/) HOLTZMAN D A.
 PA (MCCA/) MCCARTHY S A.
 PA (WRIG/) WRIGHTON N.
 PA (MACK/) MACKAY C R.
 PA (GOOD/) GOODEARL A D J.
 Query Match 7.5%; Score 235; DB 8; Length 3503;
 Best Local Similarity 52.0%; Pred. No. 2e-51;
 RESULT 603
 ID ADB90781 standard; cDNA; 3503 BP.
 DE Mouse M-Sema-F cDNA.
 PN US2003082586-A1.
 PD 01-MAY-2003.
 PA (MILL-) MILLENNIUM PHARM INC.
 Query Match 7.5%; Score 235; DB 9; Length 3503;
 Best Local Similarity 52.0%; Pred. No. 2e-51;
 RESULT 604
 ID ADF71516 standard; cDNA; 3503 BP.
 DE Murine M-Sema-F cDNA.
 PN US2003175733-A1.
 PD 18-SEP-2003.
 PA (MILL-) MILLENNIUM PHARM INC.
 Query Match 7.5%; Score 235; DB 10; Length 3503;
 Best Local Similarity 52.0%; Pred. No. 2e-51;
 RESULT 605
 ID ADQ10334 standard; cDNA; 3503 BP.
 DE Human polynucleotide #59.
 PN US2004121396-A1.
 PD 24-JUN-2004.
 PA (MILL-) MILLENNIUM PHARM INC.
 Query Match 7.5%; Score 235; DB 12; Length 3503;
 Best Local Similarity 52.0%; Pred. No. 2e-51;
 RESULT 606
 ID ADR67090 standard; cDNA; 4228 BP.
 DE Mouse cancer associated gene cDNA sequence SEQ ID NO:136.
 PN WO2004074321-A2.
 PD 02-SEP-2004.
 PA (SAGR-) SAGRES DISCOVERY INC.
 Query Match 7.5%; Score 235; DB 13; Length 4228;
 Best Local Similarity 52.0%; Pred. No. 2.2e-51;
 RESULT 607
 ID ABN83983 standard; DNA; 3776 BP.
 DE Human gene sequence #30.
 PN WO200252005-A1.
 PD 04-JUL-2002.
 PA (KAZU-) KAZUSA DNA RES INST FOUND.
 PA (CELE-) CELESTAR LEXICO-SCI LTD.
 Query Match 7.4%; Score 233.6; DB 6; Length 3776;
 Best Local Similarity 52.5%; Pred. No. 5e-51;
 RESULT 608
 ID ADR67093 standard; cDNA; 3782 BP.
 DE Human cancer associated gene cDNA sequence SEQ ID NO:139.
 PN WO2004074321-A2.
 PD 02-SEP-2004.

PA (SAGR-) SAGRES DISCOVERY INC.
 Query Match 7.4%; Score 233.6; DB 13; Length 3782;
 Best Local Similarity 52.5%; Pred. No. 5e-51;
 RESULT 609
 ID ADP83373 standard; DNA; 6164 BP.
 DE Breast specific nucleic acid of the invention #79.
 PN WO2004052290-A2.
 PD 24-JUN-2004.
 PA (DIAD-) DIADEXUS INC.
 Query Match 7.4%; Score 233.6; DB 12; Length 6164;
 Best Local Similarity 52.5%; Pred. No. 6.4e-51;
 RESULT 610
 ID ADG76098 standard; cDNA; 2739 BP.
 DE Human NOVX cDNA to treat human pathological conditions (SeqID 11).
 PN WO2003085096-A2.
 PD 16-OCT-2003.
 PA (CURA-) CURAGEN CORP.
 Query Match 7.4%; Score 233.2; DB 10; Length 2739;
 Best Local Similarity 51.9%; Pred. No. 5.4e-51;
 RESULT 611
 ID AAD28947 standard; cDNA; 3868 BP.
 DE Human MOL5a cDNA.
 PN WO200206339-A2.
 PD 24-JAN-2002.
 PA (CURA-) CURAGEN CORP.
 Query Match 7.4%; Score 233.2; DB 6; Length 3868;
 Best Local Similarity 51.9%; Pred. No. 6.4e-51;
 RESULT 612
 ID ADD18203 standard; DNA; 3868 BP.
 DE Human molecule (MOL) protein MOL5a DNA sequence.
 PN WO2003003984-A2.
 PD 16-JAN-2003.
 PA (CURA-) CURAGEN CORP.
 Query Match 7.4%; Score 233.2; DB 10; Length 3868;
 Best Local Similarity 51.9%; Pred. No. 6.4e-51;
 RESULT 613
 ID AAZ36704 standard; DNA; 2433 BP.
 DE Nucleotide sequence for GenBank accession number X85992.
 PN WO9955913-A2.
 PD 04-NOV-1999.
 PA (KIMM-) KIMMEL CANCER CENT SIDNEY.
 Query Match 7.3%; Score 230; DB 3; Length 2433;
 Best Local Similarity 50.2%; Pred. No. 3.6e-50;
 RESULT 614
 ID ADJ76087 standard; DNA; 2433 BP.
 DE Marker gene SEQ ID NO:1339.
 PN EP1394274-A2.
 PD 03-MAR-2004.
 PA (GENO-) GENOX RES INC.
 Query Match 7.3%; Score 230; DB 12; Length 2433;
 Best Local Similarity 50.2%; Pred. No. 3.6e-50;
 RESULT 615
 ID AAD28948 standard; cDNA; 2558 BP.
 DE Human MOL5b cDNA.
 PN WO200206339-A2.
 PD 24-JAN-2002.
 PA (CURA-) CURAGEN CORP.

Query Match 7.2%; Score 225.4; DB 6; Length 2558;
 Best Local Similarity 51.8%; Pred. No. 6.3e-49;
 RESULT 616
 ID ADD18205 standard; DNA; 2558 BP.
 DE Human molecule (MOL) protein MOL5b DNA sequence.
 PN WO2003003984-A2.
 PD 16-JAN-2003.
 PA (CURA-) CURAGEN CORP.
 Query Match 7.2%; Score 225.4; DB 10; Length 2558;
 Best Local Similarity 51.8%; Pred. No. 6.3e-49;
 RESULT 617
 ID AAD28949 standard; cDNA; 3112 BP.
 DE Human MOL5c cDNA.
 PN WO200206339-A2.
 PD 24-JAN-2002.
 PA (CURA-) CURAGEN CORP.
 Query Match 7.2%; Score 225.4; DB 6; Length 3112;
 Best Local Similarity 51.8%; Pred. No. 6.9e-49;
 RESULT 618
 ID ADD18207 standard; DNA; 3112 BP.
 DE Human molecule (MOL) protein MOL5c DNA sequence.
 PN WO2003003984-A2.
 PD 16-JAN-2003.
 PA (CURA-) CURAGEN CORP.
 Query Match 7.2%; Score 225.4; DB 10; Length 3112;
 Best Local Similarity 51.8%; Pred. No. 6.9e-49;
 RESULT 619
 ID ADG76092 standard; cDNA; 3112 BP.
 DE Human NOVX cDNA to treat human pathological conditions (SeqID 5).
 PN WO2003085096-A2.
 PD 16-OCT-2003.
 PA (CURA-) CURAGEN CORP.
 Query Match 7.2%; Score 225.4; DB 10; Length 3112;
 Best Local Similarity 51.8%; Pred. No. 6.9e-49;
 RESULT 620
 ID ABL62806 standard; DNA; 224 BP.
 DE Breast cancer related gene sequence SEQ ID NO:1143.
 PN WO200194629-A2.
 PD 13-DEC-2001.
 PA (AVAL-) AVALON PHARM.
 Query Match 6.9%; Score 216.2; DB 6; Length 224;
 Best Local Similarity 98.6%; Pred. No. 5.3e-47;
 RESULT 621
 ID ABL62989 standard; DNA; 224 BP.
 DE Breast cancer related gene sequence SEQ ID NO:1326.
 PN WO200194629-A2.
 PD 13-DEC-2001.
 PA (AVAL-) AVALON PHARM.
 Query Match 6.9%; Score 216.2; DB 6; Length 224;
 Best Local Similarity 98.6%; Pred. No. 5.3e-47;
 RESULT 622
 ID ACN43394 standard; cDNA; 2470 BP.
 DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:2269.
 PN WO2004023973-A2.
 PD 25-MAR-2004.
 PA (INCY-) INCYTE CORP.
 Query Match 6.5%; Score 203.2; DB 13; Length 2470;

Best Local Similarity 51.8%; Pred. No. 5.1e-43;
 RESULT 623
 ID ABQ99272 standard; cDNA; 2615 BP.
 DE Human coding sequence SEQ ID 5.
 PN WO200259260-A2.
 PD 01-AUG-2002.
 PA (HYSE-) HYSEQ INC.
 Query Match 6.4%; Score 200.8; DB 6; Length 2615;
 Best Local Similarity 51.2%; Pred. No. 2.3e-42;
 RESULT 624
 ID ADG76090 standard; cDNA; 2049 BP.
 DE Human NOVX cDNA to treat human pathological conditions (SeqID 3).
 PN WO2003085096-A2.
 PD 16-OCT-2003.
 PA (CURA-) CURAGEN CORP.
 Query Match 6.1%; Score 193; DB 10; Length 2049;
 Best Local Similarity 52.5%; Pred. No. 2.4e-40;
 RESULT 625
 ID ADG91218 standard; DNA; 6087 BP.
 DE Hepatic specific nucleic acid encoding sequence #407.
 PN WO2003066877-A2.
 PD 14-AUG-2003.
 PA (DIAD-) DIADEXUS INC.
 Query Match 6.0%; Score 189.6; DB 10; Length 6087;
 Best Local Similarity 52.7%; Pred. No. 3.4e-39;
 RESULT 626
 ID ABX92031 standard; cDNA; 8095 BP.
 DE Lung specific nucleic acid (LSNA) #73.
 PN WO200268633-A2.
 PD 06-SEP-2002.
 PA (DIAD-) DIADEXUS INC.
 Query Match 6.0%; Score 189.6; DB 6; Length 8095;
 Best Local Similarity 52.7%; Pred. No. 3.9e-39;
 RESULT 627
 ID ABT13397 standard; DNA; 8144 BP.
 DE Breast specific related polynucleotide SEQ ID No 112.
 PN WO200277232-A2.
 PD 03-OCT-2002.
 PA (DIAD-) DIADEXUS INC.
 Query Match 6.0%; Score 189.6; DB 8; Length 8144;
 Best Local Similarity 52.7%; Pred. No. 3.9e-39;
 RESULT 628
 ID AAT21456 standard; cDNA to mRNA; 164 BP.
 DE Human gene signature HUMGS02826.
 PN WO9514772-A1.
 PD 01-JUN-1995.
 PA (MATS/) MATSUBARA K.
 PA (OKUB/) OKUBO K.
 Query Match 4.9%; Score 153.8; DB 2; Length 164;
 Best Local Similarity 94.5%; Pred. No. 1.9e-30;
 RESULT 629
 ID ADA02662 standard; cDNA; 2589 BP.
 DE Human SEMA4D carcinoma associated coding sequence, SEQ ID NO:1180.
 PN WO2003057146-A2.
 PD 17-JUL-2003.
 PA (SAGR-) SAGRES DISCOVERY.
 Query Match 4.9%; Score 153.4; DB 9; Length 2589;

Best Local Similarity 50.0%; Pred. No. 9.8e-30;
 RESULT 630
 ID ADB72400 standard; cDNA; 2589 BP.
 DE Human SEMA4D cDNA.
 PN WO2003008583-A2.
 PD 30-JAN-2003.
 PA (SAGR-) SAGRES DISCOVERY.
 Query Match 4.9%; Score 153.4; DB 10; Length 2589;
 Best Local Similarity 50.0%; Pred. No. 9.8e-30;
 RESULT 631
 ID ADE95910 standard; DNA; 2589 BP.
 DE Human SEMA4D gene coding sequence.
 PN WO2003039484-A2.
 PD 15-MAY-2003.
 PA (SAGR-) SAGRES DISCOVERY.
 Query Match 4.9%; Score 153.4; DB 10; Length 2589;
 Best Local Similarity 50.0%; Pred. No. 9.8e-30;
 RESULT 632
 ID AAT60665 standard; cDNA; 4157 BP.
 DE Human CD100 antigen cDNA.
 PN WO9717368-A1.
 PD 15-MAY-1997.
 PA (DAND) DANA FARBER CANCER INST.
 Query Match 4.9%; Score 153.4; DB 2; Length 4157;
 Best Local Similarity 50.0%; Pred. No. 1.2e-29;
 RESULT 633
 ID AAC92384 standard; cDNA; 4157 BP.
 DE Human CD100 nucleotide sequence SEQ ID NO:4.
 PN WO200075655-A1.
 PD 14-DEC-2000.
 PA (TAKE) TAKEDA CHEM IND LTD.
 Query Match 4.9%; Score 153.4; DB 4; Length 4157;
 Best Local Similarity 50.0%; Pred. No. 1.2e-29;
 RESULT 634
 ID AAF77463 standard; DNA; 4157 BP.
 DE Human CD100 DNA sequence.
 PN JP2001048803-A.
 PD 20-FEB-2001.
 PA (TAKE) TAKEDA CHEM IND LTD.
 Query Match 4.9%; Score 153.4; DB 4; Length 4157;
 Best Local Similarity 50.0%; Pred. No. 1.2e-29;
 RESULT 635
 ID ADA02661 standard; cDNA; 4157 BP.
 DE Human SEMA4D carcinoma associated cDNA, SEQ ID NO:1179.
 PN WO2003057146-A2.
 PD 17-JUL-2003.
 PA (SAGR-) SAGRES DISCOVERY.
 Query Match 4.9%; Score 153.4; DB 9; Length 4157;
 Best Local Similarity 50.0%; Pred. No. 1.2e-29;
 RESULT 636
 ID ADB72399 standard; mRNA; 4157 BP.
 DE Human SEMA4D mRNA.
 PN WO2003008583-A2.
 PD 30-JAN-2003.
 PA (SAGR-) SAGRES DISCOVERY.
 Query Match 4.9%; Score 153.4; DB 10; Length 4157;
 Best Local Similarity 50.0%; Pred. No. 1.2e-29;

RESULT 637

ID ADE95909 standard; DNA; 4157 BP.
DE Human DNA related to SEMA4D gene mRNA.
PN WO2003039484-A2.
PD 15-MAY-2003.
PA (SAGR-) SAGRES DISCOVERY.

Query Match 4.9%; Score 153.4; DB 10; Length 4157;
Best Local Similarity 50.0%; Pred. No. 1.2e-29;

RESULT 638

ID ADR25414 standard; DNA; 4157 BP.
DE Breast cancer prognosis marker #1275.
PN WO2004065545-A2.
PD 05-AUG-2004.
PA (ROSE-) ROSETTA INPHARMATICS LLC.
PA (NECA-) NETHERLANDS CANCER INST.

Query Match 4.9%; Score 153.4; DB 13; Length 4157;
Best Local Similarity 50.0%; Pred. No. 1.2e-29;

RESULT 639

ID ADP23559 standard; cDNA; 4157 BP.
DE PRO polypeptide encoding cDNA SEQ ID NO:737.
PN WO2004041170-A2.
PD 21-MAY-2004.
PA (GETH) GENENTECH INC.

Query Match 4.9%; Score 153.4; DB 13; Length 4157;
Best Local Similarity 50.0%; Pred. No. 1.2e-29;

RESULT 640

ID ADE54116 standard; cDNA; 6300 BP.
DE Human prostate cancer cDNA #463.
PN US2003190640-A1.
PD 09-OCT-2003.
PA (FARI/) FARIS M.
PA (PEAR/) PEARSON C I.

Query Match 4.9%; Score 153.4; DB 10; Length 6300;
Best Local Similarity 50.0%; Pred. No. 1.5e-29;

RESULT 641

ID ADF82491 standard; DNA; 1712 BP.
DE Leukaemia-related DNA sequence #3047.
PN WO2003039443-A2.
PD 15-MAY-2003.
PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
PA (UYLU-) UNIV LUDWIG MAXIMILIANS.
PA (HAFE/) HAERLACH T.
PA (SCHO/) SCHOCH C.
PA (KERN/) KERN W.

Query Match 4.9%; Score 152.6; DB 10; Length 1712;
Best Local Similarity 50.1%; Pred. No. 1.3e-29;

RESULT 642

ID ABN85379 standard; DNA; 1024 BP.
DE Partial human NOV2, semphorin-like protein, coding sequence.
PN WO200255704-A2.
PD 18-JUL-2002.
PA (CURA-) CURAGEN CORP.

Query Match 4.7%; Score 147; DB 6; Length 1024;
Best Local Similarity 51.6%; Pred. No. 3.1e-28;

RESULT 643

ID ACN43396 standard; cDNA; 2306 BP.
DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:2271..

PN WO2004023973-A2.
 PD 25-MAR-2004.
 PA (INCY-) INCYTE CORP.
 Query Match 4.6%; Score 143.6; DB 13; Length 2306;
 Best Local Similarity 49.6%; Pred. No. 3.8e-27;
 RESULT 644
 ID ACN43392 standard; cDNA; 2555 BP.
 DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:2267.
 PN WO2004023973-A2.
 PD 25-MAR-2004.
 PA (INCY-) INCYTE CORP.
 Query Match 4.6%; Score 143.6; DB 13; Length 2555;
 Best Local Similarity 49.6%; Pred. No. 4e-27;
 RESULT 645
 ID ADA02659 standard; cDNA; 2586 BP.
 DE Mouse Sema4d carcinoma associated coding sequence, SEQ ID NO:1177.
 PN WO2003057146-A2.
 PD 17-JUL-2003.
 PA (SAGR-) SAGRES DISCOVERY.
 Query Match 4.6%; Score 143.6; DB 9; Length 2586;
 Best Local Similarity 49.4%; Pred. No. 4e-27;
 RESULT 646
 ID ADB72397 standard; cDNA; 2586 BP.
 DE Mouse Sema4d cDNA.
 PN WO2003008583-A2.
 PD 30-JAN-2003.
 PA (SAGR-) SAGRES DISCOVERY.
 Query Match 4.6%; Score 143.6; DB 10; Length 2586;
 Best Local Similarity 49.4%; Pred. No. 4e-27;
 RESULT 647
 ID ADE95907 standard; DNA; 2586 BP.
 DE Mouse Sema4d gene coding sequence.
 PN WO2003039484-A2.
 PD 15-MAY-2003.
 PA (SAGR-) SAGRES DISCOVERY.
 Query Match 4.6%; Score 143.6; DB 10; Length 2586;
 Best Local Similarity 49.4%; Pred. No. 4e-27;
 RESULT 648
 ID ADM72163 standard; cDNA; 2705 BP.
 DE Human NTRAN polypeptide encoding cDNA (clone ID 7503728CB1).
 PN WO2004022705-A2.
 PD 18-MAR-2004.
 PA (INCY-) INCYTE CORP.
 Query Match 4.6%; Score 143.6; DB 12; Length 2705;
 Best Local Similarity 49.6%; Pred. No. 4.1e-27;
 RESULT 649
 ID AAV31121 standard; cDNA; 2769 BP.
 DE Human semaphorin encoding cDNA.
 PN JP10155490-A.
 PD 16-JUN-1998.
 PA (SUMU) SUMITOMO SEIYAKU KK.
 Query Match 4.6%; Score 143.6; DB 2; Length 2769;
 Best Local Similarity 49.4%; Pred. No. 4.2e-27;
 RESULT 650
 ID AAC92383 standard; cDNA; 2769 BP.
 DE Mouse CD100 nucleotide sequence SEQ ID NO:2.
 PN WO200075655-A1.

PD 14-DEC-2000.
 PA (TAKE) TAKEDA CHEM IND LTD.
 Query Match 4.6%; Score 143.6; DB 4; Length 2769;
 Best Local Similarity 49.4%; Pred. No. 4.2e-27;
 RESULT 651
 ID AAF77462 standard; DNA; 2769 BP.
 DE Murine CD100 DNA sequence.
 PN JP2001048803-A.
 PD 20-FEB-2001.
 PA (TAKE) TAKEDA CHEM IND LTD.
 Query Match 4.6%; Score 143.6; DB 4; Length 2769;
 Best Local Similarity 49.4%; Pred. No. 4.2e-27;
 RESULT 652
 ID ADA02658 standard; cDNA; 2769 BP.
 DE Mouse Sema4d carcinoma associated cDNA, SEQ ID NO:1176.
 PN WO2003057146-A2.
 PD 17-JUL-2003.
 PA (SAGR-) SAGRES DISCOVERY.
 Query Match 4.6%; Score 143.6; DB 9; Length 2769;
 Best Local Similarity 49.4%; Pred. No. 4.2e-27;
 RESULT 653
 ID ADB72396 standard; mRNA; 2769 BP.
 DE Mouse Sema4d mRNA.
 PN WO2003008583-A2.
 PD 30-JAN-2003.
 PA (SAGR-) SAGRES DISCOVERY.
 Query Match 4.6%; Score 143.6; DB 10; Length 2769;
 Best Local Similarity 49.4%; Pred. No. 4.2e-27;
 RESULT 654
 ID ADE95906 standard; DNA; 2769 BP.
 DE Mouse DNA related to Sema4d gene mRNA.
 PN WO2003039484-A2.
 PD 15-MAY-2003.
 PA (SAGR-) SAGRES DISCOVERY.
 Query Match 4.6%; Score 143.6; DB 10; Length 2769;
 Best Local Similarity 49.4%; Pred. No. 4.2e-27;
 RESULT 655
 ID AAT60666 standard; cDNA; 4391 BP.
 DE Mouse CD100 antigen cDNA.
 PN WO9717368-A1.
 PD 15-MAY-1997.
 PA (DAND) DANA FARBER CANCER INST.
 Query Match 4.6%; Score 143.6; DB 2; Length 4391;
 Best Local Similarity 49.4%; Pred. No. 5.2e-27;
 RESULT 656
 ID AAF30193 standard; cDNA; 967 BP.
 DE Clone 14998905.0.65 encoding SECP6.
 PN WO200105971-A2.
 PD 25-JAN-2001.
 PA (CURA-) CURAGEN CORP.
 Query Match 4.5%; Score 141; DB 4; Length 967;
 Best Local Similarity 56.1%; Pred. No. 1.2e-26;
 RESULT 657
 ID ADG38841 standard; DNA; 967 BP.
 DE Human DNA encoding SECP6.
 PN US2003207348-A1.
 PD 06-NOV-2003.

PA (SHIM/) SHIMKETS R A.
PA (FERN/) FERNANDES E R.
PA (LILL/) LI L.
PA (GORM/) GORMAN L.
PA (GUSE/) GUSEV V Y.
PA (PADI/) PADIGARU M.
PA (PATT/) PATTURAJAN M.
PA (SHEN/) SHENOY S G.
PA (SPYT/) SPYTEK K A.

Query Match 4.5%; Score 141; DB 10; Length 967;
Best Local Similarity 56.1%; Pred. No. 1.2e-26;

RESULT 658

ID ACN43400 standard; cDNA; 1974 BP.
DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:2275.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.

Query Match 4.5%; Score 141; DB 13; Length 1974;
Best Local Similarity 56.1%; Pred. No. 1.7e-26;

RESULT 659

ID ACN43399 standard; cDNA; 2006 BP.
DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:2274.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.

Query Match 4.5%; Score 141; DB 13; Length 2006;
Best Local Similarity 56.1%; Pred. No. 1.7e-26;

RESULT 660

ID ACN43398 standard; cDNA; 2030 BP.
DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:2273.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.

Query Match 4.5%; Score 141; DB 13; Length 2030;
Best Local Similarity 56.1%; Pred. No. 1.8e-26;

RESULT 661

ID ACN43397 standard; cDNA; 2088 BP.
DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:2272.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.

Query Match 4.5%; Score 141; DB 13; Length 2088;
Best Local Similarity 56.1%; Pred. No. 1.8e-26;

RESULT 662

ID ACN43393 standard; cDNA; 2279 BP.
DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:2268.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.

Query Match 4.5%; Score 141; DB 13; Length 2279;
Best Local Similarity 56.1%; Pred. No. 1.9e-26;

RESULT 663

ID ACN43395 standard; cDNA; 2337 BP.
DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:2270.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.

Query Match 4.5%; Score 141; DB 13; Length 2337;
 Best Local Similarity 56.1%; Pred. No. 1.9e-26;
 RESULT 664
 ID ADR67097 standard; cDNA; 3523 BP.
 DE Human cancer associated gene cDNA sequence SEQ ID NO:143.
 PN WO2004074321-A2.
 PD 02-SEP-2004.
 PA (SAGR-) SAGRES DISCOVERY INC.
 Query Match 4.4%; Score 139.4; DB 13; Length 3523;
 Best Local Similarity 52.7%; Pred. No. 6.2e-26;
 RESULT 665
 ID ABN59626 standard; cDNA; 2813 BP.
 DE Novel human coding sequence SEQ ID NO: 37.
 PN WO200222660-A2.
 PD 21-MAR-2002.
 PA (HYSE-) HYSEQ INC.
 Query Match 4.4%; Score 139; DB 6; Length 2813;
 Best Local Similarity 52.6%; Pred. No. 7.1e-26;
 RESULT 666
 ID AAA96343 standard; cDNA; 3721 BP.
 DE cDNA encoding a novel polypeptide designated PRO4353.
 PN WO200056889-A2.
 PD 28-SEP-2000.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126.2; DB 3; Length 3721;
 Best Local Similarity 50.9%; Pred. No. 2.1e-22;
 RESULT 667
 ID AAH22914 standard; cDNA; 1801 BP.
 DE Human semaphorin R/6B protein encoding cDNA.
 PN WO200151518-A2.
 PD 19-JUL-2001.
 PA (LUDW-) LUDWIG INST CANCER RES.
 Query Match 4.0%; Score 126; DB 4; Length 1801;
 Best Local Similarity 55.3%; Pred. No. 1.7e-22;
 RESULT 668
 ID ABX08821 standard; cDNA; 1801 BP.
 DE Angiogenesis-associated human polynucleotide sequence #83.
 PN WO200279492-A2.
 PD 10-OCT-2002.
 PA (EOSB-) EOS BIOTECHNOLOGY INC.
 Query Match 4.0%; Score 126; DB 10; Length 1801;
 Best Local Similarity 55.3%; Pred. No. 1.7e-22;
 RESULT 669
 ID AAH22923 standard; cDNA; 2311 BP.
 DE Human semaphorin R/6B protein isoform encoding cDNA.
 PN WO200151518-A2.
 PD 19-JUL-2001.
 PA (LUDW-) LUDWIG INST CANCER RES.
 Query Match 4.0%; Score 126; DB 4; Length 2311;
 Best Local Similarity 55.3%; Pred. No. 1.9e-22;
 RESULT 670
 ID AAT72108 standard; cDNA to mRNA; 3524 BP.
 DE Human semaphorin Z gene.
 PN WO9720928-A1.
 PD 12-JUN-1997.
 PA (SUMU) SUMITOMO PHARM CO LTD.
 Query Match 4.0%; Score 126; DB 2; Length 3524;

Best Local Similarity 55.3%; Pred. No. 2.3e-22;
 RESULT 671
 ID ABX08822 standard; cDNA; 3524 BP.
 DE Angiogenesis-associated human polynucleotide sequence #84.
 PN WO200279492-A2.
 PD 10-OCT-2002.
 PA (EOSB-) EOS BIOTECHNOLOGY INC.
 Query Match 4.0%; Score 126; DB 10; Length 3524;
 Best Local Similarity 55.3%; Pred. No. 2.3e-22;
 RESULT 672
 ID AAS21515 standard; cDNA; 3721 BP.
 DE Human cDNA sequence encoding for PRO4353 polypeptide.
 PN WO200140466-A2.
 PD 07-JUN-2001.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 4; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 673
 ID ABL88205 standard; cDNA; 3721 BP.
 DE Human PRO4353 cDNA sequence SEQ ID NO:267.
 PN WO200200690-A2.
 PD 03-JAN-2002.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 6; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 674
 ID ABL95694 standard; cDNA; 3721 BP.
 DE Human angiogenesis related cDNA PRO4353 SEQ ID NO: 267.
 PN WO200208284-A2.
 PD 31-JAN-2002.
 PA (GETH) GENENTECH INC.
 PA (BAKE/) BAKER K P.
 PA (FERR/) FERRARA N.
 PA (GERB/) GERBER H.
 PA (GERR/) GERRITSEN M E.
 PA (GODD/) GODDARD A.
 PA (GODO/) GODOWSKI P J.
 PA (GURN/) GURNEY A L.
 PA (HILL/) HILLAN K J.
 PA (MARS/) MARSTERS S A.
 PA (PANJ/) PAN J.
 PA (PAON/) PAONI N F.
 PA (STEP/) STEPHAN J F.
 PA (WATA/) WATANABE C K.
 PA (WILL/) WILLIAMS P M.
 PA (WOOD/) WOOD W I.
 Query Match 4.0%; Score 126; DB 6; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 675
 ID ACD28820 standard; cDNA; 3721 BP.
 DE Human secreted / transmembrane polypeptide PRO1353 cDNA.
 PN US2003027249-A1.
 PD 06-FEB-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 8; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 676

ID ACA03874 standard; cDNA; 3721 BP.
 DE cDNA encoding human PRO polypeptide #272.
 PN US2003036180-A1.
 PD 20-FEB-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 8; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 677
 ID ABX89412 standard; cDNA; 3721 BP.
 DE DNA encoding novel secreted and transmembrane protein PRO4353.
 PN US2003017563-A1.
 PD 23-JAN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 8; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 678
 ID ACA06094 standard; cDNA; 3721 BP.
 DE cDNA encoding human PRO polypeptide #8.
 PN US2003008348-A1.
 PD 09-JAN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 8; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 679
 ID ACD42066 standard; cDNA; 3721 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #272.
 PN US2003036179-A1.
 PD 20-FEB-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 8; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 680
 ID ACA04295 standard; cDNA; 3721 BP.
 DE Human cDNA encoding a secreted/transmembrane protein, SEQ ID 543.
 PN US2003032155-A1.
 PD 13-FEB-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 8; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 681
 ID ACA67717 standard; cDNA; 3721 BP.
 DE cDNA encoding human secreted polypeptide PRO4353.
 PN US2002192751-A1.
 PD 19-DEC-2002.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 9; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 682
 ID ADA46062 standard; cDNA; 3721 BP.
 DE Novel human secreted and transmembrane protein PRO4353 cDNA.
 PN US2003022328-A1.
 PD 30-JAN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 9; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 683
 ID ADA76559 standard; cDNA; 3721 BP.

DE Novel human secreted and transmembrane protein PRO4353 cDNA.
 PN US2003036114-A1.
 PD 20-FEB-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 9; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 684
 ID ADA76493 standard; cDNA; 3721 BP.
 DE Human PRO polynucleotide #272.
 PN US2003073212-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 9; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 685
 ID ADA19143 standard; cDNA; 3721 BP.
 DE Human PRO polynucleotide #272.
 PN US2003054517-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 9; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 686
 ID ADA61766 standard; cDNA; 3721 BP.
 DE Homo sapiens.
 PN US2003049816-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 9; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 687
 ID ADB19551 standard; cDNA; 3721 BP.
 DE Novel human secreted and transmembrane protein PRO4353 cDNA.
 PN US2003068796-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 9; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 688
 ID ADB28092 standard; cDNA; 3721 BP.
 DE cDNA encoding human PRO polypeptide #272.
 PN US2003082704-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 9; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 689
 ID ADA86571 standard; cDNA; 3721 BP.
 DE Novel human secreted and transmembrane protein PRO4353 cDNA.
 PN US2003082711-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 9; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 690
 ID ADB16135 standard; cDNA; 3721 BP.
 DE Human PRO polynucleotide #272.

PN US2003087350-A1.
 PD 08-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 9; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 691
 ID ADA47921 standard; cDNA; 3721 BP.
 DE Human PRO polynucleotide #272.
 PN US2003073215-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 9; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 692
 ID ADA67716 standard; cDNA; 3721 BP.
 DE Human PRO polynucleotide #272.
 PN US2003068795-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 9; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 693
 ID ADB30723 standard; cDNA; 3721 BP.
 DE cDNA encoding human PRO polypeptide #272.
 PN US2003068794-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 9; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 694
 ID ADA86019 standard; cDNA; 3721 BP.
 DE Novel human secreted and transmembrane protein PRO4353 cDNA.
 PN US2003082693-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 9; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 695
 ID ADA97231 standard; cDNA; 3721 BP.
 DE Human PRO polynucleotide #272.
 PN US2003082705-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 9; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 696
 ID ADA79535 standard; cDNA; 3721 BP.
 DE Human PRO polynucleotide #272.
 PN US2003082763-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 9; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 697
 ID ADA87674 standard; cDNA; 3721 BP.
 DE Novel human secreted and transmembrane protein PRO4353 cDNA.
 PN US2003087345-A1.

PD 08-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 9; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 698
 ID ADB16876 standard; cDNA; 3721 BP.
 DE Human PRO polynucleotide #272.
 PN US2003087349-A1.
 PD 08-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 9; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 699
 ID ADA91968 standard; cDNA; 3721 BP.
 DE Novel human secreted and transmembrane protein PRO4353 cDNA.
 PN US2003082694-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 9; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 700
 ID ADB15031 standard; cDNA; 3721 BP.
 DE Human PRO polynucleotide #272.
 PN US2003087351-A1.
 PD 08-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 9; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 701
 ID ADB18992 standard; cDNA; 3721 BP.
 DE Novel human secreted and transmembrane protein PRO4353 cDNA.
 PN US2003073211-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 9; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 702
 ID ADA94207 standard; cDNA; 3721 BP.
 DE Human PRO polynucleotide #272.
 PN US2003077722-A1.
 PD 24-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 9; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 703
 ID ADB20103 standard; cDNA; 3721 BP.
 DE Novel human secreted and transmembrane protein PRO4353 cDNA.
 PN US2003082691-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 9; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 704
 ID ADB13415 standard; cDNA; 3721 BP.
 DE Human PRO polynucleotide #272.
 PN US2003082710-A1.
 PD 01-MAY-2003.

PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 9; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 705
 ID ACD98695 standard; cDNA; 3721 BP.
 DE Novel human secreted and transmembrane protein PRO4353 cDNA.
 PN US2003044945-A1.
 PD 06-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 9; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 706
 ID ADA74669 standard; cDNA; 3721 BP.
 DE Human PRO polynucleotide #272.
 PN US2003068798-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 9; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 707
 ID ADB24902 standard; cDNA; 3721 BP.
 DE Human PRO polynucleotide SEQ ID NO 543.
 PN US2003077713-A1.
 PD 24-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 9; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 708
 ID ADA82426 standard; cDNA; 3721 BP.
 DE Human PRO polynucleotide #272.
 PN US2003082701-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 9; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 709
 ID ADA75389 standard; cDNA; 3721 BP.
 DE Human PRO polynucleotide #272.
 PN US2003073216-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 9; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 710
 ID ADA85467 standard; cDNA; 3721 BP.
 DE Novel human secreted and transmembrane protein PRO4353 cDNA.
 PN US2003082695-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 9; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 711
 ID ADA84915 standard; cDNA; 3721 BP.
 DE Novel human secreted and transmembrane protein PRO4353 cDNA.
 PN US2003082708-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.

Query Match 4.0%; Score 126; DB 9; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 712
 ID ADB30171 standard; cDNA; 3721 BP.
 DE cDNA encoding human PRO polypeptide #272.
 PN US2003073214-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 9; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 713
 ID ADA80699 standard; cDNA; 3721 BP.
 DE Human PRO polynucleotide #272.
 PN US2003082761-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 9; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 714
 ID ADA75941 standard; cDNA; 3721 BP.
 DE Human PRO polynucleotide #272.
 PN US2003082703-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 9; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 715
 ID ADA47166 standard; cDNA; 3721 BP.
 DE Human PRO polynucleotide #272.
 PN US2003073210-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 9; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 716
 ID ADB25462 standard; cDNA; 3721 BP.
 DE Human PRO polynucleotide SEQ ID NO 543.
 PN US2003077715-A1.
 PD 24-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 9; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 717
 ID ADA93638 standard; cDNA; 3721 BP.
 DE Human PRO polynucleotide #272.
 PN US2003077721-A1.
 PD 24-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 9; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 718
 ID ADB26988 standard; cDNA; 3721 BP.
 DE cDNA encoding human PRO polypeptide #272.
 PN US2003092147-A1.
 PD 15-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 9; Length 3721;

Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 719
 ID ADB31275 standard; cDNA; 3721 BP.
 DE cDNA encoding human PRO polypeptide #272.
 PN US2003096386-A1.
 PD 22-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 9; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 720
 ID ADA61203 standard; cDNA; 3721 BP.
 DE Homo sapiens.
 PN US2003049817-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 9; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 721
 ID ADB24350 standard; cDNA; 3721 BP.
 DE Human PRO polynucleotide SEQ ID NO 543.
 PN US2003077714-A1.
 PD 24-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 9; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 722
 ID ADA96679 standard; cDNA; 3721 BP.
 DE Human PRO polynucleotide #272.
 PN US2003082690-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 9; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 723
 ID ADA81251 standard; cDNA; 3721 BP.
 DE Human PRO polynucleotide #272.
 PN US2003082702-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 9; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 724
 ID ADA96127 standard; cDNA; 3721 BP.
 DE Human PRO polynucleotide #272.
 PN US2003082759-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 9; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 725
 ID ADB26436 standard; cDNA; 3721 BP.
 DE cDNA encoding human PRO polypeptide #272.
 PN US2003082760-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 9; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;

RESULT 726

ID ADB21921 standard; cDNA; 3721 BP.
DE Novel human secreted and transmembrane protein PRO4353 cDNA.
PN US2003082765-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 4.0%; Score 126; DB 9; Length 3721;
Best Local Similarity 55.3%; Pred. No. 2.4e-22;

RESULT 727

ID ADA77700 standard; cDNA; 3721 BP.
DE Human PRO polynucleotide #272.
PN US2003068797-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.0%; Score 126; DB 9; Length 3721;
Best Local Similarity 55.3%; Pred. No. 2.4e-22;

RESULT 728

ID ADB18440 standard; cDNA; 3721 BP.
DE cDNA encoding human PRO polypeptide #272.
PN US2003077710-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.0%; Score 126; DB 9; Length 3721;
Best Local Similarity 55.3%; Pred. No. 2.4e-22;

RESULT 729

ID ADA87123 standard; cDNA; 3721 BP.
DE Novel human secreted and transmembrane protein PRO4353 cDNA.
PN US2003082709-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 4.0%; Score 126; DB 9; Length 3721;
Best Local Similarity 55.3%; Pred. No. 2.4e-22;

RESULT 730

ID ACD42279 standard; cDNA; 3721 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO4353.
PN US2003044842-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.0%; Score 126; DB 9; Length 3721;
Best Local Similarity 55.3%; Pred. No. 2.4e-22;

RESULT 731

ID ADA88226 standard; cDNA; 3721 BP.
DE Novel human secreted and transmembrane protein PRO4353 cDNA.
PN US2003082700-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 4.0%; Score 126; DB 9; Length 3721;
Best Local Similarity 55.3%; Pred. No. 2.4e-22;

RESULT 732

ID ADA46614 standard; cDNA; 3721 BP.
DE Novel human secreted and transmembrane protein PRO4353 cDNA.
PN US2003054516-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.0%; Score 126; DB 9; Length 3721;
Best Local Similarity 55.3%; Pred. No. 2.4e-22;

RESULT 733

ID ADB28644 standard; cDNA; 3721 BP.
 DE cDNA encoding human PRO polypeptide #272.
 PN US2003082699-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 9; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 734
 ID ADB29196 standard; cDNA; 3721 BP.
 DE cDNA encoding human PRO polypeptide #272.
 PN US2003082706-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 9; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 735
 ID ADA77148 standard; cDNA; 3721 BP.
 DE Human PRO polynucleotide #272.
 PN US2003059909-A1.
 PD 27-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 9; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 736
 ID ADA88778 standard; cDNA; 3721 BP.
 DE Novel human secreted and transmembrane protein PRO4353 cDNA.
 PN US2003073213-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 9; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 737
 ID ADA97783 standard; cDNA; 3721 BP.
 DE Human PRO polynucleotide #272.
 PN US2003082686-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 9; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 738
 ID ADB27540 standard; cDNA; 3721 BP.
 DE cDNA encoding human PRO polypeptide #272.
 PN US2003022239-A1.
 PD 30-JAN-2003.
 Query Match 4.0%; Score 126; DB 9; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 739
 ID ADB22473 standard; cDNA; 3721 BP.
 DE Novel human secreted and transmembrane protein PRO4353 cDNA.
 PN US2003087344-A1.
 PD 08-MAY-2003.
 Query Match 4.0%; Score 126; DB 9; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 740
 ID ADA67164 standard; cDNA; 3721 BP.
 DE Human PRO polynucleotide #272.
 PN US2003068793-A1.

PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 9; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 741
 ID ADB23025 standard; cDNA; 3721 BP.
 DE Human PRO polynucleotide #272.
 PN US2003077711-A1.
 PD 24-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 9; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 742
 ID ADB23798 standard; cDNA; 3721 BP.
 DE Human PRO polynucleotide SEQ ID NO 543.
 PN US2003077712-A1.
 PD 24-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 9; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 743
 ID ADA92520 standard; cDNA; 3721 BP.
 DE Novel human secreted and transmembrane protein PRO4353 cDNA.
 PN US2003082712-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 9; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 744
 ID ADB15583 standard; cDNA; 3721 BP.
 DE Human PRO polynucleotide #272.
 PN US2003087352-A1.
 PD 08-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 9; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 745
 ID ADB38835 standard; cDNA; 3721 BP.
 DE Novel human secreted and transmembrane protein PRO4353 cDNA.
 PN US2003082766-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 9; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 746
 ID ADB38283 standard; cDNA; 3721 BP.
 DE Novel human secreted and transmembrane protein PRO4353 cDNA.
 PN US2003087347-A1.
 PD 08-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 9; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 747
 ID ADB66755 standard; cDNA; 3721 BP.
 DE Novel human secreted and transmembrane protein PRO4353 cDNA.
 PN US2003082689-A1.
 PD 01-MAY-2003.

PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 9; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;

RESULT 748
 ID ADB89835 standard; cDNA; 3721 BP.
 DE Human PRO polynucleotide #272.
 PN US2003082698-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 10; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;

RESULT 749
 ID ADB90567 standard; cDNA; 3721 BP.
 DE Human PRO polynucleotide #272.
 PN US2003082762-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 10; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;

RESULT 750
 ID ADB39668 standard; cDNA; 3721 BP.
 DE Novel human secreted and transmembrane protein PRO4353 cDNA.
 PN US2003082764-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 10; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;

RESULT 751
 ID ADB47291 standard; cDNA; 3721 BP.
 DE Novel human secreted and transmembrane protein PRO4353 cDNA.
 PN US2003082687-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 10; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;

RESULT 752
 ID ADB86898 standard; cDNA; 3721 BP.
 DE Human PRO polynucleotide #272.
 PN US2003082697-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 10; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;

RESULT 753
 ID ADB77503 standard; cDNA; 3721 BP.
 DE Novel human secreted and transmembrane protein PRO4353 cDNA.
 PN US2003082696-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 10; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;

RESULT 754
 ID ADB34660 standard; cDNA; 3721 BP.
 DE Human PRO polynucleotide SEQ ID NO 543.
 PN US2003077717-A1.
 PD 24-APR-2003.
 PA (GETH) GENENTECH INC.

Query Match 4.0%; Score 126; DB 10; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 755
 ID ADB35764 standard; cDNA; 3721 BP.
 DE Human PRO polynucleotide SEQ ID NO 543.
 PN US2003077719-A1.
 PD 24-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 10; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 756
 ID ADB34108 standard; cDNA; 3721 BP.
 DE Human PRO polynucleotide SEQ ID NO 543.
 PN US2003077716-A1.
 PD 24-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 10; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 757
 ID ADB35212 standard; cDNA; 3721 BP.
 DE Human PRO polynucleotide SEQ ID NO 543.
 PN US2003077718-A1.
 PD 24-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 10; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 758
 ID ADB36316 standard; cDNA; 3721 BP.
 DE Human PRO polynucleotide SEQ ID NO 543.
 PN US2003077720-A1.
 PD 24-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 10; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 759
 ID ADB46711 standard; cDNA; 3721 BP.
 DE Novel human secreted and transmembrane protein PRO4353 cDNA.
 PN US2003082692-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 10; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 760
 ID AAD59345 standard; cDNA; 3721 BP.
 DE Human PRO4353 cDNA.
 PN US2003049733-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 10; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 761
 ID AAD59220 standard; cDNA; 3721 BP.
 DE Human PRO4353 cDNA.
 PN US2003049734-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 10; Length 3721;

Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 762
 ID ADC50584 standard; cDNA; 3721 BP.
 DE Novel human secreted and transmembrane protein PRO4353 cDNA.
 PN US2003092106-A1.
 PD 15-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 10; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 763
 ID ADC72131 standard; cDNA; 3721 BP.
 DE Novel human secreted and transmembrane protein PRO4353 cDNA.
 PN US2003092107-A1.
 PD 15-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 10; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 764
 ID ADC29790 standard; cDNA; 3721 BP.
 DE Novel human secreted and transmembrane protein PRO4353 cDNA.
 PN US2003092063-A1.
 PD 15-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 10; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 765
 ID ADC60110 standard; cDNA; 3721 BP.
 DE Novel human secreted and transmembrane protein PRO4353 cDNA.
 PN US2003092105-A1.
 PD 15-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 10; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 766
 ID ADC53117 standard; cDNA; 3721 BP.
 DE Novel human secreted and transmembrane protein cDNA Seq ID543.
 PN US2003087365-A1.
 PD 08-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 10; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 767
 ID ADC57471 standard; cDNA; 3721 BP.
 DE Novel human secreted and transmembrane protein cDNA Seq ID543.
 PN US2003087366-A1.
 PD 08-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 10; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 768
 ID ADC60662 standard; cDNA; 3721 BP.
 DE Novel human secreted and transmembrane protein PRO4353 cDNA.
 PN US2003087367-A1.
 PD 08-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 10; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;

RESULT 769

ID ADC51137 standard; cDNA; 3721 BP.
DE Novel human secreted and transmembrane protein PRO4353 cDNA.
PN US2003087361-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 4.0%; Score 126; DB 10; Length 3721;
Best Local Similarity 55.3%; Pred. No. 2.4e-22;

RESULT 770

ID ADC65664 standard; cDNA; 3721 BP.
DE Human PRO polynucleotide #272.
PN US2003087362-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 4.0%; Score 126; DB 10; Length 3721;
Best Local Similarity 55.3%; Pred. No. 2.4e-22;

RESULT 771

ID ADC54762 standard; cDNA; 3721 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID543.
PN US2003087363-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 4.0%; Score 126; DB 10; Length 3721;
Best Local Similarity 55.3%; Pred. No. 2.4e-22;

RESULT 772

ID ADC53723 standard; cDNA; 3721 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID543.
PN US2003087364-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 4.0%; Score 126; DB 10; Length 3721;
Best Local Similarity 55.3%; Pred. No. 2.4e-22;

RESULT 773

ID ADC59246 standard; cDNA; 3721 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID543.
PN US2003087359-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 4.0%; Score 126; DB 10; Length 3721;
Best Local Similarity 55.3%; Pred. No. 2.4e-22;

RESULT 774

ID ADC56124 standard; cDNA; 3721 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID543.
PN US2003087360-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 4.0%; Score 126; DB 10; Length 3721;
Best Local Similarity 55.3%; Pred. No. 2.4e-22;

RESULT 775

ID ADC58694 standard; cDNA; 3721 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID543.
PN US2003087346-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 4.0%; Score 126; DB 10; Length 3721;
Best Local Similarity 55.3%; Pred. No. 2.4e-22;

RESULT 776

ID ADD03368 standard; cDNA; 3721 BP.
 DE Novel human secreted and transmembrane protein PRO4353 cDNA.
 PN US2003092104-A1.
 PD 15-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 10; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 777
 ID ADC90360 standard; cDNA; 3721 BP.
 DE Novel human secreted and transmembrane protein PRO4353 cDNA.
 PN US2003087348-A1.
 PD 08-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 10; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 778
 ID ADC69779 standard; cDNA; 3721 BP.
 DE cDNA encoding human PRO polypeptide #272.
 PN US2003194770-A1.
 PD 16-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 10; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 779
 ID ADC48668 standard; cDNA; 3721 BP.
 DE Human PRO polynucleotide #272.
 PN US2003194773-A1.
 PD 16-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 10; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 780
 ID ADD10197 standard; cDNA; 3721 BP.
 DE Human PRO polynucleotide #272.
 PN US2003194776-A1.
 PD 16-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 10; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 781
 ID ADD04772 standard; cDNA; 3721 BP.
 DE Novel human secreted and transmembrane protein PRO4353 cDNA.
 PN US2003087354-A1.
 PD 08-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 10; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 782
 ID ADC80728 standard; cDNA; 3721 BP.
 DE Novel human secreted and transmembrane protein PRO4353 cDNA.
 PN US2003092103-A1.
 PD 15-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 10; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 783
 ID ADD11235 standard; cDNA; 3721 BP.

DE Human PRO polynucleotide #272.
 PN US2003194774-A1.
 PD 16-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 10; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 784
 ID ADD10556 standard; cDNA; 3721 BP.
 DE Human secreted/transmembrane PRO polypeptide cDNA #134.
 PN US2003105011-A1.
 PD 05-JUN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 10; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 785
 ID ADC48116 standard; cDNA; 3721 BP.
 DE Human PRO polynucleotide #272.
 PN US2003194771-A1.
 PD 16-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 10; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 786
 ID ADC80176 standard; cDNA; 3721 BP.
 DE Novel human secreted and transmembrane protein PRO4353 cDNA.
 PN US2003087358-A1.
 PD 08-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 10; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 787
 ID ADD11516 standard; cDNA; 3721 BP.
 DE Human secreted/transmembrane PRO polypeptide cDNA #134.
 PN US2003105013-A1.
 PD 05-JUN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 10; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 788
 ID ADD09645 standard; cDNA; 3721 BP.
 DE Human PRO polynucleotide #272.
 PN US2003194775-A1.
 PD 16-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 10; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 789
 ID ADD41358 standard; cDNA; 3721 BP.
 DE Novel human secreted and transmembrane protein PRO4353 cDNA.
 PN US2003203438-A1.
 PD 30-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 10; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 790
 ID ADD52497 standard; cDNA; 3721 BP.
 DE cDNA encoding human PRO polypeptide #272.

PN US2003194769-A1.
 PD 16-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 10; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 791
 ID ADD53237 standard; cDNA; 3721 BP.
 DE cDNA encoding human PRO polypeptide #272.
 PN US2003194792-A1.
 PD 16-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 10; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 792
 ID ADD53789 standard; cDNA; 3721 BP.
 DE Novel human secreted and transmembrane protein PRO4353 cDNA.
 PN US2003203437-A1.
 PD 30-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 10; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 793
 ID ADD37309 standard; cDNA; 3721 BP.
 DE Human secreted/transmembrane PRO polypeptide cDNA #134.
 PN US2003105012-A1.
 PD 05-JUN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 10; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 794
 ID ADD51945 standard; cDNA; 3721 BP.
 DE cDNA encoding human PRO polypeptide #272.
 PN US2003194779-A1.
 PD 16-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 10; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 795
 ID ADD02744 standard; cDNA; 3721 BP.
 DE Human PRO polynucleotide #272.
 PN US2003203431-A1.
 PD 30-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 10; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 796
 ID ADD02178 standard; cDNA; 3721 BP.
 DE Human PRO polynucleotide #272.
 PN US2003203430-A1.
 PD 30-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 10; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 797
 ID ADD54360 standard; cDNA; 3721 BP.
 DE Novel human secreted and transmembrane protein PRO4353 cDNA.
 PN US2003203432-A1.

PD 30-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 10; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 798
 ID ADD92677 standard; cDNA; 3721 BP.
 DE Human PRO polynucleotide #272.
 PN US2003199030-A1.
 PD 23-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 10; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 799
 ID ADD91573 standard; cDNA; 3721 BP.
 DE Human PRO polynucleotide #272.
 PN US2003199055-A1.
 PD 23-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 10; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 800
 ID ADE04187 standard; cDNA; 3721 BP.
 DE Human PRO polynucleotide #272.
 PN US2003199057-A1.
 PD 23-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 10; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 801
 ID ADE32484 standard; cDNA; 3721 BP.
 DE Novel human secreted and transmembrane protein PRO4353 cDNA.
 PN US2003194765-A1.
 PD 16-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 10; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 802
 ID ADE22416 standard; cDNA; 3721 BP.
 DE cDNA encoding human PRO polypeptide #272.
 PN US2003199056-A1.
 PD 23-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 10; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 803
 ID ADD79640 standard; cDNA; 3721 BP.
 DE cDNA encoding human PRO polypeptide #272.
 PN US2003203428-A1.
 PD 30-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 10; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 804
 ID ADE42176 standard; cDNA; 3721 BP.
 DE Human PRO polynucleotide #272.
 PN US2003194772-A1.
 PD 16-OCT-2003.

PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 10; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;

RESULT 805
 ID ADE17993 standard; cDNA; 3721 BP.
 DE Human PRO polynucleotide #272.
 PN US2003199023-A1.
 PD 23-OCT-2003.

PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 10; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;

RESULT 806
 ID ADD92125 standard; cDNA; 3721 BP.
 DE Human PRO polynucleotide #272.
 PN US2003199053-A1.
 PD 23-OCT-2003.

PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 10; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;

RESULT 807
 ID ADE33588 standard; cDNA; 3721 BP.
 DE Novel human secreted and transmembrane protein PRO4353 cDNA.
 PN US2003194767-A1.
 PD 16-OCT-2003.

PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 10; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;

RESULT 808
 ID ADE34140 standard; cDNA; 3721 BP.
 DE Novel human secreted and transmembrane protein PRO4353 cDNA.
 PN US2003194791-A1.
 PD 16-OCT-2003.

PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 10; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;

RESULT 809
 ID ADD80192 standard; cDNA; 3721 BP.
 DE cDNA encoding human PRO polypeptide #272.
 PN US2003207417-A1.
 PD 06-NOV-2003.

PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 10; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;

RESULT 810
 ID ADD93229 standard; cDNA; 3721 BP.
 DE Human PRO polynucleotide #272.
 PN US2003194768-A1.
 PD 16-OCT-2003.

PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 10; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;

RESULT 811
 ID ADE19649 standard; cDNA; 3721 BP.
 DE Human PRO polynucleotide #272.
 PN US2003199025-A1.
 PD 23-OCT-2003.

PA (GETH) GENENTECH INC.

Query Match 4.0%; Score 126; DB 10; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 812
 ID ADE19097 standard; cDNA; 3721 BP.
 DE Human PRO polynucleotide #272.
 PN US2003199026-A1.
 PD 23-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 10; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 813
 ID ADE43293 standard; cDNA; 3721 BP.
 DE Human PRO polynucleotide #272.
 PN US2003199033-A1.
 PD 23-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 10; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 814
 ID ADD96082 standard; cDNA; 3721 BP.
 DE Human PRO polynucleotide #272.
 PN US2003199059-A1.
 PD 23-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 10; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 815
 ID ADE22968 standard; cDNA; 3721 BP.
 DE cDNA encoding human PRO polypeptide #272.
 PN US2003199064-A1.
 PD 23-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 10; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 816
 ID ADD79086 standard; cDNA; 3721 BP.
 DE cDNA encoding human PRO polypeptide #272.
 PN US2003203429-A1.
 PD 30-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 10; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 817
 ID ADE33036 standard; cDNA; 3721 BP.
 DE Novel human secreted and transmembrane protein PRO4353 cDNA.
 PN US2003194766-A1.
 PD 16-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 10; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 818
 ID ADE42728 standard; cDNA; 3721 BP.
 DE Human PRO polynucleotide #272.
 PN US2003199032-A1.
 PD 23-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 10; Length 3721;

Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 819
 ID ADD80744 standard; cDNA; 3721 BP.
 DE cDNA encoding human PRO polypeptide #272.
 PN US2003207418-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 10; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 820
 ID ADD89772 standard; cDNA; 3721 BP.
 DE Human PRO polynucleotide #272.
 PN US2003199028-A1.
 PD 23-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 10; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 821
 ID ADE41056 standard; cDNA; 3721 BP.
 DE Human PRO polynucleotide #272.
 PN US2003199031-A1.
 PD 23-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 10; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 822
 ID ADE04855 standard; cDNA; 3721 BP.
 DE Human PRO polynucleotide #272.
 PN US2003199034-A1.
 PD 23-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 10; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 823
 ID ADE92984 standard; cDNA; 3721 BP.
 DE Human PRO polynucleotide #272.
 PN US2003194777-A1.
 PD 16-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 10; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 824
 ID ADG21693 standard; cDNA; 3721 BP.
 DE Novel human secreted and transmembrane protein PRO4353 cDNA.
 PN US2003207355-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 10; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 825
 ID ADG23334 standard; cDNA; 3721 BP.
 DE Novel human secreted and transmembrane protein PRO4353 cDNA.
 PN US2003207384-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 10; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;

RESULT 826

ID ADF97669 standard; cDNA; 3721 BP.

DE Human PRO polynucleotide #272.

PN US2003207370-A1.

PD 06-NOV-2003.

PA (GETH) GENENTECH INC.

Query Match 4.0%; Score 126; DB 10; Length 3721;

Best Local Similarity 55.3%; Pred. No. 2.4e-22;

RESULT 827

ID ADG80733 standard; cDNA; 3721 BP.

DE Human PRO polynucleotide #272.

PN US2003207373-A1.

PD 06-NOV-2003.

PA (GETH) GENENTECH INC.

Query Match 4.0%; Score 126; DB 10; Length 3721;

Best Local Similarity 55.3%; Pred. No. 2.4e-22;

RESULT 828

ID ADG80181 standard; cDNA; 3721 BP.

DE Human PRO polynucleotide #272.

PN US2003207372-A1.

PD 06-NOV-2003.

PA (GETH) GENENTECH INC.

Query Match 4.0%; Score 126; DB 10; Length 3721;

Best Local Similarity 55.3%; Pred. No. 2.4e-22;

RESULT 829

ID ADH55473 standard; cDNA; 3721 BP.

DE Novel human secreted and transmembrane protein PRO4353 cDNA.

PN US2003207381-A1.

PD 06-NOV-2003.

PA (GETH) GENENTECH INC.

Query Match 4.0%; Score 126; DB 10; Length 3721;

Best Local Similarity 55.3%; Pred. No. 2.4e-22;

RESULT 830

ID ADH56025 standard; cDNA; 3721 BP.

DE Novel human secreted and transmembrane protein PRO4353 cDNA.

PN US2003207379-A1.

PD 06-NOV-2003.

PA (GETH) GENENTECH INC.

Query Match 4.0%; Score 126; DB 10; Length 3721;

Best Local Similarity 55.3%; Pred. No. 2.4e-22;

RESULT 831

ID ADI64244 standard; cDNA; 3721 BP.

DE Novel human secreted and transmembrane protein PRO4353 cDNA.

PN US2003207385-A1.

PD 06-NOV-2003.

PA (GETH) GENENTECH INC.

Query Match 4.0%; Score 126; DB 10; Length 3721;

Best Local Similarity 55.3%; Pred. No. 2.4e-22;

RESULT 832

ID ADI65193 standard; cDNA; 3721 BP.

DE Novel human secreted and transmembrane protein PRO4353 cDNA.

PN US2003207386-A1.

PD 06-NOV-2003.

PA (GETH) GENENTECH INC.

Query Match 4.0%; Score 126; DB 10; Length 3721;

Best Local Similarity 55.3%; Pred. No. 2.4e-22;

RESULT 833

ID ADI63692 standard; cDNA; 3721 BP.
 DE Novel human secreted and transmembrane protein PRO4353 cDNA.
 PN US2003207387-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 10; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 834
 ID ADH82106 standard; cDNA; 3721 BP.
 DE Novel human secreted and transmembrane protein PRO4353 cDNA.
 PN US2003207388-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 10; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 835
 ID ADH81554 standard; cDNA; 3721 BP.
 DE Novel human secreted and transmembrane protein PRO4353 cDNA.
 PN US2003207377-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 10; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 836
 ID ACD24124 standard; cDNA; 3721 BP.
 DE Novel human secreted and transmembrane protein PRO4353 cDNA.
 PN US2003032156-A1.
 PD 13-FEB-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 10; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 837
 ID ACA06151 standard; cDNA; 3721 BP.
 DE cDNA encoding human PRO polypeptide #8.
 PN US2003032061-A1.
 PD 13-FEB-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 10; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 838
 ID ACA67265 standard; cDNA; 3721 BP.
 DE cDNA encoding human PRO polypeptide #272.
 PN US2003004311-A1.
 PD 02-JAN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 10; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 839
 ID ADM82723 standard; cDNA; 3721 BP.
 DE Novel human secreted and transmembrane protein PRO4353 cDNA.
 PN US2003087355-A1.
 PD 08-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 11; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 840
 ID ADN16122 standard; cDNA; 3721 BP.

DE Novel human secreted and transmembrane protein PRO4353 cDNA.
 PN US2003087353-A1.
 PD 08-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 11; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 841
 ID ADN16751 standard; cDNA; 3721 BP.
 DE Novel human secreted and transmembrane protein PRO4353 cDNA.
 PN US2003087385-A1.
 PD 08-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 11; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 842
 ID ADN15570 standard; cDNA; 3721 BP.
 DE Novel human secreted and transmembrane protein PRO4353 cDNA.
 PN US2003087356-A1.
 PD 08-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 11; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 843
 ID ADN15018 standard; cDNA; 3721 BP.
 DE Novel human secreted and transmembrane protein PRO4353 cDNA.
 PN US2003087357-A1.
 PD 08-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 11; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 844
 ID ADC81280 standard; cDNA; 3721 BP.
 DE Novel human secreted and transmembrane protein PRO4353 cDNA.
 PN US2003092115-A1.
 PD 15-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 12; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 845
 ID ADD76728 standard; cDNA; 3721 BP.
 DE Human PRO polynucleotide #272.
 PN US2003100087-A1.
 PD 29-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 12; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 846
 ID ADD88092 standard; cDNA; 3721 BP.
 DE Human PRO polynucleotide #272.
 PN US2003092113-A1.
 PD 15-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 12; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 847
 ID ADD86496 standard; cDNA; 3721 BP.
 DE Human PRO polynucleotide #272.

PN US2003203440-A1.
 PD 30-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 12; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 848
 ID ADE75944 standard; cDNA; 3721 BP.
 DE Human PRO polynucleotide #272.
 PN US2003211571-A1.
 PD 13-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 12; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 849
 ID ADE41517 standard; cDNA; 3721 BP.
 DE Human secreted/transmembrane PRO polypeptide cDNA #134.
 PN US2003100497-A1.
 PD 29-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 12; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 850
 ID ADE23520 standard; cDNA; 3721 BP.
 DE cDNA encoding human PRO polypeptide #272.
 PN US2003092108-A1.
 PD 15-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 12; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 851
 ID ADE24072 standard; cDNA; 3721 BP.
 DE cDNA encoding human PRO polypeptide #272.
 PN US2003092110-A1.
 PD 15-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 12; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 852
 ID ADE24715 standard; cDNA; 3721 BP.
 DE cDNA encoding human PRO polypeptide #272.
 PN US2003092111-A1.
 PD 15-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 12; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 853
 ID ADD87540 standard; cDNA; 3721 BP.
 DE Human PRO polynucleotide #272.
 PN US2003203439-A1.
 PD 30-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 12; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 854
 ID ADE89406 standard; cDNA; 3721 BP.
 DE Human PRO polynucleotide #272.
 PN US2003199062-A1.

PD 23-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 12; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 855
 ID ADE18545 standard; cDNA; 3721 BP.
 DE Human PRO polynucleotide #272.
 PN US2003194794-A1.
 PD 16-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 12; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 856
 ID ADE88854 standard; cDNA; 3721 BP.
 DE Human PRO polynucleotide #272.
 PN US2003199054-A1.
 PD 23-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 12; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 857
 ID ADE94874 standard; cDNA; 3721 BP.
 DE cDNA encoding human PRO polypeptide #272.
 PN US2003199027-A1.
 PD 23-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 12; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 858
 ID ADE91285 standard; cDNA; 3721 BP.
 DE Human PRO polynucleotide #272.
 PN US2003199061-A1.
 PD 23-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 12; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 859
 ID ADE95426 standard; cDNA; 3721 BP.
 DE cDNA encoding human PRO polypeptide #272.
 PN US2003199052-A1.
 PD 23-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 12; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 860
 ID ADE93536 standard; cDNA; 3721 BP.
 DE Human PRO polynucleotide #272.
 PN US2003199060-A1.
 PD 23-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 12; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 861
 ID ADF35117 standard; cDNA; 3721 BP.
 DE cDNA encoding human PRO polypeptide #272.
 PN US2003199029-A1.
 PD 23-OCT-2003.

PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 12; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;

RESULT 862
 ID ADE92432 standard; cDNA; 3721 BP.
 DE Novel human secreted and transmembrane protein PRO4353 cDNA.
 PN US2003199051-A1.
 PD 23-OCT-2003.

PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 12; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;

RESULT 863
 ID ADE90733 standard; cDNA; 3721 BP.
 DE Human PRO polynucleotide #272.
 PN US2003199063-A1.
 PD 23-OCT-2003.

PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 12; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;

RESULT 864
 ID ADF09233 standard; cDNA; 3721 BP.
 DE Human secreted and transmembrane protein PRO4353 cDNA.
 PN US2003134327-A1.
 PD 17-JUL-2003.

PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 12; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;

RESULT 865
 ID ADE91880 standard; cDNA; 3721 BP.
 DE Novel human secreted and transmembrane protein PRO4353 cDNA.
 PN US2003199058-A1.
 PD 23-OCT-2003.

PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 12; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;

RESULT 866
 ID ADG02459 standard; cDNA; 3721 BP.
 DE Human PRO polynucleotide #272.
 PN US2003207352-A1.
 PD 06-NOV-2003.

PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 12; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;

RESULT 867
 ID ADG22245 standard; cDNA; 3721 BP.
 DE Novel human secreted and transmembrane protein PRO4353 cDNA.
 PN US2003207360-A1.
 PD 06-NOV-2003.

PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 12; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;

RESULT 868
 ID ADG20315 standard; cDNA; 3721 BP.
 DE cDNA encoding human PRO polypeptide #272.
 PN US2003207376-A1.
 PD 06-NOV-2003.

PA (GETH) GENENTECH INC.

Query Match 4.0%; Score 126; DB 12; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 869
 ID ADF98221 standard; cDNA; 3721 BP.
 DE Human PRO polynucleotide #272.
 PN US2003207422-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 12; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 870
 ID ADG24438 standard; cDNA; 3721 BP.
 DE Novel human secreted and transmembrane protein PRO4353 cDNA.
 PN US2003207426-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 12; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 871
 ID ADF98792 standard; cDNA; 3721 BP.
 DE Human PRO polynucleotide #272.
 PN US2003208055-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 12; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 872
 ID ADG03623 standard; cDNA; 3721 BP.
 DE Human PRO polynucleotide #272.
 PN US2003207351-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 12; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 873
 ID ADF99344 standard; cDNA; 3721 BP.
 DE Human PRO polynucleotide #272.
 PN US2003207353-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 12; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 874
 ID ADG16929 standard; cDNA; 3721 BP.
 DE cDNA encoding human PRO polypeptide #272.
 PN US2003207359-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 12; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 875
 ID ADG05388 standard; cDNA; 3721 BP.
 DE Human PRO polynucleotide #272.
 PN US2003207375-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 12; Length 3721;

Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 876
 ID ADG19655 standard; cDNA; 3721 BP.
 DE cDNA encoding human PRO polypeptide #272.
 PN US2003207425-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 12; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 877
 ID ADG13492 standard; cDNA; 3721 BP.
 DE cDNA encoding human PRO polypeptide #272.
 PN US2003207357-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 12; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 878
 ID ADG08549 standard; cDNA; 3721 BP.
 DE Novel human secreted and transmembrane protein PRO4353 cDNA.
 PN US2003207424-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 12; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 879
 ID ADG15719 standard; cDNA; 3721 BP.
 DE cDNA encoding human PRO polypeptide #272.
 PN US2003219885-A1.
 PD 27-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 12; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 880
 ID ADF97117 standard; cDNA; 3721 BP.
 DE Human PRO polynucleotide #272.
 PN US2003207371-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 12; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 881
 ID ADG06302 standard; cDNA; 3721 BP.
 DE Human PRO polynucleotide #272.
 PN US2003207374-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 12; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 882
 ID ADG23886 standard; cDNA; 3721 BP.
 DE Novel human secreted and transmembrane protein PRO4353 cDNA.
 PN US2003207389-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 12; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;

RESULT 883

ID ADG04175 standard; cDNA; 3721 BP.

DE Human PRO polynucleotide #272.

PN US2003207423-A1.

PD 06-NOV-2003.

PA (GETH) GENENTECH INC.

Query Match 4.0%; Score 126; DB 12; Length 3721;

Best Local Similarity 55.3%; Pred. No. 2.4e-22;

RESULT 884

ID ADG25076 standard; cDNA; 3721 BP.

DE Novel human secreted and transmembrane protein PRO4353 cDNA.

PN US2003207427-A1.

PD 06-NOV-2003.

PA (GETH) GENENTECH INC.

Query Match 4.0%; Score 126; DB 12; Length 3721;

Best Local Similarity 55.3%; Pred. No. 2.4e-22;

RESULT 885

ID ADG07373 standard; cDNA; 3721 BP.

DE Novel human secreted and transmembrane protein PRO4353 cDNA.

PN US2003207350-A1.

PD 06-NOV-2003.

PA (GETH) GENENTECH INC.

Query Match 4.0%; Score 126; DB 12; Length 3721;

Best Local Similarity 55.3%; Pred. No. 2.4e-22;

RESULT 886

ID ADG07925 standard; cDNA; 3721 BP.

DE Novel human secreted and transmembrane protein PRO4353 cDNA.

PN US2003207356-A1.

PD 06-NOV-2003.

PA (GETH) GENENTECH INC.

Query Match 4.0%; Score 126; DB 12; Length 3721;

Best Local Similarity 55.3%; Pred. No. 2.4e-22;

RESULT 887

ID ADG55420 standard; cDNA; 3721 BP.

DE Novel human secreted and transmembrane protein PRO4353 cDNA.

PN US2003194778-A1.

PD 16-OCT-2003.

PA (GETH) GENENTECH INC.

Query Match 4.0%; Score 126; DB 12; Length 3721;

Best Local Similarity 55.3%; Pred. No. 2.4e-22;

RESULT 888

ID ADG61084 standard; cDNA; 3721 BP.

DE Novel human secreted and transmembrane protein PRO4353 cDNA.

PN US2003207390-A1.

PD 06-NOV-2003.

PA (GETH) GENENTECH INC.

Query Match 4.0%; Score 126; DB 12; Length 3721;

Best Local Similarity 55.3%; Pred. No. 2.4e-22;

RESULT 889

ID ADG62188 standard; cDNA; 3721 BP.

DE Novel human secreted and transmembrane protein PRO4353 cDNA.

PN US2003207428-A1.

PD 06-NOV-2003.

PA (GETH) GENENTECH INC.

Query Match 4.0%; Score 126; DB 12; Length 3721;

Best Local Similarity 55.3%; Pred. No. 2.4e-22;

RESULT 890

ID ADG82389 standard; cDNA; 3721 BP.
 DE Human PRO polynucleotide #272.
 PN US2003207358-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 12; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 891
 ID ADG57628 standard; cDNA; 3721 BP.
 DE Novel human secreted and transmembrane protein PRO4353 cDNA.
 PN US2003207362-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 12; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 892
 ID ADG57076 standard; cDNA; 3721 BP.
 DE Novel human secreted and transmembrane protein PRO4353 cDNA.
 PN US2003207364-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 12; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 893
 ID ADG55972 standard; cDNA; 3721 BP.
 DE Novel human secreted and transmembrane protein PRO4353 cDNA.
 PN US2003207365-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 12; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 894
 ID ADG58732 standard; cDNA; 3721 BP.
 DE Novel human secreted and transmembrane protein PRO4353 cDNA.
 PN US2003207368-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 12; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 895
 ID ADG71098 standard; cDNA; 3721 BP.
 DE Novel human secreted and transmembrane protein PRO4353 cDNA.
 PN US2003207420-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 12; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 896
 ID ADG58180 standard; cDNA; 3721 BP.
 DE Novel human secreted and transmembrane protein PRO4353 cDNA.
 PN US2003207363-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 12; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 897
 ID ADG53764 standard; cDNA; 3721 BP.

DE Novel human secreted and transmembrane protein PRO4353 cDNA.
 PN US2003207415-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 12; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 898
 ID ADG71650 standard; cDNA; 3721 BP.
 DE Novel human secreted and transmembrane protein PRO4353 cDNA.
 PN US2003207421-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 12; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 899
 ID ADG81837 standard; cDNA; 3721 BP.
 DE Human PRO polynucleotide #272.
 PN US2003207805-A1.
 PD 06-NOV-2003.
 Query Match 4.0%; Score 126; DB 12; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 900
 ID ADH30799 standard; cDNA; 3721 BP.
 DE Human PRO polynucleotide #272.
 PN US2003077723-A1.
 PD 24-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 12; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 901
 ID ADH12166 standard; cDNA; 3721 BP.
 DE Novel human secreted and transmembrane protein PRO4353 cDNA.
 PN US2003207419-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 12; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 902
 ID ADG52588 standard; cDNA; 3721 BP.
 DE Novel human secreted and transmembrane protein PRO4353 cDNA.
 PN US2003207414-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 12; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 903
 ID ADG54316 standard; cDNA; 3721 BP.
 DE Novel human secreted and transmembrane protein PRO4353 cDNA.
 PN US2003207416-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 12; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 904
 ID ADG81285 standard; cDNA; 3721 BP.
 DE Human PRO polynucleotide #272.
 PN US2003194793-A1.

PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 4.0%; Score 126; DB 12; Length 3721;
Best Local Similarity 55.3%; Pred. No. 2.4e-22;
RESULT 905
ID ADG56524 standard; cDNA; 3721 BP.
DE Novel human secreted and transmembrane protein PRO4353 cDNA.
PN US2003207366-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 4.0%; Score 126; DB 12; Length 3721;
Best Local Similarity 55.3%; Pred. No. 2.4e-22;
RESULT 906
ID ADH12790 standard; cDNA; 3721 BP.
DE Novel human secreted and transmembrane protein PRO4353 cDNA.
PN US2003207378-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 4.0%; Score 126; DB 12; Length 3721;
Best Local Similarity 55.3%; Pred. No. 2.4e-22;
RESULT 907
ID ADG61636 standard; cDNA; 3721 BP.
DE Novel human secreted and transmembrane protein PRO4353 cDNA.
PN US2003207429-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 4.0%; Score 126; DB 12; Length 3721;
Best Local Similarity 55.3%; Pred. No. 2.4e-22;
RESULT 908
ID ADH28723 standard; cDNA; 3721 BP.
DE Human PRO polynucleotide #272.
PN US2003022331-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 4.0%; Score 126; DB 12; Length 3721;
Best Local Similarity 55.3%; Pred. No. 2.4e-22;
RESULT 909
ID ADG54868 standard; cDNA; 3721 BP.
DE Novel human secreted and transmembrane protein PRO4353 cDNA.
PN US2003207367-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 4.0%; Score 126; DB 12; Length 3721;
Best Local Similarity 55.3%; Pred. No. 2.4e-22;
RESULT 910
ID ADG59908 standard; cDNA; 3721 BP.
DE Novel human secreted and transmembrane protein PRO4353 cDNA.
PN US2003207369-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 4.0%; Score 126; DB 12; Length 3721;
Best Local Similarity 55.3%; Pred. No. 2.4e-22;
RESULT 911
ID ADH43700 standard; cDNA; 3721 BP.
DE Human PRO polynucleotide #134.
PN US2003224984-A1.
PD 04-DEC-2003.

PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 12; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;

RESULT 912
 ID ADI81332 standard; cDNA; 3721 BP.
 DE cDNA encoding human PRO polypeptide #272.
 PN US2003207361-A1.
 PD 06-NOV-2003.

PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 12; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;

RESULT 913
 ID ADG10075 standard; cDNA; 3721 BP.
 DE Novel human secreted and transmembrane protein PRO4353 cDNA.
 PN US2004009548-A1.
 PD 15-JAN-2004.

PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 12; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;

RESULT 914
 ID ADI15546 standard; cDNA; 3721 BP.
 DE Novel human secreted and transmembrane protein PRO4353 cDNA.
 PN US2003207382-A1.
 PD 06-NOV-2003.

PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 12; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;

RESULT 915
 ID ADG09423 standard; cDNA; 3721 BP.
 DE Novel human secreted and transmembrane protein PRO4353 cDNA.
 PN US2004009547-A1.
 PD 15-JAN-2004.

PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 12; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;

RESULT 916
 ID ADI14878 standard; cDNA; 3721 BP.
 DE Novel human secreted and transmembrane protein PRO4353 cDNA.
 PN US2003207383-A1.
 PD 06-NOV-2003.

PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 12; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;

RESULT 917
 ID ADI18473 standard; cDNA; 3721 BP.
 DE Novel human secreted and transmembrane protein PRO4353 cDNA.
 PN US2003207349-A1.
 PD 06-NOV-2003.

PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 12; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;

RESULT 918
 ID ADJ63754 standard; cDNA; 3721 BP.
 DE Novel human secreted and transmembrane protein PRO4353 cDNA.
 PN US2004039164-A1.
 PD 26-FEB-2004.

PA (GETH) GENENTECH INC.

Query Match 4.0%; Score 126; DB 12; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 919
 ID ADJ77649 standard; cDNA; 3721 BP.
 DE Human PRO polynucleotide #272.
 PN US2004038336-A1.
 PD 26-FEB-2004.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 12; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 920
 ID ADK83045 standard; cDNA; 3721 BP.
 DE Human PRO polynucleotide #134.
 PN US2004043927-A1.
 PD 04-MAR-2004.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 12; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 921
 ID ADJ65771 standard; cDNA; 3721 BP.
 DE cDNA encoding human PRO polypeptide #272.
 PN US2004038335-A1.
 PD 26-FEB-2004.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 12; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 922
 ID ADM27907 standard; cDNA; 3721 BP.
 DE cDNA encoding human PRO polypeptide #272.
 PN US2004048333-A1.
 PD 11-MAR-2004.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 12; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 923
 ID ADM42631 standard; cDNA; 3721 BP.
 DE cDNA encoding human PRO polypeptide #272.
 PN US2004058424-A1.
 PD 25-MAR-2004.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 12; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 924
 ID ADM28493 standard; cDNA; 3721 BP.
 DE cDNA encoding human PRO polypeptide #272.
 PN US2004077064-A1.
 PD 22-APR-2004.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 12; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 925
 ID ADI95975 standard; cDNA; 3721 BP.
 DE cDNA encoding human PRO polypeptide #272.
 PN US2003077659-A1.
 PD 24-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 13; Length 3721;

Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 926
 ID ADI96527 standard; cDNA; 3721 BP.
 DE Novel human secreted and transmembrane protein PRO4353 cDNA.
 PN US2003207354-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 4.0%; Score 126; DB 13; Length 3721;
 Best Local Similarity 55.3%; Pred. No. 2.4e-22;
 RESULT 927
 ID AAD08306 standard; cDNA; 888 BP.
 DE Human secreted protein-encoding gene 1 cDNA clone HKAHL26, SEQ ID NO: 34.
 PN WO200136440-A1.
 PD 25-MAY-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 4.0%; Score 125.4; DB 4; Length 888;
 Best Local Similarity 51.0%; Pred. No. 1.7e-22;
 RESULT 928
 ID AAT72107 standard; cDNA to mRNA; 3692 BP.
 DE Rat semaphorin Z gene.
 PN WO9720928-A1.
 PD 12-JUN-1997.
 PA (SUMU) SUMITOMO PHARM CO LTD.
 Query Match 4.0%; Score 125.4; DB 2; Length 3692;
 Best Local Similarity 58.5%; Pred. No. 3.4e-22;
 RESULT 929
 ID ADS73258 standard; cDNA; 3279 BP.
 DE Human kidney tumour specific cDNA K1622P ORF #3.
 PN US2003109434-A1.
 PD 12-JUN-2003.
 PA (CORI-) CORIXA CORP.
 Query Match 3.9%; Score 121.8; DB 7; Length 3279;
 Best Local Similarity 49.6%; Pred. No. 2.9e-21;
 RESULT 930
 ID ADS73257 standard; cDNA; 3453 BP.
 DE Human kidney tumour specific cDNA K1622P ORF #2.
 PN US2003109434-A1.
 PD 12-JUN-2003.
 PA (CORI-) CORIXA CORP.
 Query Match 3.9%; Score 121.8; DB 7; Length 3453;
 Best Local Similarity 49.6%; Pred. No. 3e-21;
 RESULT 931
 ID ADS73256 standard; cDNA; 3606 BP.
 DE Human kidney tumour specific cDNA K1622P ORF #1.
 PN US2003109434-A1.
 PD 12-JUN-2003.
 PA (CORI-) CORIXA CORP.
 Query Match 3.9%; Score 121.8; DB 7; Length 3606;
 Best Local Similarity 49.6%; Pred. No. 3.1e-21;
 RESULT 932
 ID ADD18221 standard; DNA; 3631 BP.
 DE Human molecule (MOL) protein MOL4c DNA sequence.
 PN WO2003003984-A2.
 PD 16-JAN-2003.
 PA (CURA-) CURAGEN CORP.
 Query Match 3.9%; Score 121.8; DB 10; Length 3631;
 Best Local Similarity 49.6%; Pred. No. 3.1e-21;

RESULT 933

ID ADJ34118 standard; cDNA; 3631 BP.

DE Human cDNA encoding secreted protein NOV2b.

PN WO2004000997-A2.

PD 31-DEC-2003.

PA (CURA-) CURAGEN CORP.

Query Match 3.9%; Score 121.8; DB 12; Length 3631;

Best Local Similarity 49.6%; Pred. No. 3.1e-21;

RESULT 934

ID ADF72677 standard; cDNA; 3938 BP.

DE Human cancer-related gene nucleotide sequence SEQ ID NO:7.

PN WO2003101400-A2.

PD 11-DEC-2003.

PA (AVAL-) AVALON PHARM INC.

Query Match 3.9%; Score 121.8; DB 12; Length 3938;

Best Local Similarity 49.6%; Pred. No. 3.2e-21;

RESULT 935

ID ADF72703 standard; cDNA; 3938 BP.

DE Human cancer-related gene nucleotide sequence SEQ ID NO:33.

PN WO2003101400-A2.

PD 11-DEC-2003.

PA (AVAL-) AVALON PHARM INC.

Query Match 3.9%; Score 121.8; DB 12; Length 3938;

Best Local Similarity 49.6%; Pred. No. 3.2e-21;

RESULT 936

ID ADF72690 standard; cDNA; 3938 BP.

DE Human cancer-related gene nucleotide sequence SEQ ID NO:20.

PN WO2003101400-A2.

PD 11-DEC-2003.

PA (AVAL-) AVALON PHARM INC.

Query Match 3.9%; Score 121.8; DB 12; Length 3938;

Best Local Similarity 49.6%; Pred. No. 3.2e-21;

RESULT 937

ID ADJ34128 standard; cDNA; 4233 BP.

DE Human cDNA encoding secreted protein NOV2g.

PN WO2004000997-A2.

PD 31-DEC-2003.

PA (CURA-) CURAGEN CORP.

Query Match 3.9%; Score 121.8; DB 12; Length 4233;

Best Local Similarity 49.6%; Pred. No. 3.3e-21;

RESULT 938

ID ADF72702 standard; cDNA; 4405 BP.

DE Human cancer-related gene nucleotide sequence SEQ ID NO:32.

PN WO2003101400-A2.

PD 11-DEC-2003.

PA (AVAL-) AVALON PHARM INC.

Query Match 3.9%; Score 121.8; DB 12; Length 4405;

Best Local Similarity 49.6%; Pred. No. 3.4e-21;

RESULT 939

ID ADF72689 standard; cDNA; 4405 BP.

DE Human cancer-related gene nucleotide sequence SEQ ID NO:19.

PN WO2003101400-A2.

PD 11-DEC-2003.

PA (AVAL-) AVALON PHARM INC.

Query Match 3.9%; Score 121.8; DB 12; Length 4405;

Best Local Similarity 49.6%; Pred. No. 3.4e-21;

RESULT 940

ID ADF72676 standard; cDNA; 4405 BP.
 DE Human cancer-related gene nucleotide sequence SEQ ID NO:6.
 PN WO2003101400-A2.
 PD 11-DEC-2003.
 PA (AVAL-) AVALON PHARM INC.
 Query Match 3.9%; Score 121.8; DB 12; Length 4405;
 Best Local Similarity 49.6%; Pred. No. 3.4e-21;
 RESULT 941
 ID ABA00058 standard; cDNA; 4456 BP.
 DE CADHP-5 coding sequence, Incyte ID No: 2496174CB1.
 PN WO200259312-A2.
 PD 01-AUG-2002.
 PA (INCY-) INCYTE GENOMICS INC.
 Query Match 3.9%; Score 121.8; DB 6; Length 4456;
 Best Local Similarity 49.6%; Pred. No. 3.4e-21;
 RESULT 942
 ID ADS73255 standard; cDNA; 4559 BP.
 DE Human kidney tumour specific full length cDNA K1622P.
 PN US2003109434-A1.
 PD 12-JUN-2003.
 PA (CORI-) CORIXA CORP.
 Query Match 3.9%; Score 121.8; DB 7; Length 4559;
 Best Local Similarity 49.6%; Pred. No. 3.5e-21;
 RESULT 943
 ID ADR44043 standard; DNA; 4559 BP.
 DE Human kidney tumour associated gene clone-54 SEQ ID NO:53.
 PN WO2004074506-A2.
 PD 02-SEP-2004.
 PA (MERG-) MERGEN LTD.
 Query Match 3.9%; Score 121.8; DB 13; Length 4559;
 Best Local Similarity 49.6%; Pred. No. 3.5e-21;
 RESULT 944
 ID ADF72671 standard; cDNA; 4567 BP.
 DE Human cancer-related gene nucleotide sequence SEQ ID NO:1.
 PN WO2003101400-A2.
 PD 11-DEC-2003.
 PA (AVAL-) AVALON PHARM INC.
 Query Match 3.9%; Score 121.8; DB 12; Length 4567;
 Best Local Similarity 49.6%; Pred. No. 3.5e-21;
 RESULT 945
 ID ADF72697 standard; cDNA; 4567 BP.
 DE Human cancer-related gene nucleotide sequence SEQ ID NO:27.
 PN WO2003101400-A2.
 PD 11-DEC-2003.
 PA (AVAL-) AVALON PHARM INC.
 Query Match 3.9%; Score 121.8; DB 12; Length 4567;
 Best Local Similarity 49.6%; Pred. No. 3.5e-21;
 RESULT 946
 ID ADF72684 standard; cDNA; 4567 BP.
 DE Human cancer-related gene nucleotide sequence SEQ ID NO:14.
 PN WO2003101400-A2.
 PD 11-DEC-2003.
 PA (AVAL-) AVALON PHARM INC.
 Query Match 3.9%; Score 121.8; DB 12; Length 4567;
 Best Local Similarity 49.6%; Pred. No. 3.5e-21;
 RESULT 947
 ID ADE07460 standard; DNA; 4650 BP.

DE Novel coding sequence (useful for identifying genetic disorders) #526.
PN WO2003054152-A2.
PD 03-JUL-2003.
PA (HYSE-) HYSEQ INC.
Query Match 3.9%; Score 121.8; DB 10; Length 4650;
Best Local Similarity 49.6%; Pred. No. 3.5e-21;
RESULT 948
ID ADF72699 standard; cDNA; 4675 BP.
DE Human cancer-related gene nucleotide sequence SEQ ID NO:29.
PN WO2003101400-A2.
PD 11-DEC-2003.
PA (AVAL-) AVALON PHARM INC.
Query Match 3.9%; Score 121.8; DB 12; Length 4675;
Best Local Similarity 49.6%; Pred. No. 3.5e-21;
RESULT 949
ID ADF72673 standard; cDNA; 4675 BP.
DE Human cancer-related gene nucleotide sequence SEQ ID NO:3.
PN WO2003101400-A2.
PD 11-DEC-2003.
PA (AVAL-) AVALON PHARM INC.
Query Match 3.9%; Score 121.8; DB 12; Length 4675;
Best Local Similarity 49.6%; Pred. No. 3.5e-21;
RESULT 950
ID ADF72686 standard; cDNA; 4675 BP.
DE Human cancer-related gene nucleotide sequence SEQ ID NO:16.
PN WO2003101400-A2.
PD 11-DEC-2003.
PA (AVAL-) AVALON PHARM INC.
Query Match 3.9%; Score 121.8; DB 12; Length 4675;
Best Local Similarity 49.6%; Pred. No. 3.5e-21;
RESULT 951
ID ADF72701 standard; cDNA; 4703 BP.
DE Human cancer-related gene nucleotide sequence SEQ ID NO:31.
PN WO2003101400-A2.
PD 11-DEC-2003.
PA (AVAL-) AVALON PHARM INC.
Query Match 3.9%; Score 121.8; DB 12; Length 4703;
Best Local Similarity 49.6%; Pred. No. 3.5e-21;
RESULT 952
ID ADF72688 standard; cDNA; 4703 BP.
DE Human cancer-related gene nucleotide sequence SEQ ID NO:18.
PN WO2003101400-A2.
PD 11-DEC-2003.
PA (AVAL-) AVALON PHARM INC.
Query Match 3.9%; Score 121.8; DB 12; Length 4703;
Best Local Similarity 49.6%; Pred. No. 3.5e-21;
RESULT 953
ID ADF72675 standard; cDNA; 4703 BP.
DE Human cancer-related gene nucleotide sequence SEQ ID NO:5.
PN WO2003101400-A2.
PD 11-DEC-2003.
PA (AVAL-) AVALON PHARM INC.
Query Match 3.9%; Score 121.8; DB 12; Length 4703;
Best Local Similarity 49.6%; Pred. No. 3.5e-21;
RESULT 954
ID ABK70008 standard; DNA; 4725 BP.
DE cDNA encoding human Pro peptide #48.

PN WO200224888-A2.
 PD 28-MAR-2002.
 PA (GETH) GENENTECH INC.
 Query Match 3.9%; Score 121.8; DB 6; Length 4725;
 Best Local Similarity 49.6%; Pred. No. 3.5e-21;
 RESULT 955
 ID ADA01363 standard; cDNA; 4725 BP.
 DE Human PRO polynucleotide #48.
 PN US2003068779-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 3.9%; Score 121.8; DB 9; Length 4725;
 Best Local Similarity 49.6%; Pred. No. 3.5e-21;
 RESULT 956
 ID ADA43792 standard; cDNA; 4725 BP.
 DE Human cDNA encoding secreted/transmembrane polypeptide PRO34001.
 PN US2003064474-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 3.9%; Score 121.8; DB 9; Length 4725;
 Best Local Similarity 49.6%; Pred. No. 3.5e-21;
 RESULT 957
 ID ADA43560 standard; cDNA; 4725 BP.
 DE Human cDNA encoding secreted/transmembrane polypeptide PRO34001.
 PN US2003073196-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 3.9%; Score 121.8; DB 9; Length 4725;
 Best Local Similarity 49.6%; Pred. No. 3.5e-21;
 RESULT 958
 ID ADA01235 standard; cDNA; 4725 BP.
 DE Human PRO polynucleotide #48.
 PN US2003068782-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 3.9%; Score 121.8; DB 9; Length 4725;
 Best Local Similarity 49.6%; Pred. No. 3.5e-21;
 RESULT 959
 ID ADA01119 standard; cDNA; 4725 BP.
 DE Human cDNA encoding secreted/transmembrane polypeptide PRO34001.
 PN US2003068780-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 3.9%; Score 121.8; DB 9; Length 4725;
 Best Local Similarity 49.6%; Pred. No. 3.5e-21;
 RESULT 960
 ID ADA43676 standard; cDNA; 4725 BP.
 DE Human cDNA encoding secreted/transmembrane polypeptide PRO34001.
 PN US2003073190-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 3.9%; Score 121.8; DB 9; Length 4725;
 Best Local Similarity 49.6%; Pred. No. 3.5e-21;
 RESULT 961
 ID ADA06938 standard; cDNA; 4725 BP.
 DE Human PRO polynucleotide #48.
 PN US2003068781-A1.

PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.9%; Score 121.8; DB 9; Length 4725;
Best Local Similarity 49.6%; Pred. No. 3.5e-21;
RESULT 962
ID ADA08426 standard; cDNA; 4725 BP.
DE Novel human secreted and transmembrane protein PRO34001 cDNA.
PN US2003068783-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.9%; Score 121.8; DB 9; Length 4725;
Best Local Similarity 49.6%; Pred. No. 3.5e-21;
RESULT 963
ID ADB99719 standard; cDNA; 4725 BP.
DE Human PRO polynucleotide SEQ ID 95.
PN US2003082728-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 3.9%; Score 121.8; DB 9; Length 4725;
Best Local Similarity 49.6%; Pred. No. 3.5e-21;
RESULT 964
ID ADB87002 standard; cDNA; 4725 BP.
DE Human PRO polynucleotide #48.
PN US2003082726-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 3.9%; Score 121.8; DB 9; Length 4725;
Best Local Similarity 49.6%; Pred. No. 3.5e-21;
RESULT 965
ID ADB66157 standard; cDNA; 4725 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO34001.
PN US2003082729-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 3.9%; Score 121.8; DB 9; Length 4725;
Best Local Similarity 49.6%; Pred. No. 3.5e-21;
RESULT 966
ID ADB99835 standard; cDNA; 4725 BP.
DE Human PRO polynucleotide SEQ ID 95.
PN US2003073192-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.9%; Score 121.8; DB 10; Length 4725;
Best Local Similarity 49.6%; Pred. No. 3.5e-21;
RESULT 967
ID ADB99490 standard; cDNA; 4725 BP.
DE Novel human secreted and transmembrane protein PRO34001 cDNA.
PN US2003082731-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 3.9%; Score 121.8; DB 10; Length 4725;
Best Local Similarity 49.6%; Pred. No. 3.5e-21;
RESULT 968
ID ADB66041 standard; cDNA; 4725 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO34001.
PN US2003082732-A1.
PD 01-MAY-2003.

PA (GETH) GENENTECH INC.
 Query Match 3.9%; Score 121.8; DB 10; Length 4725;
 Best Local Similarity 49.6%; Pred. No. 3.5e-21;
 RESULT 969
 ID ADC23439 standard; cDNA; 4725 BP.
 DE Human cDNA clone (SeqID 95) encoding the transmembrane PRO protein.
 PN US2003073193-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 3.9%; Score 121.8; DB 10; Length 4725;
 Best Local Similarity 49.6%; Pred. No. 3.5e-21;
 RESULT 970
 ID ADC26132 standard; cDNA; 4725 BP.
 DE Human PRO34001 cDNA.
 PN US2003073194-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 3.9%; Score 121.8; DB 10; Length 4725;
 Best Local Similarity 49.6%; Pred. No. 3.5e-21;
 RESULT 971
 ID ADE04959 standard; cDNA; 4725 BP.
 DE Human PRO polynucleotide #48.
 PN US2003068778-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 3.9%; Score 121.8; DB 10; Length 4725;
 Best Local Similarity 49.6%; Pred. No. 3.5e-21;
 RESULT 972
 ID ADE11265 standard; cDNA; 4725 BP.
 DE Human PRO polynucleotide #48.
 PN US2003073191-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 3.9%; Score 121.8; DB 10; Length 4725;
 Best Local Similarity 49.6%; Pred. No. 3.5e-21;
 RESULT 973
 ID ADD88196 standard; cDNA; 4725 BP.
 DE Human PRO polynucleotide #48.
 PN US2003082733-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 3.9%; Score 121.8; DB 10; Length 4725;
 Best Local Similarity 49.6%; Pred. No. 3.5e-21;
 RESULT 974
 ID ADD95491 standard; cDNA; 4725 BP.
 DE Human cDNA encoding secreted/transmembrane polypeptide PRO34001.
 PN US2003064473-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 3.9%; Score 121.8; DB 10; Length 4725;
 Best Local Similarity 49.6%; Pred. No. 3.5e-21;
 RESULT 975
 ID ADE06421 standard; cDNA; 4725 BP.
 DE Human PRO polynucleotide #48.
 PN US2003073195-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC.

Query Match 3.9%; Score 121.8; DB 10; Length 4725;
 Best Local Similarity 49.6%; Pred. No. 3.5e-21;
 RESULT 976
 ID ADE38196 standard; cDNA; 4725 BP.
 DE Human PRO polynucleotide #48.
 PN US2003119120-A1.
 PD 26-JUN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 3.9%; Score 121.8; DB 10; Length 4725;
 Best Local Similarity 49.6%; Pred. No. 3.5e-21;
 RESULT 977
 ID ADD88312 standard; cDNA; 4725 BP.
 DE Human PRO polynucleotide #48.
 PN US2003073189-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 3.9%; Score 121.8; DB 10; Length 4725;
 Best Local Similarity 49.6%; Pred. No. 3.5e-21;
 RESULT 978
 ID ADD90893 standard; cDNA; 4725 BP.
 DE Human cDNA encoding secreted/transmembrane polypeptide PRO34001.
 PN US2003073188-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 3.9%; Score 121.8; DB 10; Length 4725;
 Best Local Similarity 49.6%; Pred. No. 3.5e-21;
 RESULT 979
 ID ADF99448 standard; cDNA; 4725 BP.
 DE Human cDNA encoding secreted/transmembrane polypeptide PRO34001.
 PN US2003078401-A1.
 PD 24-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 3.9%; Score 121.8; DB 10; Length 4725;
 Best Local Similarity 49.6%; Pred. No. 3.5e-21;
 RESULT 980
 ID ADG06541 standard; cDNA; 4725 BP.
 DE Human PRO polynucleotide #48.
 PN US2003077742-A1.
 PD 24-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 3.9%; Score 121.8; DB 10; Length 4725;
 Best Local Similarity 49.6%; Pred. No. 3.5e-21;
 RESULT 981
 ID ADG05492 standard; cDNA; 4725 BP.
 DE Human PRO polynucleotide #48.
 PN US2003077741-A1.
 PD 24-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 3.9%; Score 121.8; DB 10; Length 4725;
 Best Local Similarity 49.6%; Pred. No. 3.5e-21;
 RESULT 982
 ID ADG82493 standard; cDNA; 4725 BP.
 DE Human PRO polynucleotide #48.
 PN US2003077744-A1.
 PD 24-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 3.9%; Score 121.8; DB 10; Length 4725;

Best Local Similarity 49.6%; Pred. No. 3.5e-21;
 RESULT 983
 ID ADE51746 standard; cDNA; 4725 BP.
 DE Human cDNA encoding secreted/transmembrane polypeptide PRO34001.
 PN US2003104560-A1.
 PD 05-JUN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 3.9%; Score 121.8; DB 12; Length 4725;
 Best Local Similarity 49.6%; Pred. No. 3.5e-21;
 RESULT 984
 ID ADE51862 standard; cDNA; 4725 BP.
 DE Human cDNA encoding secreted/transmembrane polypeptide PRO34001.
 PN US2003104561-A1.
 PD 05-JUN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 3.9%; Score 121.8; DB 12; Length 4725;
 Best Local Similarity 49.6%; Pred. No. 3.5e-21;
 RESULT 985
 ID ADE37720 standard; cDNA; 4725 BP.
 DE Human cDNA encoding secreted/transmembrane polypeptide PRO34001.
 PN US2003104564-A1.
 PD 05-JUN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 3.9%; Score 121.8; DB 12; Length 4725;
 Best Local Similarity 49.6%; Pred. No. 3.5e-21;
 RESULT 986
 ID ADE37604 standard; cDNA; 4725 BP.
 DE Human cDNA encoding secreted/transmembrane polypeptide PRO34001.
 PN US2003104565-A1.
 PD 05-JUN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 3.9%; Score 121.8; DB 12; Length 4725;
 Best Local Similarity 49.6%; Pred. No. 3.5e-21;
 RESULT 987
 ID ADD95375 standard; cDNA; 4725 BP.
 DE Human cDNA encoding secreted/transmembrane polypeptide PRO34001.
 PN US2003138901-A1.
 PD 24-JUL-2003.
 PA (GETH) GENENTECH INC.
 Query Match 3.9%; Score 121.8; DB 12; Length 4725;
 Best Local Similarity 49.6%; Pred. No. 3.5e-21;
 RESULT 988
 ID ADE38075 standard; cDNA; 4725 BP.
 DE Human PRO polynucleotide #48.
 PN US2003104566-A1.
 PD 05-JUN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 3.9%; Score 121.8; DB 12; Length 4725;
 Best Local Similarity 49.6%; Pred. No. 3.5e-21;
 RESULT 989
 ID ADE76164 standard; cDNA; 4725 BP.
 DE Human PRO polynucleotide #48.
 PN US2003124665-A1.
 PD 03-JUL-2003.
 PA (GETH) GENENTECH INC.
 Query Match 3.9%; Score 121.8; DB 12; Length 4725;
 Best Local Similarity 49.6%; Pred. No. 3.5e-21;

RESULT 990

ID ADE39487 standard; cDNA; 4725 BP.

DE Human PRO polynucleotide #48.

PN US2003119117-A1.

PD 26-JUN-2003.

PA (GETH) GENENTECH INC.

Query Match 3.9%; Score 121.8; DB 12; Length 4725;

Best Local Similarity 49.6%; Pred. No. 3.5e-21;

RESULT 991

ID ADE04291 standard; cDNA; 4725 BP.

DE Human PRO polynucleotide #48.

PN US2003096364-A1.

PD 22-MAY-2003.

PA (GETH) GENENTECH INC.

Query Match 3.9%; Score 121.8; DB 12; Length 4725;

Best Local Similarity 49.6%; Pred. No. 3.5e-21;

RESULT 992

ID ADE39888 standard; cDNA; 4725 BP.

DE Human PRO polynucleotide #48.

PN US2003138896-A1.

PD 24-JUL-2003.

PA (GETH) GENENTECH INC.

Query Match 3.9%; Score 121.8; DB 12; Length 4725;

Best Local Similarity 49.6%; Pred. No. 3.5e-21;

RESULT 993

ID ADE19753 standard; cDNA; 4725 BP.

DE Human PRO polynucleotide #48.

PN US2003138903-A1.

PD 24-JUL-2003.

PA (GETH) GENENTECH INC.

Query Match 3.9%; Score 121.8; DB 12; Length 4725;

Best Local Similarity 49.6%; Pred. No. 3.5e-21;

RESULT 994

ID ADE77331 standard; cDNA; 4725 BP.

DE Human cDNA encoding secreted/transmembrane polypeptide PRO34001.

PN US2003124666-A1.

PD 03-JUL-2003.

PA (GETH) GENENTECH INC.

Query Match 3.9%; Score 121.8; DB 12; Length 4725;

Best Local Similarity 49.6%; Pred. No. 3.5e-21;

RESULT 995

ID ADE65439 standard; cDNA; 4725 BP.

DE Human PRO polynucleotide #48.

PN US2003119116-A1.

PD 26-JUN-2003.

PA (GETH) GENENTECH INC.

Query Match 3.9%; Score 121.8; DB 12; Length 4725;

Best Local Similarity 49.6%; Pred. No. 3.5e-21;

RESULT 996

ID ADE76048 standard; cDNA; 4725 BP.

DE Human PRO polynucleotide #48.

PN US2003124663-A1.

PD 03-JUL-2003.

PA (GETH) GENENTECH INC.

Query Match 3.9%; Score 121.8; DB 12; Length 4725;

Best Local Similarity 49.6%; Pred. No. 3.5e-21;

RESULT 997

ID ADE37959 standard; cDNA; 4725 BP.
 DE Human PRO polynucleotide #48.
 PN US2003119119-A1.
 PD 26-JUN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 3.9%; Score 121.8; DB 12; Length 4725;
 Best Local Similarity 49.6%; Pred. No. 3.5e-21;
 RESULT 998
 ID ADE64569 standard; cDNA; 4725 BP.
 DE Human PRO polynucleotide #48.
 PN US2003119114-A1.
 PD 26-JUN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 3.9%; Score 121.8; DB 12; Length 4725;
 Best Local Similarity 49.6%; Pred. No. 3.5e-21;
 RESULT 999
 ID ADE38904 standard; cDNA; 4725 BP.
 DE Human PRO polynucleotide #48.
 PN US2003096363-A1.
 PD 22-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 3.9%; Score 121.8; DB 12; Length 4725;
 Best Local Similarity 49.6%; Pred. No. 3.5e-21;
 RESULT 1000
 ID ADE51978 standard; cDNA; 4725 BP.
 DE Human cDNA encoding secreted/transmembrane polypeptide PRO34001.
 PN US2003104562-A1.
 PD 05-JUN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 3.9%; Score 121.8; DB 12; Length 4725;
 Best Local Similarity 49.6%; Pred. No. 3.5e-21;
 RESULT 1001
 ID ADD91009 standard; cDNA; 4725 BP.
 DE Human cDNA encoding secreted/transmembrane polypeptide PRO34001.
 PN US2003138902-A1.
 PD 24-JUL-2003.
 PA (GETH) GENENTECH INC.
 Query Match 3.9%; Score 121.8; DB 12; Length 4725;
 Best Local Similarity 49.6%; Pred. No. 3.5e-21;
 RESULT 1002
 ID ADE38788 standard; cDNA; 4725 BP.
 DE Human PRO polynucleotide #48.
 PN US2003108996-A1.
 PD 12-JUN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 3.9%; Score 121.8; DB 12; Length 4725;
 Best Local Similarity 49.6%; Pred. No. 3.5e-21;
 RESULT 1003
 ID ADE37488 standard; cDNA; 4725 BP.
 DE Human cDNA encoding secreted/transmembrane polypeptide PRO34001.
 PN US2003104563-A1.
 PD 05-JUN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 3.9%; Score 121.8; DB 12; Length 4725;
 Best Local Similarity 49.6%; Pred. No. 3.5e-21;
 RESULT 1004
 ID ADE06304 standard; cDNA; 4725 BP.

DE Human PRO polynucleotide #48.
 PN US2003138898-A1.
 PD 24-JUL-2003.
 PA (GETH) GENENTECH INC.
 Query Match 3.9%; Score 121.8; DB 12; Length 4725;
 Best Local Similarity 49.6%; Pred. No. 3.5e-21;
 RESULT 1005
 ID ADD90164 standard; cDNA; 4725 BP.
 DE Human cDNA encoding secreted/transmembrane polypeptide PRO34001.
 PN US2003138904-A1.
 PD 24-JUL-2003.
 PA (GETH) GENENTECH INC.
 Query Match 3.9%; Score 121.8; DB 12; Length 4725;
 Best Local Similarity 49.6%; Pred. No. 3.5e-21;
 RESULT 1006
 ID ADE38672 standard; cDNA; 4725 BP.
 DE Human PRO polynucleotide #48.
 PN US2003119086-A1.
 PD 26-JUN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 3.9%; Score 121.8; DB 12; Length 4725;
 Best Local Similarity 49.6%; Pred. No. 3.5e-21;
 RESULT 1007
 ID ADE39603 standard; cDNA; 4725 BP.
 DE Human PRO polynucleotide #48.
 PN US2003119118-A1.
 PD 26-JUN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 3.9%; Score 121.8; DB 12; Length 4725;
 Best Local Similarity 49.6%; Pred. No. 3.5e-21;
 RESULT 1008
 ID ADD89208 standard; cDNA; 4725 BP.
 DE Human PRO polynucleotide #48.
 PN US2003138897-A1.
 PD 24-JUL-2003.
 PA (GETH) GENENTECH INC.
 Query Match 3.9%; Score 121.8; DB 12; Length 4725;
 Best Local Similarity 49.6%; Pred. No. 3.5e-21;
 RESULT 1009
 ID ADD88975 standard; cDNA; 4725 BP.
 DE Human PRO polynucleotide #48.
 PN US2003138899-A1.
 PD 24-JUL-2003.
 PA (GETH) GENENTECH INC.
 Query Match 3.9%; Score 121.8; DB 12; Length 4725;
 Best Local Similarity 49.6%; Pred. No. 3.5e-21;
 RESULT 1010
 ID ADE19869 standard; cDNA; 4725 BP.
 DE Human PRO polynucleotide #48.
 PN US2003138900-A1.
 PD 24-JUL-2003.
 PA (GETH) GENENTECH INC.
 Query Match 3.9%; Score 121.8; DB 12; Length 4725;
 Best Local Similarity 49.6%; Pred. No. 3.5e-21;
 RESULT 1011
 ID ADE77447 standard; cDNA; 4725 BP.
 DE Human cDNA encoding secreted/transmembrane polypeptide PRO34001.

PN US2003124667-A1.
 PD 03-JUL-2003.
 PA (GETH) GENENTECH INC.
 Query Match 3.9%; Score 121.8; DB 12; Length 4725;
 Best Local Similarity 49.6%; Pred. No. 3.5e-21;
 RESULT 1012
 ID ADE65323 standard; cDNA; 4725 BP.
 DE Human PRO polynucleotide #48.
 PN US2003119113-A1.
 PD 26-JUN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 3.9%; Score 121.8; DB 12; Length 4725;
 Best Local Similarity 49.6%; Pred. No. 3.5e-21;
 RESULT 1013
 ID ADE39371 standard; cDNA; 4725 BP.
 DE Human PRO polynucleotide #48.
 PN US2003119115-A1.
 PD 26-JUN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 3.9%; Score 121.8; DB 12; Length 4725;
 Best Local Similarity 49.6%; Pred. No. 3.5e-21;
 RESULT 1014
 ID ADE38556 standard; cDNA; 4725 BP.
 DE Human cDNA encoding secreted/transmembrane polypeptide PRO34001.
 PN US2003104559-A1.
 PD 05-JUN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 3.9%; Score 121.8; DB 12; Length 4725;
 Best Local Similarity 49.6%; Pred. No. 3.5e-21;
 RESULT 1015
 ID ADG11109 standard; cDNA; 4725 BP.
 DE Human cDNA encoding secreted/transmembrane polypeptide PRO34001.
 PN US2003170809-A1.
 PD 11-SEP-2003.
 PA (GETH) GENENTECH INC.
 Query Match 3.9%; Score 121.8; DB 12; Length 4725;
 Best Local Similarity 49.6%; Pred. No. 3.5e-21;
 RESULT 1016
 ID ADG10993 standard; cDNA; 4725 BP.
 DE Human cDNA encoding secreted/transmembrane polypeptide PRO34001.
 PN US2003077743-A1.
 PD 24-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 3.9%; Score 121.8; DB 12; Length 4725;
 Best Local Similarity 49.6%; Pred. No. 3.5e-21;
 RESULT 1017
 ID ADH31521 standard; cDNA; 4725 BP.
 DE Human PRO polynucleotide #48.
 PN US2003119139-A1.
 PD 26-JUN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 3.9%; Score 121.8; DB 12; Length 4725;
 Best Local Similarity 49.6%; Pred. No. 3.5e-21;
 RESULT 1018
 ID ADH38769 standard; cDNA; 4725 BP.
 DE Human cDNA encoding secreted/transmembrane polypeptide PRO34001.
 PN US2003119140-A1.

PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 3.9%; Score 121.8; DB 12; Length 4725;
Best Local Similarity 49.6%; Pred. No. 3.5e-21;
RESULT 1019
ID ADH29404 standard; cDNA; 4725 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO34001.
PN US2003119137-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 3.9%; Score 121.8; DB 12; Length 4725;
Best Local Similarity 49.6%; Pred. No. 3.5e-21;
RESULT 1020
ID ADH23707 standard; cDNA; 4725 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO34001.
PN US2003119143-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 3.9%; Score 121.8; DB 12; Length 4725;
Best Local Similarity 49.6%; Pred. No. 3.5e-21;
RESULT 1021
ID ADH27037 standard; cDNA; 4725 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO34001.
PN US2003119135-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 3.9%; Score 121.8; DB 12; Length 4725;
Best Local Similarity 49.6%; Pred. No. 3.5e-21;
RESULT 1022
ID ADH38305 standard; cDNA; 4725 BP.
DE Novel human secreted and transmembrane protein PRO34001 cDNA.
PN US2003119124-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 3.9%; Score 121.8; DB 12; Length 4725;
Best Local Similarity 49.6%; Pred. No. 3.5e-21;
RESULT 1023
ID ADH26921 standard; cDNA; 4725 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO34001.
PN US2003119134-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 3.9%; Score 121.8; DB 12; Length 4725;
Best Local Similarity 49.6%; Pred. No. 3.5e-21;
RESULT 1024
ID ADH38189 standard; cDNA; 4725 BP.
DE Novel human secreted and transmembrane protein PRO34001 cDNA.
PN US2003119123-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 3.9%; Score 121.8; DB 12; Length 4725;
Best Local Similarity 49.6%; Pred. No. 3.5e-21;
RESULT 1025
ID ADH38885 standard; cDNA; 4725 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO34001.
PN US2003119141-A1.
PD 26-JUN-2003.

PA (GETH) GENENTECH INC.
 Query Match 3.9%; Score 121.8; DB 12; Length 4725;
 Best Local Similarity 49.6%; Pred. No. 3.5e-21;
 RESULT 1026
 ID ADH23823 standard; cDNA; 4725 BP.
 DE Human cDNA encoding secreted/transmembrane polypeptide PRO34001.
 PN US2003119142-A1.
 PD 26-JUN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 3.9%; Score 121.8; DB 12; Length 4725;
 Best Local Similarity 49.6%; Pred. No. 3.5e-21;
 RESULT 1027
 ID ADH40198 standard; cDNA; 4725 BP.
 DE Human PRO34001 cDNA.
 PN US2003119132-A1.
 PD 26-JUN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 3.9%; Score 121.8; DB 12; Length 4725;
 Best Local Similarity 49.6%; Pred. No. 3.5e-21;
 RESULT 1028
 ID ADH40083 standard; cDNA; 4725 BP.
 DE Human PRO34001 cDNA.
 PN US2003119133-A1.
 PD 26-JUN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 3.9%; Score 121.8; DB 12; Length 4725;
 Best Local Similarity 49.6%; Pred. No. 3.5e-21;
 RESULT 1029
 ID ADH31405 standard; cDNA; 4725 BP.
 DE Human PRO polynucleotide #48.
 PN US2003119138-A1.
 PD 26-JUN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 3.9%; Score 121.8; DB 12; Length 4725;
 Best Local Similarity 49.6%; Pred. No. 3.5e-21;
 RESULT 1030
 ID ADH29283 standard; cDNA; 4725 BP.
 DE Human cDNA encoding secreted/transmembrane polypeptide PRO34001.
 PN US2003119136-A1.
 PD 26-JUN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 3.9%; Score 121.8; DB 12; Length 4725;
 Best Local Similarity 49.6%; Pred. No. 3.5e-21;
 RESULT 1031
 ID ADH49498 standard; cDNA; 4725 BP.
 DE Novel human secreted and transmembrane protein PRO34001 cDNA.
 PN US2003119127-A1.
 PD 26-JUN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 3.9%; Score 121.8; DB 12; Length 4725;
 Best Local Similarity 49.6%; Pred. No. 3.5e-21;
 RESULT 1032
 ID ADH51962 standard; cDNA; 4725 BP.
 DE Novel human secreted and transmembrane protein PRO34001 cDNA.
 PN US2003119125-A1.
 PD 26-JUN-2003.
 PA (GETH) GENENTECH INC.

Query Match 3.9%; Score 121.8; DB 12; Length 4725;
 Best Local Similarity 49.6%; Pred. No. 3.5e-21;
 RESULT 1033
 ID ADH49817 standard; cDNA; 4725 BP.
 DE Novel human secreted and transmembrane protein PRO34001 cDNA.
 PN US2003119128-A1.
 PD 26-JUN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 3.9%; Score 121.8; DB 12; Length 4725;
 Best Local Similarity 49.6%; Pred. No. 3.5e-21;
 RESULT 1034
 ID ADH52418 standard; cDNA; 4725 BP.
 DE Novel human secreted and transmembrane protein PRO34001 cDNA.
 PN US2003119130-A1.
 PD 26-JUN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 3.9%; Score 121.8; DB 12; Length 4725;
 Best Local Similarity 49.6%; Pred. No. 3.5e-21;
 RESULT 1035
 ID ADH52534 standard; cDNA; 4725 BP.
 DE Novel human secreted and transmembrane protein PRO34001 cDNA.
 PN US2003119129-A1.
 PD 26-JUN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 3.9%; Score 121.8; DB 12; Length 4725;
 Best Local Similarity 49.6%; Pred. No. 3.5e-21;
 RESULT 1036
 ID ADH58531 standard; cDNA; 4725 BP.
 DE Novel human secreted and transmembrane protein PRO34001 cDNA.
 PN US2003119121-A1.
 PD 26-JUN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 3.9%; Score 121.8; DB 12; Length 4725;
 Best Local Similarity 49.6%; Pred. No. 3.5e-21;
 RESULT 1037
 ID ADH51846 standard; cDNA; 4725 BP.
 DE Novel human secreted and transmembrane protein PRO34001 cDNA.
 PN US2003119126-A1.
 PD 26-JUN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 3.9%; Score 121.8; DB 12; Length 4725;
 Best Local Similarity 49.6%; Pred. No. 3.5e-21;
 RESULT 1038
 ID ADH58407 standard; cDNA; 4725 BP.
 DE Novel human secreted and transmembrane protein PRO34001 cDNA.
 PN US2003119122-A1.
 PD 26-JUN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 3.9%; Score 121.8; DB 12; Length 4725;
 Best Local Similarity 49.6%; Pred. No. 3.5e-21;
 RESULT 1039
 ID ADI13604 standard; cDNA; 4725 BP.
 DE Novel human secreted and transmembrane protein PRO34001 cDNA.
 PN US2003119131-A1.
 PD 26-JUN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 3.9%; Score 121.8; DB 12; Length 4725;

Best Local Similarity 49.6%; Pred. No. 3.5e-21;

RESULT 1040

ID ADK00860 standard; cDNA; 4725 BP.

DE Human PRO polynucleotide #48.

PN US2003186373-A1.

PD 02-OCT-2003.

PA (GETH) GENENTECH INC.

Query Match 3.9%; Score 121.8; DB 12; Length 4725;

Best Local Similarity 49.6%; Pred. No. 3.5e-21;

RESULT 1041

ID ADL08601 standard; cDNA; 4725 BP.

DE Human cDNA encoding secreted/transmembrane polypeptide PRO34001.

PN US2003186372-A1.

PD 02-OCT-2003.

PA (GETH) GENENTECH INC.

Query Match 3.9%; Score 121.8; DB 12; Length 4725;

Best Local Similarity 49.6%; Pred. No. 3.5e-21;

RESULT 1042

ID ADL06475 standard; cDNA; 4725 BP.

DE Human tumour-associated antigenic target (TAT) cDNA sequence #55.

PN WO2004016225-A2.

PD 26-FEB-2004.

PA (GETH) GENENTECH INC.

Query Match 3.9%; Score 121.8; DB 12; Length 4725;

Best Local Similarity 49.6%; Pred. No. 3.5e-21;

RESULT 1043

ID ADF72687 standard; cDNA; 4731 BP.

DE Human cancer-related gene nucleotide sequence SEQ ID NO:17.

PN WO2003101400-A2.

PD 11-DEC-2003.

PA (AVAL-) AVALON PHARM INC.

Query Match 3.9%; Score 121.8; DB 12; Length 4731;

Best Local Similarity 49.6%; Pred. No. 3.5e-21;

RESULT 1044

ID ADF72700 standard; cDNA; 4731 BP.

DE Human cancer-related gene nucleotide sequence SEQ ID NO:30.

PN WO2003101400-A2.

PD 11-DEC-2003.

PA (AVAL-) AVALON PHARM INC.

Query Match 3.9%; Score 121.8; DB 12; Length 4731;

Best Local Similarity 49.6%; Pred. No. 3.5e-21;

RESULT 1045

ID ADF72674 standard; cDNA; 4731 BP.

DE Human cancer-related gene nucleotide sequence SEQ ID NO:4.

PN WO2003101400-A2.

PD 11-DEC-2003.

PA (AVAL-) AVALON PHARM INC.

Query Match 3.9%; Score 121.8; DB 12; Length 4731;

Best Local Similarity 49.6%; Pred. No. 3.5e-21;

RESULT 1046

ID AAD28946 standard; cDNA; 6408 BP.

DE Human MOL4 cDNA.

PN WO200206339-A2.

PD 24-JAN-2002.

PA (CURA-) CURAGEN CORP.

Query Match 3.9%; Score 121.8; DB 6; Length 6408;

Best Local Similarity 49.6%; Pred. No. 4.1e-21;

RESULT 1047

ID ADD18201 standard; DNA; 6408 BP.
DE Human molecule (MOL) protein MOL4a DNA sequence.
PN WO2003003984-A2.
PD 16-JAN-2003.
PA (CURA-) CURAGEN CORP.
Query Match 3.9%; Score 121.8; DB 10; Length 6408;
Best Local Similarity 49.6%; Pred. No. 4.1e-21;

RESULT 1048

ID ADJ34132 standard; cDNA; 6408 BP.
DE Human cDNA encoding secreted protein NOV2i.
PN WO2004000997-A2.
PD 31-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 3.9%; Score 121.8; DB 12; Length 6408;
Best Local Similarity 49.6%; Pred. No. 4.1e-21;

RESULT 1049

ID ADJ34116 standard; cDNA; 6408 BP.
DE Human cDNA encoding secreted protein NOV2a.
PN WO2004000997-A2.
PD 31-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 3.9%; Score 121.8; DB 12; Length 6408;
Best Local Similarity 49.6%; Pred. No. 4.1e-21;

RESULT 1050

ID ABA04069 standard; cDNA; 2820 BP.
DE Human semaphorin G-like NHP encoding cDNA SEQ ID NO:15.
PN WO200188133-A2.
PD 22-NOV-2001.
PA (LEXI-) LEXICON GENETICS INC.
Query Match 3.9%; Score 121.4; DB 6; Length 2820;
Best Local Similarity 49.5%; Pred. No. 3.5e-21;

RESULT 1051

ID ABA04068 standard; cDNA; 2865 BP.
DE Human semaphorin G-like NHP encoding cDNA SEQ ID NO:13.
PN WO200188133-A2.
PD 22-NOV-2001.
PA (LEXI-) LEXICON GENETICS INC.
Query Match 3.9%; Score 121.4; DB 6; Length 2865;
Best Local Similarity 49.5%; Pred. No. 3.5e-21;

RESULT 1052

ID ABA04064 standard; cDNA; 3105 BP.
DE Human semaphorin G-like NHP encoding cDNA SEQ ID NO:5.
PN WO200188133-A2.
PD 22-NOV-2001.
PA (LEXI-) LEXICON GENETICS INC.
Query Match 3.9%; Score 121.4; DB 6; Length 3105;
Best Local Similarity 49.5%; Pred. No. 3.6e-21;

RESULT 1053

ID ABA04062 standard; cDNA; 3150 BP.
DE Human semaphorin G-like NHP encoding cDNA SEQ ID NO:1.
PN WO200188133-A2.
PD 22-NOV-2001.
PA (LEXI-) LEXICON GENETICS INC.
Query Match 3.9%; Score 121.4; DB 6; Length 3150;
Best Local Similarity 49.5%; Pred. No. 3.7e-21;

RESULT 1054

ID ABA04065 standard; cDNA; 3237 BP.
 DE Human semaphorin G-like NHP encoding cDNA SEQ ID NO:7.
 PN WO200188133-A2.
 PD 22-NOV-2001.
 PA (LEXI-) LEXICON GENETICS INC.
 Query Match 3.9%; Score 121.4; DB 6; Length 3237;
 Best Local Similarity 49.5%; Pred. No. 3.7e-21;
 RESULT 1055
 ID ABA04063 standard; cDNA; 3282 BP.
 DE Human semaphorin G-like NHP encoding cDNA SEQ ID NO:3.
 PN WO200188133-A2.
 PD 22-NOV-2001.
 PA (LEXI-) LEXICON GENETICS INC.
 Query Match 3.9%; Score 121.4; DB 6; Length 3282;
 Best Local Similarity 49.5%; Pred. No. 3.7e-21;
 RESULT 1056
 ID ABA04067 standard; cDNA; 3411 BP.
 DE Human semaphorin G-like NHP encoding cDNA SEQ ID NO:11.
 PN WO200188133-A2.
 PD 22-NOV-2001.
 PA (LEXI-) LEXICON GENETICS INC.
 Query Match 3.9%; Score 121.4; DB 6; Length 3411;
 Best Local Similarity 49.5%; Pred. No. 3.8e-21;
 RESULT 1057
 ID ABA04066 standard; cDNA; 3456 BP.
 DE Human semaphorin G-like NHP encoding cDNA SEQ ID NO:9.
 PN WO200188133-A2.
 PD 22-NOV-2001.
 PA (LEXI-) LEXICON GENETICS INC.
 Query Match 3.9%; Score 121.4; DB 6; Length 3456;
 Best Local Similarity 49.5%; Pred. No. 3.8e-21;
 RESULT 1058
 ID ABA04070 standard; cDNA; 4074 BP.
 DE Human semaphorin G-like NHP polynucleotide sequence SEQ ID NO:17.
 PN WO200188133-A2.
 PD 22-NOV-2001.
 PA (LEXI-) LEXICON GENETICS INC.
 Query Match 3.9%; Score 121.4; DB 6; Length 4074;
 Best Local Similarity 49.5%; Pred. No. 4.2e-21;
 RESULT 1059
 ID ADD18219 standard; DNA; 4233 BP.
 DE Human molecule (MOL) protein MOL4b DNA sequence.
 PN WO2003003984-A2.
 PD 16-JAN-2003.
 PA (CURA-) CURAGEN CORP.
 Query Match 3.8%; Score 120.2; DB 10; Length 4233;
 Best Local Similarity 49.5%; Pred. No. 8.9e-21;
 RESULT 1060
 ID AAX84077 standard; DNA; 963 BP.
 DE Degenerate Mouse ZSMF-3 coding sequence.
 PN WO9932622-A2.
 PD 01-JUL-1999.
 PA (ZYMO) ZYMOGENETICS INC.
 Query Match 3.8%; Score 120; DB 2; Length 963;
 Best Local Similarity 33.2%; Pred. No. 4.8e-21;
 RESULT 1061
 ID AAA23432 standard; cDNA; 4144 BP.

DE cDNA encoding human secreted protein vb21_1, SEQ ID NO:19.
PN WO200011015-A1.
PD 02-MAR-2000.
PA (ALPH-) ALPHAGENE INC.
Query Match 3.8%; Score 119.2; DB 3; Length 4144;
Best Local Similarity 49.4%; Pred. No. 1.6e-20;
RESULT 1062
ID AAX84067 standard; DNA; 963 BP.
DE Degenerate Human ZSMF-3 coding sequence.
PN WO9932622-A2.
PD 01-JUL-1999.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 3.8%; Score 118.4; DB 2; Length 963;
Best Local Similarity 34.3%; Pred. No. 1.3e-20;
RESULT 1063
ID AAF29451 standard; cDNA; 2811 BP.
DE Human TANGO 276 cDNA.
PN WO200100638-A2.
PD 04-JAN-2001.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 3.7%; Score 115.6; DB 4; Length 2811;
Best Local Similarity 51.9%; Pred. No. 1.2e-19;
RESULT 1064
ID ACD66760 standard; cDNA; 2811 BP.
DE Secreted polypeptide-related cDNA #44.
PN US2003022279-A1.
PD 30-JAN-2003.
PA (FRAS/) FRASER C C.
PA (BARN/) BARNES T M.
PA (SHAR/) SHARP J D.
PA (KIRS/) KIRST S J.
PA (MYER/) MYERS P S.
PA (LEIB/) LEIBY K R.
PA (HOLT/) HOLTZMAN D A.
PA (MCCA/) MCCARTHY S A.
PA (WRIG/) WRIGHTON N.
PA (MACK/) MACKAY C R.
PA (GOOD/) GOODEARL A D J.
Query Match 3.7%; Score 115.6; DB 8; Length 2811;
Best Local Similarity 51.9%; Pred. No. 1.2e-19;
RESULT 1065
ID ADB90748 standard; cDNA; 2811 BP.
DE Human cDNA encoding TANGO 276.
PN US2003082586-A1.
PD 01-MAY-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 3.7%; Score 115.6; DB 9; Length 2811;
Best Local Similarity 51.9%; Pred. No. 1.2e-19;
RESULT 1066
ID ADF71483 standard; cDNA; 2811 BP.
DE Human TANGO 276 cDNA.
PN US2003175733-A1.
PD 18-SEP-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 3.7%; Score 115.6; DB 10; Length 2811;
Best Local Similarity 51.9%; Pred. No. 1.2e-19;
RESULT 1067

ID ADQ10309 standard; cDNA; 2811 BP.
 DE Human polynucleotide #51.
 PN US2004121396-A1.
 PD 24-JUN-2004.
 PA (MILL-) MILLENNIUM PHARM INC.
 Query Match 3.7%; Score 115.6; DB 12; Length 2811;
 Best Local Similarity 51.9%; Pred. No. 1.2e-19;
 RESULT 1068
 ID ABD32607 standard; cDNA; 2675 BP.
 DE Mouse cancer-associated cDNA MR7-239.1.
 PN WO2004074320-A2.
 PD 02-SEP-2004.
 PA (SAGR-) SAGRES DISCOVERY INC.
 Query Match 3.6%; Score 114.4; DB 13; Length 2675;
 Best Local Similarity 50.4%; Pred. No. 2.5e-19;
 RESULT 1069
 ID AAV07280 standard; cDNA to mRNA; 2331 BP.
 DE Rat semaphorin W encoding cDNA.
 PN WO9815628-A1.
 PD 16-APR-1998.
 PA (SUMU) SUMITOMO PHARM CO LTD.
 Query Match 3.6%; Score 113.8; DB 2; Length 2331;
 Best Local Similarity 48.7%; Pred. No. 3.4e-19;
 RESULT 1070
 ID AAV07279 standard; cDNA to mRNA; 4008 BP.
 DE Rat semaphorin W encoding cDNA with 5'UTR and 3'UTR.
 PN WO9815628-A1.
 PD 16-APR-1998.
 PA (SUMU) SUMITOMO PHARM CO LTD.
 Query Match 3.6%; Score 113.8; DB 2; Length 4008;
 Best Local Similarity 48.7%; Pred. No. 4.4e-19;
 RESULT 1071
 ID AAF93776 standard; cDNA; 2971 BP.
 DE Human cDNA encoding a membrane or secretory protein clone PSEC0074.
 PN EP1067182-A2.
 PD 10-JAN-2001.
 PA (HELI-) HELIX RES INST.
 Query Match 3.5%; Score 111; DB 5; Length 2971;
 Best Local Similarity 51.4%; Pred. No. 2.1e-18;
 RESULT 1072
 ID ABK62744 standard; cDNA; 344 BP.
 DE Rat sequence differentially expressed in response to a hepatotoxin #651.
 PN WO200210453-A2.
 PD 07-FEB-2002.
 PA (GENE-) GENE LOGIC INC.
 Query Match 3.5%; Score 110; DB 6; Length 344;
 Best Local Similarity 70.6%; Pred. No. 1.3e-18;
 RESULT 1073
 ID ADB56646 standard; DNA; 344 BP.
 DE Toxicity-related gene, SEQ ID 1672.
 PN WO2003064624-A2.
 PD 07-AUG-2003.
 PA (GENE-) GENE LOGIC INC.
 Query Match 3.5%; Score 110; DB 10; Length 344;
 Best Local Similarity 70.6%; Pred. No. 1.3e-18;
 RESULT 1074
 ID ADB51177 standard; DNA; 344 BP.

DE Primary rat hepatocyte toxicity modelling related gene SEQ ID NO:1719.
PN WO2003065993-A2.
PD 14-AUG-2003.
PA (GENE-) GENE LOGIC INC.
Query Match 3.5%; Score 110; DB 10; Length 344;
Best Local Similarity 70.6%; Pred. No. 1.3e-18;
RESULT 1075
ID AAH10459 standard; cDNA; 557 BP.
DE Human cDNA clone (3'-primer) SEQ ID NO:7294.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 3.4%; Score 107.8; DB 4; Length 557;
Best Local Similarity 98.2%; Pred. No. 6.5e-18;
RESULT 1076
ID ADR67095 standard; cDNA; 2606 BP.
DE Human cancer associated gene cDNA sequence SEQ ID NO:141.
PN WO2004074321-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 3.4%; Score 106.8; DB 13; Length 2606;
Best Local Similarity 51.8%; Pred. No. 2.6e-17;
RESULT 1077
ID ABA04074 standard; cDNA; 2094 BP.
DE Human semaphorin G-like NHP encoding cDNA SEQ ID NO:24.
PN WO200188133-A2.
PD 22-NOV-2001.
PA (LEXI-) LEXICON GENETICS INC.
Query Match 3.4%; Score 105.4; DB 6; Length 2094;
Best Local Similarity 47.2%; Pred. No. 5.5e-17;
RESULT 1078
ID ABA04076 standard; cDNA; 2517 BP.
DE Human semaphorin G-like NHP encoding cDNA SEQ ID NO:28.
PN WO200188133-A2.
PD 22-NOV-2001.
PA (LEXI-) LEXICON GENETICS INC.
Query Match 3.4%; Score 105.4; DB 6; Length 2517;
Best Local Similarity 47.2%; Pred. No. 6e-17;
RESULT 1079
ID ABA04078 standard; cDNA; 2598 BP.
DE Human semaphorin G-like NHP encoding cDNA SEQ ID NO:32.
PN WO200188133-A2.
PD 22-NOV-2001.
PA (LEXI-) LEXICON GENETICS INC.
Query Match 3.4%; Score 105.4; DB 6; Length 2598;
Best Local Similarity 47.2%; Pred. No. 6.1e-17;
RESULT 1080
ID ABA04087 standard; cDNA; 2951 BP.
DE Human semaphorin G-like NHP polynucleotide sequence SEQ ID NO:50.
PN WO200188133-A2.
PD 22-NOV-2001.
PA (LEXI-) LEXICON GENETICS INC.
Query Match 3.4%; Score 105.4; DB 6; Length 2951;
Best Local Similarity 47.2%; Pred. No. 6.5e-17;
RESULT 1081
ID AAX84076 standard; DNA; 1047 BP.
DE Mouse ZSMF-3 coding sequence.

PN WO9932622-A2.
 PD 01-JUL-1999.
 PA (ZYMO) ZYMOGENETICS INC.
 Query Match 3.3%; Score 104.8; DB 2; Length 1047;
 Best Local Similarity 53.0%; Pred. No. 5.6e-17;
 RESULT 1082
 ID AAF90251 standard; DNA; 2337 BP.
 DE Nucleotide sequence of a semaphorin polypeptide designated ZSMF-16.
 PN WO200140278-A2.
 PD 07-JUN-2001.
 PA (ZYMO) ZYMOGENETICS INC.
 Query Match 3.3%; Score 102.8; DB 4; Length 2337;
 Best Local Similarity 31.2%; Pred. No. 2.9e-16;
 RESULT 1083
 ID ABA97363 standard; cDNA; 2337 BP.
 DE Degenerate nucleotide sequence of human ZSMF-16.
 PN US2001049432-A1.
 PD 06-DEC-2001.
 PA (HOLL/) HOLLOWAY J L.
 PA (FOLE/) FOLEY K P.
 Query Match 3.3%; Score 102.8; DB 6; Length 2337;
 Best Local Similarity 31.2%; Pred. No. 2.9e-16;
 RESULT 1084
 ID AAZ87977 standard; DNA; 4024 BP.
 DE Mouse semaphorin W polypeptide encoding DNA.
 PN WO200006725-A1.
 PD 10-FEB-2000.
 PA (SUMU) SUMITOMO PHARM CO LTD.
 Query Match 3.3%; Score 102.6; DB 3; Length 4024;
 Best Local Similarity 48.0%; Pred. No. 4.3e-16;
 RESULT 1085
 ID AAH94461 standard; cDNA; 2036 BP.
 DE Human foetal cDNA, SEQ ID NO: 1148.
 PN WO200155339-A2.
 PD 02-AUG-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match 3.3%; Score 102.4; DB 5; Length 2036;
 Best Local Similarity 47.1%; Pred. No. 3.4e-16;
 RESULT 1086
 ID ABA04073 standard; cDNA; 2109 BP.
 DE Human semaphorin G-like NHP encoding cDNA SEQ ID NO:22.
 PN WO200188133-A2.
 PD 22-NOV-2001.
 PA (LEXI-) LEXICON GENETICS INC.
 Query Match 3.3%; Score 102.4; DB 6; Length 2109;
 Best Local Similarity 47.1%; Pred. No. 3.5e-16;
 RESULT 1087
 ID ABA04075 standard; cDNA; 2532 BP.
 DE Human semaphorin G-like NHP encoding cDNA SEQ ID NO:26.
 PN WO200188133-A2.
 PD 22-NOV-2001.
 PA (LEXI-) LEXICON GENETICS INC.
 Query Match 3.3%; Score 102.4; DB 6; Length 2532;
 Best Local Similarity 47.1%; Pred. No. 3.8e-16;
 RESULT 1088
 ID ABX70813 standard; cDNA; 2575 BP.
 DE Novel human cDNA sequence #38.

PN WO200281731-A2.
 PD 17-OCT-2002.
 PA (HYSE-) HYSEQ INC.
 PA (GOOD/) GOODRICH R W.
 Query Match 3.3%; Score 102.4; DB 8; Length 2575;
 Best Local Similarity 47.1%; Pred. No. 3.9e-16;
 RESULT 1089
 ID ABA04077 standard; cDNA; 2613 BP.
 DE Human semaphorin G-like NHP encoding cDNA SEQ ID NO:30.
 PN WO200188133-A2.
 PD 22-NOV-2001.
 PA (LEXI-) LEXICON GENETICS INC.
 Query Match 3.3%; Score 102.4; DB 6; Length 2613;
 Best Local Similarity 47.1%; Pred. No. 3.9e-16;
 RESULT 1090
 ID ADG76108 standard; cDNA; 1327 BP.
 DE Human NOVX cDNA to treat human pathological conditions (SeqID 21).
 PN WO2003085096-A2.
 PD 16-OCT-2003.
 PA (CURA-) CURAGEN CORP.
 Query Match 3.2%; Score 102; DB 10; Length 1327;
 Best Local Similarity 50.0%; Pred. No. 3.5e-16;
 RESULT 1091
 ID ADF45331 standard; cDNA; 1327 BP.
 DE Human semaphorin-like protein NOV2e encoding cDNA SEQ ID NO:21.
 PN WO2003102584-A2.
 PD 11-DEC-2003.
 PA (CURA-) CURAGEN CORP.
 Query Match 3.2%; Score 102; DB 12; Length 1327;
 Best Local Similarity 50.0%; Pred. No. 3.5e-16;
 RESULT 1092
 ID ADO40265 standard; cDNA; 1327 BP.
 DE Human cDNA encoding semaphorin-like protein NOV2e.
 PN US2004018977-A1.
 PD 29-JAN-2004.
 PA (ALVA/) ALVAREZ E.
 PA (ANDE/) ANDERSON D W.
 PA (DHAN/) DHANABAL M.
 PA (KHRA/) KHRAMTSOV N V.
 PA (LARO/) LAROCHELLE W J.
 PA (LICH/) LICHENSTEIN H S.
 PA (LILL/) LI L.
 PA (OOIC/) OOI C E.
 PA (PADI/) PADIGARU M.
 PA (SHIM/) SHIMKETS R A.
 PA (ZHON/) ZHONG M.
 Query Match 3.2%; Score 102; DB 12; Length 1327;
 Best Local Similarity 50.0%; Pred. No. 3.5e-16;
 RESULT 1093
 ID ADG76110 standard; cDNA; 1492 BP.
 DE Human NOVX cDNA to treat human pathological conditions (SeqID 23).
 PN WO2003085096-A2.
 PD 16-OCT-2003.
 PA (CURA-) CURAGEN CORP.
 Query Match 3.2%; Score 102; DB 10; Length 1492;
 Best Local Similarity 50.0%; Pred. No. 3.8e-16;
 RESULT 1094

ID ADF45333 standard; cDNA; 1492 BP.
DE Human semaphorin-like protein NOV2f encoding cDNA SEQ ID NO:23.
PN WO2003102584-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.

Query Match 3.2%; Score 102; DB 12; Length 1492;
Best Local Similarity 50.0%; Pred. No. 3.8e-16;

RESULT 1095

ID ADO40267 standard; cDNA; 1492 BP.
DE Human cDNA encoding semaphorin-like protein NOV2f.
PN US2004018977-A1.
PD 29-JAN-2004.
PA (ALVA/) ALVAREZ E.
PA (ANDE/) ANDERSON D W.
PA (DHAN/) DHANABAL M.
PA (KHRA/) KHRAMTSOV N V.
PA (LARO/) LAROCHELLE W J.
PA (LICH/) LICHENSTEIN H S.
PA (LILL/) LI L.
PA (OOIC/) OOI C E.
PA (PADI/) PADIGARU M.
PA (SHIM/) SHIMKETS R A.
PA (ZHON/) ZHONG M.

Query Match 3.2%; Score 102; DB 12; Length 1492;
Best Local Similarity 50.0%; Pred. No. 3.8e-16;

RESULT 1096

ID ADG76120 standard; cDNA; 1878 BP.
DE Human NOVX cDNA to treat human pathological conditions (SeqID 33).
PN WO2003085096-A2.
PD 16-OCT-2003.
PA (CURA-) CURAGEN CORP.

Query Match 3.2%; Score 102; DB 10; Length 1878;
Best Local Similarity 50.0%; Pred. No. 4.2e-16;

RESULT 1097

ID ADF45343 standard; cDNA; 1878 BP.
DE Human semaphorin-like protein NOV2k encoding cDNA SEQ ID NO:33.
PN WO2003102584-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.

Query Match 3.2%; Score 102; DB 12; Length 1878;
Best Local Similarity 50.0%; Pred. No. 4.2e-16;

RESULT 1098

ID ADO40277 standard; cDNA; 1878 BP.
DE Human cDNA encoding semaphorin-like protein NOV2k.
PN US2004018977-A1.
PD 29-JAN-2004.
PA (ALVA/) ALVAREZ E.
PA (ANDE/) ANDERSON D W.
PA (DHAN/) DHANABAL M.
PA (KHRA/) KHRAMTSOV N V.
PA (LARO/) LAROCHELLE W J.
PA (LICH/) LICHENSTEIN H S.
PA (LILL/) LI L.
PA (OOIC/) OOI C E.
PA (PADI/) PADIGARU M.
PA (SHIM/) SHIMKETS R A.
PA (ZHON/) ZHONG M.

Query Match 3.2%; Score 102; DB 12; Length 1878;
 Best Local Similarity 50.0%; Pred. No. 4.2e-16;
 RESULT 1099
 ID AAA93630 standard; cDNA; 1890 BP.
 DE Human semaphorin protein-like splice variant SECX pCR2.1-2864933 cDNA.
 PN WO200053742-A2.
 PD 14-SEP-2000.
 PA (CURA-) CURAGEN CORP.
 Query Match 3.2%; Score 102; DB 3; Length 1890;
 Best Local Similarity 50.0%; Pred. No. 4.2e-16;
 RESULT 1100
 ID ADA23359 standard; cDNA; 1890 BP.
 DE cDNA encoding human SECX polypeptide, SEC3 #2.
 PN US2003054514-A1.
 PD 20-MAR-2003.
 PA (SHIM/) SHIMKETS R A.
 PA (LARO/) LAROCHELLE W J.
 Query Match 3.2%; Score 102; DB 9; Length 1890;
 Best Local Similarity 50.0%; Pred. No. 4.2e-16;
 RESULT 1101
 ID ADA23306 standard; cDNA; 1890 BP.
 DE cDNA encoding human SECX polypeptide.
 PN US2003054514-A1.
 PD 20-MAR-2003.
 PA (SHIM/) SHIMKETS R A.
 PA (LARO/) LAROCHELLE W J.
 Query Match 3.2%; Score 102; DB 9; Length 1890;
 Best Local Similarity 50.0%; Pred. No. 4.2e-16;
 RESULT 1102
 ID ADG76122 standard; cDNA; 1908 BP.
 DE Human NOVX cDNA to treat human pathological conditions (SeqID 35).
 PN WO2003085096-A2.
 PD 16-OCT-2003.
 PA (CURA-) CURAGEN CORP.
 Query Match 3.2%; Score 102; DB 10; Length 1908;
 Best Local Similarity 50.0%; Pred. No. 4.2e-16;
 RESULT 1103
 ID ADF45345 standard; cDNA; 1908 BP.
 DE Human semaphorin-like protein NOV21 encoding cDNA SEQ ID NO:35.
 PN WO2003102584-A2.
 PD 11-DEC-2003.
 PA (CURA-) CURAGEN CORP.
 Query Match 3.2%; Score 102; DB 12; Length 1908;
 Best Local Similarity 50.0%; Pred. No. 4.2e-16;
 RESULT 1104
 ID ADO40279 standard; cDNA; 1908 BP.
 DE Human cDNA encoding semaphorin-like protein NOV21.
 PN US2004018977-A1.
 PD 29-JAN-2004.
 PA (ALVA/) ALVAREZ E.
 PA (ANDE/) ANDERSON D W.
 PA (DHAN/) DHANABAL M.
 PA (KHRA/) KHRAMTSOV N V.
 PA (LARO/) LAROCHELLE W J.
 PA (LICH/) LICHENSTEIN H S.
 PA (LILL/) LI L.
 PA (OOIC/) OOI C E.

PA (PADI/) PADIGARU M.
PA (SHIM/) SHIMKETS R A.
PA (ZHON/) ZHONG M.
Query Match 3.2%; Score 102; DB 12; Length 1908;
Best Local Similarity 50.0%; Pred. No. 4.2e-16;
RESULT 1105
ID ADG76102 standard; cDNA; 1921 BP.
DE Human NOVX cDNA to treat human pathological conditions (SeqID 15).
PN WO2003085096-A2.
PD 16-OCT-2003.
PA (CURA-) CURAGEN CORP.
Query Match 3.2%; Score 102; DB 10; Length 1921;
Best Local Similarity 50.0%; Pred. No. 4.3e-16;
RESULT 1106
ID ADF45325 standard; cDNA; 1921 BP.
DE Human semaphorin-like protein NOV2b encoding cDNA SEQ ID NO:15.
PN WO2003102584-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 3.2%; Score 102; DB 12; Length 1921;
Best Local Similarity 50.0%; Pred. No. 4.3e-16;
RESULT 1107
ID ADO40259 standard; cDNA; 1921 BP.
DE Human cDNA encoding semaphorin-like protein NOV2b.
PN US2004018977-A1.
PD 29-JAN-2004.
PA (ALVA/) ALVAREZ E.
PA (ANDE/) ANDERSON D W.
PA (DHAN/) DHANABAL M.
PA (KHRA/) KHRAMTSOV N V.
PA (LARO/) LAROCHELLE W J.
PA (LICH/) LICHENSTEIN H S.
PA (LILL/) LI L.
PA (OOIC/) OOI C E.
PA (PADI/) PADIGARU M.
PA (SHIM/) SHIMKETS R A.
PA (ZHON/) ZHONG M.
Query Match 3.2%; Score 102; DB 12; Length 1921;
Best Local Similarity 50.0%; Pred. No. 4.3e-16;
RESULT 1108
ID ADG76136 standard; cDNA; 1948 BP.
DE Human NOVX cDNA to treat human pathological conditions (SeqID 49).
PN WO2003085096-A2.
PD 16-OCT-2003.
PA (CURA-) CURAGEN CORP.
Query Match 3.2%; Score 102; DB 10; Length 1948;
Best Local Similarity 50.0%; Pred. No. 4.3e-16;
RESULT 1109
ID ADF45359 standard; cDNA; 1948 BP.
DE Human semaphorin-like protein NOV2s encoding cDNA SEQ ID NO:49.
PN WO2003102584-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 3.2%; Score 102; DB 12; Length 1948;
Best Local Similarity 50.0%; Pred. No. 4.3e-16;
RESULT 1110
ID ADO40293 standard; cDNA; 1948 BP.

DE Human cDNA encoding semaphorin-like protein NOV2s.
 PN US2004018977-A1.
 PD 29-JAN-2004.
 PA (ALVA/) ALVAREZ E.
 PA (ANDE/) ANDERSON D W.
 PA (DHAN/) DHANABAL M.
 PA (KHRA/) KHRAMTSOV N V.
 PA (LARO/) LAROCHELLE W J.
 PA (LICH/) LICHENSTEIN H S.
 PA (LILL/) LI L.
 PA (OOIC/) OOI C E.
 PA (PADI/) PADIGARU M.
 PA (SHIM/) SHIMKETS R A.
 PA (ZHON/) ZHONG M.
 Query Match 3.2%; Score 102; DB 12; Length 1948;
 Best Local Similarity 50.0%; Pred. No. 4.3e-16;
 RESULT 1111
 ID ADL13273 standard; cDNA; 2278 BP.
 DE Human steroid-induced C3A liver cell cDNA #1002.
 PN US6673549-B1.
 PD 06-JAN-2004.
 PA (INCY-) INCYTE CORP.
 Query Match 3.2%; Score 102; DB 12; Length 2278;
 Best Local Similarity 50.0%; Pred. No. 4.6e-16;
 RESULT 1112
 ID ADG76138 standard; cDNA; 2583 BP.
 DE Human NOVX cDNA to treat human pathological conditions (SeqID 51).
 PN WO2003085096-A2.
 PD 16-OCT-2003.
 PA (CURA-) CURAGEN CORP.
 Query Match 3.2%; Score 102; DB 10; Length 2583;
 Best Local Similarity 50.0%; Pred. No. 4.9e-16;
 RESULT 1113
 ID ADF45361 standard; cDNA; 2583 BP.
 DE Human semaphorin-like protein NOV2t encoding cDNA SEQ ID NO:51.
 PN WO2003102584-A2.
 PD 11-DEC-2003.
 PA (CURA-) CURAGEN CORP.
 Query Match 3.2%; Score 102; DB 12; Length 2583;
 Best Local Similarity 50.0%; Pred. No. 4.9e-16;
 RESULT 1114
 ID ADO40295 standard; cDNA; 2583 BP.
 DE Human cDNA encoding semaphorin-like protein NOV2t.
 PN US2004018977-A1.
 PD 29-JAN-2004.
 PA (ALVA/) ALVAREZ E.
 PA (ANDE/) ANDERSON D W.
 PA (DHAN/) DHANABAL M.
 PA (KHRA/) KHRAMTSOV N V.
 PA (LARO/) LAROCHELLE W J.
 PA (LICH/) LICHENSTEIN H S.
 PA (LILL/) LI L.
 PA (OOIC/) OOI C E.
 PA (PADI/) PADIGARU M.
 PA (SHIM/) SHIMKETS R A.
 PA (ZHON/) ZHONG M.
 Query Match 3.2%; Score 102; DB 12; Length 2583;

Best Local Similarity 50.0%; Pred. No. 4.9e-16;
 RESULT 1115
 ID ADG76140 standard; cDNA; 2634 BP.
 DE Human NOVX cDNA to treat human pathological conditions (SeqID 53).
 PN WO2003085096-A2.
 PD 16-OCT-2003.
 PA (CURA-) CURAGEN CORP.
 Query Match 3.2%; Score 102; DB 10; Length 2634;
 Best Local Similarity 50.0%; Pred. No. 5e-16;
 RESULT 1116
 ID ADF45363 standard; cDNA; 2634 BP.
 DE Human semaphorin-like protein NOV2u encoding cDNA SEQ ID NO:53.
 PN WO2003102584-A2.
 PD 11-DEC-2003.
 PA (CURA-) CURAGEN CORP.
 Query Match 3.2%; Score 102; DB 12; Length 2634;
 Best Local Similarity 50.0%; Pred. No. 5e-16;
 RESULT 1117
 ID ADO40297 standard; cDNA; 2634 BP.
 DE Human cDNA encoding semaphorin-like protein NOV2u.
 PN US2004018977-A1.
 PD 29-JAN-2004.
 PA (ALVA/) ALVAREZ E.
 PA (ANDE/) ANDERSON D W.
 PA (DHAN/) DHANABAL M.
 PA (KHRA/) KHRAMTSOV N V.
 PA (LARO/) LAROCHELLE W J.
 PA (LICH/) LICHENSTEIN H S.
 PA (LILL/) LI L.
 PA (OOIC/) OOI C E.
 PA (PADI/) PADIGARU M.
 PA (SHIM/) SHIMKETS R A.
 PA (ZHON/) ZHONG M.
 Query Match 3.2%; Score 102; DB 12; Length 2634;
 Best Local Similarity 50.0%; Pred. No. 5e-16;
 RESULT 1118
 ID ADG76116 standard; cDNA; 2944 BP.
 DE Human NOVX cDNA to treat human pathological conditions (SeqID 29).
 PN WO2003085096-A2.
 PD 16-OCT-2003.
 PA (CURA-) CURAGEN CORP.
 Query Match 3.2%; Score 102; DB 10; Length 2944;
 Best Local Similarity 50.0%; Pred. No. 5.3e-16;
 RESULT 1119
 ID ADF45339 standard; cDNA; 2944 BP.
 DE Human semaphorin-like protein NOV2i encoding cDNA SEQ ID NO:29.
 PN WO2003102584-A2.
 PD 11-DEC-2003.
 PA (CURA-) CURAGEN CORP.
 Query Match 3.2%; Score 102; DB 12; Length 2944;
 Best Local Similarity 50.0%; Pred. No. 5.3e-16;
 RESULT 1120
 ID ADO40273 standard; cDNA; 2944 BP.
 DE Human cDNA encoding semaphorin-like protein NOV2i.
 PN US2004018977-A1.
 PD 29-JAN-2004.
 PA (ALVA/) ALVAREZ E.

PA (ANDE/) ANDERSON D W.
PA (DHAN/) DHANABAL M.
PA (KHRA/) KHRAMTSOV N V.
PA (LARO/) LAROCHELLE W J.
PA (LICH/) LICHENSTEIN H S.
PA (LILL/) LI L.
PA (OOIC/) OOI C E.
PA (PADI/) PADIGARU M.
PA (SHIM/) SHIMKETS R A.
PA (ZHON/) ZHONG M.

Query Match 3.2%; Score 102; DB 12; Length 2944;
Best Local Similarity 50.0%; Pred. No. 5.3e-16;

RESULT 1121

ID ADG76106 standard; cDNA; 2995 BP.
DE Human NOVX cDNA to treat human pathological conditions (SeqID 19).
PN WO2003085096-A2.
PD 16-OCT-2003.
PA (CURA-) CURAGEN CORP.

Query Match 3.2%; Score 102; DB 10; Length 2995;
Best Local Similarity 50.0%; Pred. No. 5.3e-16;

RESULT 1122

ID ADF45329 standard; cDNA; 2995 BP.
DE Human semaphorin-like protein NOV2d encoding cDNA SEQ ID NO:19.
PN WO2003102584-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.

Query Match 3.2%; Score 102; DB 12; Length 2995;
Best Local Similarity 50.0%; Pred. No. 5.3e-16;

RESULT 1123

ID ADO40263 standard; cDNA; 2995 BP.
DE Human cDNA encoding semaphorin-like protein NOV2d.
PN US2004018977-A1.
PD 29-JAN-2004.

PA (ALVA/) ALVAREZ E.
PA (ANDE/) ANDERSON D W.
PA (DHAN/) DHANABAL M.
PA (KHRA/) KHRAMTSOV N V.
PA (LARO/) LAROCHELLE W J.
PA (LICH/) LICHENSTEIN H S.
PA (LILL/) LI L.
PA (OOIC/) OOI C E.
PA (PADI/) PADIGARU M.
PA (SHIM/) SHIMKETS R A.
PA (ZHON/) ZHONG M.

Query Match 3.2%; Score 102; DB 12; Length 2995;
Best Local Similarity 50.0%; Pred. No. 5.3e-16;

RESULT 1124

ID ADG76114 standard; cDNA; 3055 BP.
DE Human NOVX cDNA to treat human pathological conditions (SeqID 27).
PN WO2003085096-A2.
PD 16-OCT-2003.
PA (CURA-) CURAGEN CORP.

Query Match 3.2%; Score 102; DB 10; Length 3055;
Best Local Similarity 50.0%; Pred. No. 5.4e-16;

RESULT 1125

ID ADF45337 standard; cDNA; 3055 BP.
DE Human semaphorin-like protein NOV2h encoding cDNA SEQ ID NO:27.

PN WO2003102584-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.

Query Match 3.2%; Score 102; DB 12; Length 3055;
Best Local Similarity 50.0%; Pred. No. 5.4e-16;

RESULT 1126

ID ADO40271 standard; cDNA; 3055 BP.
DE Human cDNA encoding semaphorin-like protein NOV2h.
PN US2004018977-A1.
PD 29-JAN-2004.
PA (ALVA/) ALVAREZ E.
PA (ANDE/) ANDERSON D W.
PA (DHAN/) DHANABAL M.
PA (KHRA/) KHRAMTSOV N V.
PA (LARO/) LAROCHELLE W J.
PA (LICH/) LICHENSTEIN H S.
PA (LILL/) LI L.
PA (OOIC/) OOI C E.
PA (PADI/) PADIGARU M.
PA (SHIM/) SHIMKETS R A.
PA (ZHON/) ZHONG M.

Query Match 3.2%; Score 102; DB 12; Length 3055;
Best Local Similarity 50.0%; Pred. No. 5.4e-16;

RESULT 1127

ID ADG76104 standard; cDNA; 3106 BP.
DE Human NOVX cDNA to treat human pathological conditions (SeqID 17).
PN WO2003085096-A2.
PD 16-OCT-2003.
PA (CURA-) CURAGEN CORP.

Query Match 3.2%; Score 102; DB 10; Length 3106;
Best Local Similarity 50.0%; Pred. No. 5.4e-16;

RESULT 1128

ID ADF45327 standard; cDNA; 3106 BP.
DE Human semaphorin-like protein NOV2c encoding cDNA SEQ ID NO:17.
PN WO2003102584-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.

Query Match 3.2%; Score 102; DB 12; Length 3106;
Best Local Similarity 50.0%; Pred. No. 5.4e-16;

RESULT 1129

ID ADO40261 standard; cDNA; 3106 BP.
DE Human cDNA encoding semaphorin-like protein NOV2c.
PN US2004018977-A1.
PD 29-JAN-2004.
PA (ALVA/) ALVAREZ E.
PA (ANDE/) ANDERSON D W.
PA (DHAN/) DHANABAL M.
PA (KHRA/) KHRAMTSOV N V.
PA (LARO/) LAROCHELLE W J.
PA (LICH/) LICHENSTEIN H S.
PA (LILL/) LI L.
PA (OOIC/) OOI C E.
PA (PADI/) PADIGARU M.
PA (SHIM/) SHIMKETS R A.
PA (ZHON/) ZHONG M.

Query Match 3.2%; Score 102; DB 12; Length 3106;
Best Local Similarity 50.0%; Pred. No. 5.4e-16;

RESULT 1130

ID ADG76134 standard; cDNA; 3165 BP.
DE Human NOVX cDNA to treat human pathological conditions (SeqID 47).
PN WO2003085096-A2.
PD 16-OCT-2003.
PA (CURA-) CURAGEN CORP.

Query Match 3.2%; Score 102; DB 10; Length 3165;
Best Local Similarity 50.0%; Pred. No. 5.5e-16;

RESULT 1131

ID ADF45357 standard; cDNA; 3165 BP.
DE Human semaphorin-like protein NOV2r encoding cDNA SEQ ID NO:47.
PN WO2003102584-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.

Query Match 3.2%; Score 102; DB 12; Length 3165;
Best Local Similarity 50.0%; Pred. No. 5.5e-16;

RESULT 1132

ID ADO40291 standard; cDNA; 3165 BP.
DE Human cDNA encoding semaphorin-like protein NOV2r.
PN US2004018977-A1.
PD 29-JAN-2004.
PA (ALVA/) ALVAREZ E.
PA (ANDE/) ANDERSON D W.
PA (DHAN/) DHANABAL M.
PA (KHRA/) KHRAMTSOV N V.
PA (LARO/) LAROCHELLE W J.
PA (LICH/) LICHENSTEIN H S.
PA (LILL/) LI L.
PA (OOIC/) OOI C E.
PA (PADI/) PADIGARU M.
PA (SHIM/) SHIMKETS R A.
PA (ZHON/) ZHONG M.

Query Match 3.2%; Score 102; DB 12; Length 3165;
Best Local Similarity 50.0%; Pred. No. 5.5e-16;

RESULT 1133

ID AAA93618 standard; DNA; 3333 BP.
DE Human semaphorin protein-like splice variant SECX 2864933-2 DNA.
PN WO200053742-A2.
PD 14-SEP-2000.
PA (CURA-) CURAGEN CORP.

Query Match 3.2%; Score 102; DB 3; Length 3333;
Best Local Similarity 50.0%; Pred. No. 5.6e-16;

RESULT 1134

ID ADA23282 standard; cDNA; 3333 BP.
DE cDNA encoding human SECX polypeptide, SEC3 #1.
PN US2003054514-A1.
PD 20-MAR-2003.
PA (SHIM/) SHIMKETS R A.
PA (LARO/) LAROCHELLE W J.

Query Match 3.2%; Score 102; DB 9; Length 3333;
Best Local Similarity 50.0%; Pred. No. 5.6e-16;

RESULT 1135

ID AAA93617 standard; DNA; 3498 BP.
DE Human semaphorin protein-like splice variant SECX 2864933-1 DNA.
PN WO200053742-A2.
PD 14-SEP-2000.
PA (CURA-) CURAGEN CORP.

Query Match 3.2%; Score 102; DB 3; Length 3498;
Best Local Similarity 50.0%; Pred. No. 5.7e-16;

RESULT 1136

ID ADA23280 standard; cDNA; 3498 BP.
DE cDNA encoding human SECX polypeptide, SEC2.
PN US2003054514-A1.
PD 20-MAR-2003.
PA (SHIM/) SHIMKETS R A.
PA (LARO/) LAROCHELLE W J.

Query Match 3.2%; Score 102; DB 9; Length 3498;
Best Local Similarity 50.0%; Pred. No. 5.7e-16;

RESULT 1137

ID ADG76118 standard; cDNA; 3498 BP.
DE Human NOVX cDNA to treat human pathological conditions (SeqID 31).
PN WO2003085096-A2.
PD 16-OCT-2003.
PA (CURA-) CURAGEN CORP.

Query Match 3.2%; Score 102; DB 10; Length 3498;
Best Local Similarity 50.0%; Pred. No. 5.7e-16;

RESULT 1138

ID ADF45341 standard; cDNA; 3498 BP.
DE Human semaphorin-like protein NOV2j encoding cDNA SEQ ID NO:31.
PN WO2003102584-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.

Query Match 3.2%; Score 102; DB 12; Length 3498;
Best Local Similarity 50.0%; Pred. No. 5.7e-16;

RESULT 1139

ID ADO40275 standard; cDNA; 3498 BP.
DE Human cDNA encoding semaphorin-like protein NOV2j.
PN US2004018977-A1.
PD 29-JAN-2004.
PA (ALVA/) ALVAREZ E.
PA (ANDE/) ANDERSON D W.
PA (DHAN/) DHANABAL M.
PA (KHRA/) KHRAMTSOV N V.
PA (LARO/) LAROCHELLE W J.
PA (LICH/) LICHENSTEIN H S.
PA (LILL/) LI L.
PA (OOIC/) OOI C E.
PA (PADI/) PADIGARU M.
PA (SHIM/) SHIMKETS R A.
PA (ZHON/) ZHONG M.

Query Match 3.2%; Score 102; DB 12; Length 3498;
Best Local Similarity 50.0%; Pred. No. 5.7e-16;

RESULT 1140

ID AAV44295 standard; cDNA; 3550 BP.
DE Human secreted protein clone CJ145_1 cDNA.
PN WO9827205-A2.
PD 25-JUN-1998.
PA (GEMY) GENETICS INST INC.

Query Match 3.2%; Score 102; DB 2; Length 3550;
Best Local Similarity 50.0%; Pred. No. 5.8e-16;

RESULT 1141

ID AAF98469 standard; cDNA; 3550 BP.
DE Human cDNA clone CJ145_1 sequence SEQ ID 160.
PN WO200119988-A1.

PD 22-MAR-2001.
PA (GEMY) GENETICS INST INC.
Query Match 3.2%; Score 102; DB 5; Length 3550;
Best Local Similarity 50.0%; Pred. No. 5.8e-16;
RESULT 1142
ID AAD01233 standard; DNA; 3862 BP.
DE Human semaphorin 6A-1 cDNA.
PN WO200031252-A1.
PD 02-JUN-2000.
PA (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
Query Match 3.2%; Score 102; DB 3; Length 3862;
Best Local Similarity 50.0%; Pred. No. 6e-16;
RESULT 1143
ID ADA23361 standard; cDNA; 4250 BP.
DE cDNA encoding human SECX polypeptide, SEC15.
PN US2003054514-A1.
PD 20-MAR-2003.
PA (SHIM/) SHIMKETS R A.
PA (LARO/) LAROCHELLE W J.
Query Match 3.2%; Score 102; DB 9; Length 4250;
Best Local Similarity 50.0%; Pred. No. 6.3e-16;
RESULT 1144
ID ADG76100 standard; cDNA; 4250 BP.
DE Human NOVX cDNA to treat human pathological conditions (SeqID 13).
PN WO2003085096-A2.
PD 16-OCT-2003.
PA (CURA-) CURAGEN CORP.
Query Match 3.2%; Score 102; DB 10; Length 4250;
Best Local Similarity 50.0%; Pred. No. 6.3e-16;
RESULT 1145
ID ADG39670 standard; cDNA; 4250 BP.
DE Human cDNA #30 of gene differentially expressed in colorectal cancer.
PN US2003186302-A1.
PD 02-OCT-2003.
PA (WANG/) WANG Y.
Query Match 3.2%; Score 102; DB 12; Length 4250;
Best Local Similarity 50.0%; Pred. No. 6.3e-16;
RESULT 1146
ID ADG39719 standard; cDNA; 4250 BP.
DE Human cDNA #30 of gene differentially expressed in colorectal cancer.
PN US2003186303-A1.
PD 02-OCT-2003.
PA (WANG/) WANG Y.
Query Match 3.2%; Score 102; DB 12; Length 4250;
Best Local Similarity 50.0%; Pred. No. 6.3e-16;
RESULT 1147
ID ADF45323 standard; cDNA; 4250 BP.
DE Human semaphorin-like protein NOV2a encoding cDNA SEQ ID NO:13.
PN WO2003102584-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 3.2%; Score 102; DB 12; Length 4250;
Best Local Similarity 50.0%; Pred. No. 6.3e-16;
RESULT 1148
ID ADO40257 standard; cDNA; 4250 BP.
DE Human cDNA encoding semaphorin-like protein NOV2a.
PN US2004018977-A1.

PD 29-JAN-2004.
 PA (ALVA/) ALVAREZ E.
 PA (ANDE/) ANDERSON D W.
 PA (DHAN/) DHANABAL M.
 PA (KHRA/) KHRAMTSOV N V.
 PA (LARO/) LAROCHELLE W J.
 PA (LICH/) LICHENSTEIN H S.
 PA (LILL/) LI L.
 PA (OOIC/) OOI C E.
 PA (PADI/) PADIGARU M.
 PA (SHIM/) SHIMKETS R A.
 PA (ZHON/) ZHONG M.
 Query Match 3.2%; Score 102; DB 12; Length 4250;
 Best Local Similarity 50.0%; Pred. No. 6.3e-16;
 RESULT 1149
 ID ADQ19980 standard; DNA; 4250 BP.
 DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 2800.
 PN WO2004048938-A2.
 PD 10-JUN-2004.
 PA (PROT-) PROTEIN DESIGN LABS INC.
 Query Match 3.2%; Score 102; DB 12; Length 4250;
 Best Local Similarity 50.0%; Pred. No. 6.3e-16;
 RESULT 1150
 ID ABX71103 standard; cDNA; 4280 BP.
 DE Novel human cDNA sequence #328.
 PN WO200281731-A2.
 PD 17-OCT-2002.
 PA (HYSE-) HYSEQ INC.
 PA (GOOD/) GOODRICH R W.
 Query Match 3.2%; Score 102; DB 8; Length 4280;
 Best Local Similarity 50.0%; Pred. No. 6.3e-16;
 RESULT 1151
 ID ABD32609 standard; cDNA; 4612 BP.
 DE Human cancer-associated cDNA HR7-239.1.
 PN WO2004074320-A2.
 PD 02-SEP-2004.
 PA (SAGR-) SAGRES DISCOVERY INC.
 Query Match 3.2%; Score 102; DB 13; Length 4612;
 Best Local Similarity 50.0%; Pred. No. 6.6e-16;
 RESULT 1152
 ID AAH18729 standard; cDNA; 6060 BP.
 DE Human cDNA sequence SEQ ID NO:19004.
 PN EP1074617-A2.
 PD 07-FEB-2001.
 PA (HELI-) HELIX RES INST.
 Query Match 3.2%; Score 102; DB 4; Length 6060;
 Best Local Similarity 50.0%; Pred. No. 7.5e-16;
 RESULT 1153
 ID ADN05230 standard; cDNA; 6060 BP.
 DE Antipsoriatic cDNA sequence #833.
 PN WO2004028479-A2.
 PD 08-APR-2004.
 PA (GETH) GENENTECH INC.
 Query Match 3.2%; Score 102; DB 12; Length 6060;
 Best Local Similarity 50.0%; Pred. No. 7.5e-16;
 RESULT 1154
 ID ADQ22776 standard; DNA; 7281 BP.

DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5596.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 3.2%; Score 102; DB 12; Length 7281;
Best Local Similarity 50.0%; Pred. No. 8.3e-16;
RESULT 1155
ID ADM72166 standard; cDNA; 2082 BP.
DE Human NTRAN polypeptide encoding cDNA (clone ID 7523644CB1).
PN WO2004022705-A2.
PD 18-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 3.2%; Score 100.6; DB 12; Length 2082;
Best Local Similarity 52.8%; Pred. No. 1e-15;
RESULT 1156
ID ADG76112 standard; cDNA; 1438 BP.
DE Human NOVX cDNA to treat human pathological conditions (SeqID 25).
PN WO2003085096-A2.
PD 16-OCT-2003.
PA (CURA-) CURAGEN CORP.
Query Match 3.2%; Score 100.4; DB 10; Length 1438;
Best Local Similarity 49.9%; Pred. No. 9.8e-16;
RESULT 1157
ID ADO40269 standard; cDNA; 1438 BP.
DE Human cDNA encoding semaphorin-like protein NOV2g.
PN US2004018977-A1.
PD 29-JAN-2004.
PA (ALVA/) ALVAREZ E.
PA (ANDE/) ANDERSON D W.
PA (DHAN/) DHANABAL M.
PA (KHRA/) KHRAMTSOV N V.
PA (LARO/) LAROCHELLE W J.
PA (LICH/) LICHENSTEIN H S.
PA (LILL/) LI L.
PA (OOIC/) OOI C E.
PA (PADI/) PADIGARU M.
PA (SHIM/) SHIMKETS R A.
PA (ZHON/) ZHONG M.
Query Match 3.2%; Score 100.4; DB 12; Length 1438;
Best Local Similarity 49.9%; Pred. No. 9.8e-16;
RESULT 1158
ID ADG76142 standard; cDNA; 2113 BP.
DE Human NOVX cDNA to treat human pathological conditions (SeqID 55).
PN WO2003085096-A2.
PD 16-OCT-2003.
PA (CURA-) CURAGEN CORP.
Query Match 3.2%; Score 100.4; DB 10; Length 2113;
Best Local Similarity 49.9%; Pred. No. 1.2e-15;
RESULT 1159
ID ADF45365 standard; cDNA; 2113 BP.
DE Human semaphorin-like protein NOV2v encoding cDNA SEQ ID NO:55.
PN WO2003102584-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 3.2%; Score 100.4; DB 12; Length 2113;
Best Local Similarity 49.9%; Pred. No. 1.2e-15;
RESULT 1160

ID ADO40299 standard; cDNA; 2113 BP.
 DE Human cDNA encoding semaphorin-like protein NOV2v.
 PN US2004018977-A1.
 PD 29-JAN-2004.
 PA (ALVA/) ALVAREZ E.
 PA (ANDE/) ANDERSON D W.
 PA (DHAN/) DHANABAL M.
 PA (KHRA/) KHRAMTSOV N V.
 PA (LARO/) LAROCHELLE W J.
 PA (LICH/) LICHENSTEIN H S.
 PA (LILL/) LI L.
 PA (OOIC/) OOI C E.
 PA (PADI/) PADIGARU M.
 PA (SHIM/) SHIMKETS R A.
 PA (ZHON/) ZHONG M.
 Query Match 3.2%; Score 100.4; DB 12; Length 2113;
 Best Local Similarity 49.9%; Pred. No. 1.2e-15;
 RESULT 1161
 ID ADG76132 standard; cDNA; 3983 BP.
 DE Human NOVX cDNA to treat human pathological conditions (SeqID 45).
 PN WO2003085096-A2.
 PD 16-OCT-2003.
 PA (CURA-) CURAGEN CORP.
 Query Match 3.2%; Score 100.4; DB 10; Length 3983;
 Best Local Similarity 49.9%; Pred. No. 1.6e-15;
 RESULT 1162
 ID ADF45355 standard; cDNA; 3983 BP.
 DE Human semaphorin-like protein NOV2q encoding cDNA SEQ ID NO:45.
 PN WO2003102584-A2.
 PD 11-DEC-2003.
 PA (CURA-) CURAGEN CORP.
 Query Match 3.2%; Score 100.4; DB 12; Length 3983;
 Best Local Similarity 49.9%; Pred. No. 1.6e-15;
 RESULT 1163
 ID ADO40289 standard; cDNA; 3983 BP.
 DE Human cDNA encoding semaphorin-like protein NOV2q.
 PN US2004018977-A1.
 PD 29-JAN-2004.
 PA (ALVA/) ALVAREZ E.
 PA (ANDE/) ANDERSON D W.
 PA (DHAN/) DHANABAL M.
 PA (KHRA/) KHRAMTSOV N V.
 PA (LARO/) LAROCHELLE W J.
 PA (LICH/) LICHENSTEIN H S.
 PA (LILL/) LI L.
 PA (OOIC/) OOI C E.
 PA (PADI/) PADIGARU M.
 PA (SHIM/) SHIMKETS R A.
 PA (ZHON/) ZHONG M.
 Query Match 3.2%; Score 100.4; DB 12; Length 3983;
 Best Local Similarity 49.9%; Pred. No. 1.6e-15;
 RESULT 1164
 ID ADE31378 standard; DNA; 4230 BP.
 DE Human diagnostic and therapeutic polynucleotide (dithp), SEQ ID No 133.
 PN WO2003062376-A2.
 PD 31-JUL-2003.
 PA (INCY-) INCYTE GENOMICS INC.

Query Match 3.2%; Score 100.2; DB 10; Length 4230;
 Best Local Similarity 50.2%; Pred. No. 1.9e-15;
 RESULT 1165
 ID ADF45335 standard; cDNA; 1437 BP.
 DE Human semaphorin-like protein NOV2g encoding cDNA SEQ ID NO:25.
 PN WO2003102584-A2.
 PD 11-DEC-2003.
 PA (CURA-) CURAGEN CORP.
 Query Match 3.2%; Score 100; DB 12; Length 1437;
 Best Local Similarity 49.9%; Pred. No. 1.3e-15;
 RESULT 1166
 ID AAX86126 standard; DNA; 2893 BP.
 DE DNA encoding SBSEMN1, a semaphorin family polypeptide.
 PN EP933425-A1.
 PD 04-AUG-1999.
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 Query Match 3.1%; Score 99; DB 2; Length 2893;
 Best Local Similarity 52.6%; Pred. No. 3.3e-15;
 RESULT 1167
 ID AAX86127 standard; DNA; 2894 BP.
 DE EST sequence for DNA encoding SBSEMN1.
 PN EP933425-A1.
 PD 04-AUG-1999.
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 Query Match 3.1%; Score 99; DB 2; Length 2894;
 Best Local Similarity 52.6%; Pred. No. 3.3e-15;
 RESULT 1168
 ID ABA04082 standard; cDNA; 1797 BP.
 DE Human semaphorin G-like NHP encoding cDNA SEQ ID NO:40.
 PN WO200188133-A2.
 PD 22-NOV-2001.
 PA (LEXI-) LEXICON GENETICS INC.
 Query Match 3.1%; Score 98.6; DB 6; Length 1797;
 Best Local Similarity 47.4%; Pred. No. 3.3e-15;
 RESULT 1169
 ID ABA04084 standard; cDNA; 2220 BP.
 DE Human semaphorin G-like NHP encoding cDNA SEQ ID NO:44.
 PN WO200188133-A2.
 PD 22-NOV-2001.
 PA (LEXI-) LEXICON GENETICS INC.
 Query Match 3.1%; Score 98.6; DB 6; Length 2220;
 Best Local Similarity 47.4%; Pred. No. 3.7e-15;
 RESULT 1170
 ID ABA04086 standard; cDNA; 2301 BP.
 DE Human semaphorin G-like NHP encoding cDNA SEQ ID NO:48.
 PN WO200188133-A2.
 PD 22-NOV-2001.
 PA (LEXI-) LEXICON GENETICS INC.
 Query Match 3.1%; Score 98.6; DB 6; Length 2301;
 Best Local Similarity 47.4%; Pred. No. 3.8e-15;
 RESULT 1171
 ID AAV28916 standard; cDNA to mRNA; 2790 BP.
 DE Human semaphorin Y encoding cDNA, CDS only.
 PN WO9811216-A1.
 PD 19-MAR-1998.
 PA (SUMU) SUMITOMO PHARM CO LTD.
 Query Match 3.1%; Score 98.6; DB 2; Length 2790;

Best Local Similarity 50.1%; Pred. No. 4.1e-15;
 RESULT 1172
 ID AAV28915 standard; cDNA to mRNA; 3432 BP.
 DE Human semaphorin Y encoding cDNA.
 PN WO9811216-A1.
 PD 19-MAR-1998.
 PA (SUMU) SUMITOMO PHARM CO LTD.
 Query Match 3.1%; Score 98.6; DB 2; Length 3432;
 Best Local Similarity 50.1%; Pred. No. 4.6e-15;
 RESULT 1173
 ID ABA04081 standard; cDNA; 1812 BP.
 DE Human semaphorin G-like NHP encoding cDNA SEQ ID NO:38.
 PN WO200188133-A2.
 PD 22-NOV-2001.
 PA (LEXI-) LEXICON GENETICS INC.
 Query Match 3.0%; Score 95.6; DB 6; Length 1812;
 Best Local Similarity 48.8%; Pred. No. 2.1e-14;
 RESULT 1174
 ID ABA04083 standard; cDNA; 2235 BP.
 DE Human semaphorin G-like NHP encoding cDNA SEQ ID NO:42.
 PN WO200188133-A2.
 PD 22-NOV-2001.
 PA (LEXI-) LEXICON GENETICS INC.
 Query Match 3.0%; Score 95.6; DB 6; Length 2235;
 Best Local Similarity 48.8%; Pred. No. 2.3e-14;
 RESULT 1175
 ID ABA04085 standard; cDNA; 2316 BP.
 DE Human semaphorin G-like NHP encoding cDNA SEQ ID NO:46.
 PN WO200188133-A2.
 PD 22-NOV-2001.
 PA (LEXI-) LEXICON GENETICS INC.
 Query Match 3.0%; Score 95.6; DB 6; Length 2316;
 Best Local Similarity 48.8%; Pred. No. 2.4e-14;
 RESULT 1176
 ID AAS68807 standard; cDNA; 3039 BP.
 DE DNA encoding novel human diagnostic protein #4611.
 PN WO200175067-A2.
 PD 11-OCT-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match 3.0%; Score 93; DB 5; Length 3039;
 Best Local Similarity 49.9%; Pred. No. 1.3e-13;
 RESULT 1177
 ID AAS89721 standard; cDNA; 3039 BP.
 DE DNA encoding novel human diagnostic protein #25525.
 PN WO200175067-A2.
 PD 11-OCT-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match 3.0%; Score 93; DB 5; Length 3039;
 Best Local Similarity 49.9%; Pred. No. 1.3e-13;
 RESULT 1178
 ID AAF29452 standard; cDNA; 729 BP.
 DE Human TANGO 276 cDNA open reading frame.
 PN WO200100638-A2.
 PD 04-JAN-2001.
 PA (MILL-) MILLENNIUM PHARM INC.
 Query Match 3.0%; Score 92.8; DB 4; Length 729;
 Best Local Similarity 56.6%; Pred. No. 7.4e-14;

RESULT 1179

ID ACD66761 standard; cDNA; 729 BP.
DE Secreted polypeptide-related cDNA #45.
PN US2003022279-A1.
PD 30-JAN-2003.
PA (FRAS/) FRASER C C.
PA (BARN/) BARNES T M.
PA (SHAR/) SHARP J D.
PA (KIRS/) KIRST S J.
PA (MYER/) MYERS P S.
PA (LEIB/) LEIBY K R.
PA (HOLT/) HOLTZMAN D A.
PA (MCCA/) MCCARTHY S A.
PA (WRIG/) WRIGHTON N.
PA (MACK/) MACKAY C R.
PA (GOOD/) GOODEARL A D J.

Query Match 3.0%; Score 92.8; DB 8; Length 729;
Best Local Similarity 56.6%; Pred. No. 7.4e-14;

RESULT 1180

ID ADB90749 standard; cDNA; 729 BP.
DE Human TANGO 276 open reading frame.
PN US2003082586-A1.
PD 01-MAY-2003.
PA (MILL-) MILLENNIUM PHARM INC.

Query Match 3.0%; Score 92.8; DB 9; Length 729;
Best Local Similarity 56.6%; Pred. No. 7.4e-14;

RESULT 1181

ID ADF71484 standard; cDNA; 729 BP.
DE Human TANGO 276 CDS.
PN US2003175733-A1.
PD 18-SEP-2003.
PA (MILL-) MILLENNIUM PHARM INC.

Query Match 3.0%; Score 92.8; DB 10; Length 729;
Best Local Similarity 56.6%; Pred. No. 7.4e-14;

RESULT 1182

ID ADQ10310 standard; cDNA; 729 BP.
DE Human polynucleotide #52.
PN US2004121396-A1.
PD 24-JUN-2004.
PA (MILL-) MILLENNIUM PHARM INC.

Query Match 3.0%; Score 92.8; DB 12; Length 729;
Best Local Similarity 56.6%; Pred. No. 7.4e-14;

RESULT 1183

ID AAX84066 standard; DNA; 1054 BP.
DE Human ZSMF-3 coding sequence.
PN WO9932622-A2.
PD 01-JUL-1999.
PA (ZYMO) ZYMOGENETICS INC.

Query Match 2.9%; Score 92; DB 2; Length 1054;
Best Local Similarity 53.2%; Pred. No. 1.5e-13;

RESULT 1184

ID ADR68485 standard; DNA; 1173 BP.
DE Apoptosis-associated polypeptide encoding cDNA #4.
PN WO2004072111-A2.
PD 26-AUG-2004.
PA (XANT-) XANTOS BIOMEDICINE AG.

Query Match 2.9%; Score 92; DB 13; Length 1173;

Best Local Similarity 53.2%; Pred. No. 1.5e-13;
 RESULT 1185
 ID ADF82146 standard; DNA; 4982 BP.
 DE Leukaemia-related DNA sequence #2702.
 PN WO2003039443-A2.
 PD 15-MAY-2003.
 PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
 PA (UYLU-) UNIV LUDWIG MAXIMILIANS.
 PA (HAFE/) HAERLACH T.
 PA (SCHO/) SCHOCH C.
 PA (KERN/) KERN W.
 Query Match 2.9%; Score 91.2; DB 10; Length 4982;
 Best Local Similarity 49.8%; Pred. No. 5.2e-13;
 RESULT 1186
 ID ADL83281 standard; cDNA; 2505 BP.
 DE Human PRO80846 cDNA, SEQ ID 483.
 PN WO2004024097-A2.
 PD 25-MAR-2004.
 PA (GETH) GENENTECH INC.
 Query Match 2.9%; Score 90.2; DB 12; Length 2505;
 Best Local Similarity 55.3%; Pred. No. 6.8e-13;
 RESULT 1187
 ID ACN37741 standard; cDNA; 2505 BP.
 DE Tumour-associated antigenic target (TAT) cDNA DNA324145, SEQ ID NO:825.
 PN WO2004030615-A2.
 PD 15-APR-2004.
 PA (GETH) GENENTECH INC.
 Query Match 2.9%; Score 90.2; DB 13; Length 2505;
 Best Local Similarity 55.3%; Pred. No. 6.8e-13;
 RESULT 1188
 ID AAV28914 standard; cDNA to mRNA; 2787 BP.
 DE Rat semaphorin Y encoding cDNA, CDS only.
 PN WO9811216-A1.
 PD 19-MAR-1998.
 PA (SUMU) SUMITOMO PHARM CO LTD.
 Query Match 2.9%; Score 89.8; DB 2; Length 2787;
 Best Local Similarity 50.1%; Pred. No. 9.2e-13;
 RESULT 1189
 ID AAV28913 standard; cDNA to mRNA; 3195 BP.
 DE Rat semaphorin Y encoding cDNA.
 PN WO9811216-A1.
 PD 19-MAR-1998.
 PA (SUMU) SUMITOMO PHARM CO LTD.
 Query Match 2.9%; Score 89.8; DB 2; Length 3195;
 Best Local Similarity 50.1%; Pred. No. 9.8e-13;
 RESULT 1190
 ID ADQ22240 standard; DNA; 4003 BP.
 DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5060.
 PN WO2004048938-A2.
 PD 10-JUN-2004.
 PA (PROT-) PROTEIN DESIGN LABS INC.
 Query Match 2.8%; Score 89.4; DB 12; Length 4003;
 Best Local Similarity 50.8%; Pred. No. 1.4e-12;
 RESULT 1191
 ID ADQ92047 standard; DNA; 557 BP.
 DE Human autoantigen DNA fragment MPMGp800B24597.
 PN WO2004058972-A1.

PD 15-JUL-2004.
 PA (THIE/) THIESEN H.
 PA (LORE/) LORENZ P.
 Query Match 2.8%; Score 88; DB 12; Length 557;
 Best Local Similarity 56.7%; Pred. No. 1.2e-12;
 RESULT 1192
 ID ABL39763 standard; cDNA; 1419 BP.
 DE Human NS cDNA sequence SEQ ID NO:73.
 PN WO200206315-A2.
 PD 24-JAN-2002.
 PA (COMP-) COMPUGEN LTD.
 Query Match 2.7%; Score 86.2; DB 6; Length 1419;
 Best Local Similarity 48.3%; Pred. No. 6e-12;
 RESULT 1193
 ID ADL12903 standard; cDNA; 4286 BP.
 DE Human steroid-induced C3A liver cell cDNA #632.
 PN US6673549-B1.
 PD 06-JAN-2004.
 PA (INCY-) INCYTE CORP.
 Query Match 2.7%; Score 84.2; DB 12; Length 4286;
 Best Local Similarity 50.3%; Pred. No. 3.5e-11;
 RESULT 1194
 ID ABX34490 standard; cDNA; 4388 BP.
 DE Human mddt cDNA SEQ ID 51.
 PN WO200279449-A2.
 PD 10-OCT-2002.
 PA (INCY-) INCYTE GENOMICS INC.
 Query Match 2.7%; Score 84.2; DB 8; Length 4388;
 Best Local Similarity 50.3%; Pred. No. 3.6e-11;
 RESULT 1195
 ID ABZ35865 standard; cDNA; 2506 BP.
 DE Human secretory polynucleotide SPTM SEQ ID NO 29.
 PN WO200283876-A2.
 PD 24-OCT-2002.
 PA (INCY-) INCYTE GENOMICS INC.
 Query Match 2.6%; Score 83; DB 8; Length 2506;
 Best Local Similarity 48.1%; Pred. No. 5.6e-11;
 RESULT 1196
 ID ADQ87204 standard; cDNA; 2918 BP.
 DE Human tumour-associated antigenic target (TAT) cDNA sequence #4081.
 PN WO2004060270-A2.
 PD 22-JUL-2004.
 PA (GETH) GENENTECH INC.
 PA (WUTD/) WU T D.
 PA (ZHOU/) ZHOU Y.
 Query Match 2.6%; Score 83; DB 12; Length 2918;
 Best Local Similarity 48.1%; Pred. No. 6.1e-11;
 RESULT 1197
 ID ADQ84927 standard; cDNA; 2918 BP.
 DE Human tumour-associated antigenic target (TAT) cDNA sequence #1741.
 PN WO2004060270-A2.
 PD 22-JUL-2004.
 PA (GETH) GENENTECH INC.
 PA (WUTD/) WU T D.
 PA (ZHOU/) ZHOU Y.
 Query Match 2.6%; Score 83; DB 12; Length 2918;
 Best Local Similarity 48.1%; Pred. No. 6.1e-11;

RESULT 1198

ID ADD08935 standard; cDNA; 2919 BP.
DE Human semaphorin 3B encoding cDNA SEQ ID NO:11.
PN WO2003029814-A2.
PD 10-APR-2003.
PA (LUDW-) LUDWIG INST CANCER RES.
PA (LICN) LICENTIA LTD.

Query Match 2.6%; Score 83; DB 10; Length 2919;
Best Local Similarity 48.1%; Pred. No. 6.1e-11;

RESULT 1199

ID ADL82794 standard; cDNA; 2919 BP.
DE Human semaphorin3B, SEMA3B, cDNA.
PN US2003166557-A1.
PD 04-SEP-2003.
PA (TEXA) UNIV TEXAS SYSTEM.

Query Match 2.6%; Score 83; DB 11; Length 2919;
Best Local Similarity 48.1%; Pred. No. 6.1e-11;

RESULT 1200

ID ACN37936 standard; cDNA; 2919 BP.
DE Tumour-associated antigenic target (TAT) cDNA DNA103505, SEQ ID NO:1149.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.

Query Match 2.6%; Score 83; DB 13; Length 2919;
Best Local Similarity 48.1%; Pred. No. 6.1e-11;

RESULT 1201

ID AAV07282 standard; cDNA to mRNA; 1761 BP.
DE Human semaphorin W encoding cDNA.
PN WO9815628-A1.
PD 16-APR-1998.
PA (SUMU) SUMITOMO PHARM CO LTD.

Query Match 2.6%; Score 81.4; DB 2; Length 1761;
Best Local Similarity 55.8%; Pred. No. 1.3e-10;

RESULT 1202

ID AAV07281 standard; cDNA to mRNA; 2315 BP.
DE Human semaphorin W encoding cDNA with 3'UTR.
PN WO9815628-A1.
PD 16-APR-1998.
PA (SUMU) SUMITOMO PHARM CO LTD.

Query Match 2.6%; Score 81.4; DB 2; Length 2315;
Best Local Similarity 55.8%; Pred. No. 1.4e-10;

RESULT 1203

ID ABL15029 standard; cDNA; 3780 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 39569.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.

Query Match 2.6%; Score 80.2; DB 4; Length 3780;
Best Local Similarity 49.4%; Pred. No. 3.9e-10;

RESULT 1204

ID ADE28132 standard; cDNA; 2892 BP.
DE Human NTRAN cDNA - SEQ ID 37.
PN WO2003051902-A1.
PD 26-JUN-2003.
PA (INCY-) INCYTE GENOMICS INC.

Query Match 2.5%; Score 79.8; DB 10; Length 2892;
Best Local Similarity 49.5%; Pred. No. 4.3e-10;

RESULT 1205

ID AAH47791 standard; cDNA; 2349 BP.
DE Novel human protein (NHP) encoding cDNA sequence.
PN WO200170806-A2.
PD 27-SEP-2001.
PA (LEXI-) LEXICON GENETICS INC.
Query Match 2.5%; Score 79.6; DB 4; Length 2349;
Best Local Similarity 50.6%; Pred. No. 4.4e-10;

RESULT 1206

ID ADJ34112 standard; cDNA; 2414 BP.
DE Human cDNA encoding secreted protein NOV1a.
PN WO2004000997-A2.
PD 31-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 2.5%; Score 79.6; DB 12; Length 2414;
Best Local Similarity 50.6%; Pred. No. 4.5e-10;

RESULT 1207

ID AAH47790 standard; cDNA; 2628 BP.
DE Novel human protein (NHP) encoding cDNA sequence.
PN WO200170806-A2.
PD 27-SEP-2001.
PA (LEXI-) LEXICON GENETICS INC.
Query Match 2.5%; Score 79.6; DB 4; Length 2628;
Best Local Similarity 50.6%; Pred. No. 4.7e-10;

RESULT 1208

ID AAH47792 standard; DNA; 3568 BP.
DE Novel human protein (NHP) polynucleotide sequence.
PN WO200170806-A2.
PD 27-SEP-2001.
PA (LEXI-) LEXICON GENETICS INC.
Query Match 2.5%; Score 79.6; DB 4; Length 3568;
Best Local Similarity 50.6%; Pred. No. 5.4e-10;

RESULT 1209

ID ADJ34114 standard; cDNA; 4690 BP.
DE Human cDNA encoding secreted protein NOV1b.
PN WO2004000997-A2.
PD 31-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 2.5%; Score 79.6; DB 12; Length 4690;
Best Local Similarity 50.6%; Pred. No. 6.2e-10;

RESULT 1210

ID ADN04921 standard; cDNA; 4700 BP.
DE Antipsoriatic cDNA sequence #675.
PN WO2004028479-A2.
PD 08-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 79.6; DB 12; Length 4700;
Best Local Similarity 50.6%; Pred. No. 6.2e-10;

RESULT 1211

ID ADQ20124 standard; DNA; 4700 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 2944.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 2.5%; Score 79.6; DB 12; Length 4700;
Best Local Similarity 50.6%; Pred. No. 6.2e-10;

RESULT 1212

ID ADR25963 standard; DNA; 4700 BP.
 DE Breast cancer prognosis marker #1824.
 PN WO2004065545-A2.
 PD 05-AUG-2004.
 PA (ROSE-) ROSETTA INPHARMATICS LLC.
 PA (NECA-) NETHERLANDS CANCER INST.
 Query Match 2.5%; Score 79.6; DB 13; Length 4700;
 Best Local Similarity 50.6%; Pred. No. 6.2e-10;
 RESULT 1213
 ID AAA93109 standard; cDNA; 4859 BP.
 DE Human secreted protein coding sequence SEQ ID NO: 17.
 PN WO200049134-A1.
 PD 24-AUG-2000.
 PA (ALPH-) ALPHAGENE INC.
 Query Match 2.5%; Score 79.6; DB 3; Length 4859;
 Best Local Similarity 50.6%; Pred. No. 6.3e-10;
 RESULT 1214
 ID ADQ24174 standard; DNA; 4936 BP.
 DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 6994.
 PN WO2004048938-A2.
 PD 10-JUN-2004.
 PA (PROT-) PROTEIN DESIGN LABS INC.
 Query Match 2.5%; Score 79.6; DB 12; Length 4936;
 Best Local Similarity 50.6%; Pred. No. 6.4e-10;
 RESULT 1215
 ID AAQ87444 standard; cDNA; 3560 BP.
 DE Drosophila semaphorin I cDNA.
 PN WO9507706-A1.
 PD 23-MAR-1995.
 PA (REGC) UNIV CALIFORNIA.
 Query Match 2.5%; Score 78.6; DB 2; Length 3560;
 Best Local Similarity 49.2%; Pred. No. 1e-09;
 RESULT 1216
 ID AAH42598 standard; cDNA; 1923 BP.
 DE Partial cDNA sequence of semaphorin-like polypeptide.
 PN WO200153466-A1.
 PD 26-JUL-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match 2.5%; Score 78.2; DB 4; Length 1923;
 Best Local Similarity 51.9%; Pred. No. 9.4e-10;
 RESULT 1217
 ID AAH42597 standard; cDNA; 3694 BP.
 DE Nucleotide sequence of a human semaphorin-like polypeptide.
 PN WO200153466-A1.
 PD 26-JUL-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match 2.5%; Score 78.2; DB 4; Length 3694;
 Best Local Similarity 51.9%; Pred. No. 1.3e-09;
 RESULT 1218
 ID ADS10319 standard; DNA; 3694 BP.
 DE Human therapeutic DNA - SEQ ID 556.
 PN WO2004080148-A2.
 PD 23-SEP-2004.
 PA (NUVE-) NUVELO INC.
 Query Match 2.5%; Score 78.2; DB 13; Length 3694;
 Best Local Similarity 51.9%; Pred. No. 1.3e-09;
 RESULT 1219

ID ABA04072 standard; cDNA; 1491 BP.
 DE Human semaphorin G-like NHP encoding cDNA SEQ ID NO:20.
 PN WO200188133-A2.
 PD 22-NOV-2001.
 PA (LEXI-) LEXICON GENETICS INC.
 Query Match 2.5%; Score 78; DB 6; Length 1491;
 Best Local Similarity 47.2%; Pred. No. 9.4e-10;
 RESULT 1220
 ID AAH03722 standard; cDNA; 862 BP.
 DE Human cDNA clone (5'-primer) SEQ ID NO:557.
 PN EP1074617-A2.
 PD 07-FEB-2001.
 PA (HELI-) HELIX RES INST.
 Query Match 2.4%; Score 76.6; DB 4; Length 862;
 Best Local Similarity 51.7%; Pred. No. 1.7e-09;
 RESULT 1221
 ID ADJ34314 standard; cDNA; 1383 BP.
 DE Human cDNA encoding secreted protein NOV16e.
 PN WO2004000997-A2.
 PD 31-DEC-2003.
 PA (CURA-) CURAGEN CORP.
 Query Match 2.4%; Score 76.6; DB 12; Length 1383;
 Best Local Similarity 51.7%; Pred. No. 2.1e-09;
 RESULT 1222
 ID ADJ34308 standard; cDNA; 1383 BP.
 DE Human cDNA encoding secreted protein NOV16b.
 PN WO2004000997-A2.
 PD 31-DEC-2003.
 PA (CURA-) CURAGEN CORP.
 Query Match 2.4%; Score 76.6; DB 12; Length 1383;
 Best Local Similarity 51.7%; Pred. No. 2.1e-09;
 RESULT 1223
 ID AAH15312 standard; cDNA; 1588 BP.
 DE Human cDNA sequence SEQ ID NO:13470.
 PN EP1074617-A2.
 PD 07-FEB-2001.
 PA (HELI-) HELIX RES INST.
 Query Match 2.4%; Score 76.6; DB 4; Length 1588;
 Best Local Similarity 51.7%; Pred. No. 2.3e-09;
 RESULT 1224
 ID ADJ34312 standard; cDNA; 1713 BP.
 DE Human cDNA encoding secreted protein NOV16d.
 PN WO2004000997-A2.
 PD 31-DEC-2003.
 PA (CURA-) CURAGEN CORP.
 Query Match 2.4%; Score 76.6; DB 12; Length 1713;
 Best Local Similarity 51.7%; Pred. No. 2.4e-09;
 RESULT 1225
 ID ADJ34316 standard; cDNA; 1713 BP.
 DE Human cDNA encoding secreted protein NOV16f.
 PN WO2004000997-A2.
 PD 31-DEC-2003.
 PA (CURA-) CURAGEN CORP.
 Query Match 2.4%; Score 76.6; DB 12; Length 1713;
 Best Local Similarity 51.7%; Pred. No. 2.4e-09;
 RESULT 1226
 ID ADJ34336 standard; cDNA; 1894 BP.

DE Human cDNA encoding secreted protein NOV16p.
 PN WO2004000997-A2.
 PD 31-DEC-2003.
 PA (CURA-) CURAGEN CORP.
 Query Match 2.4%; Score 76.6; DB 12; Length 1894;
 Best Local Similarity 51.7%; Pred. No. 2.5e-09;
 RESULT 1227
 ID ADJ34306 standard; cDNA; 1894 BP.
 DE Human cDNA encoding secreted protein NOV16a.
 PN WO2004000997-A2.
 PD 31-DEC-2003.
 PA (CURA-) CURAGEN CORP.
 Query Match 2.4%; Score 76.6; DB 12; Length 1894;
 Best Local Similarity 51.7%; Pred. No. 2.5e-09;
 RESULT 1228
 ID ADJ34338 standard; cDNA; 1894 BP.
 DE Human cDNA encoding secreted protein NOV16q.
 PN WO2004000997-A2.
 PD 31-DEC-2003.
 PA (CURA-) CURAGEN CORP.
 Query Match 2.4%; Score 76.6; DB 12; Length 1894;
 Best Local Similarity 51.7%; Pred. No. 2.5e-09;
 RESULT 1229
 ID ADJ34334 standard; cDNA; 1894 BP.
 DE Human cDNA encoding secreted protein NOV16o.
 PN WO2004000997-A2.
 PD 31-DEC-2003.
 PA (CURA-) CURAGEN CORP.
 Query Match 2.4%; Score 76.6; DB 12; Length 1894;
 Best Local Similarity 51.7%; Pred. No. 2.5e-09;
 RESULT 1230
 ID ADJ34330 standard; cDNA; 1894 BP.
 DE Human cDNA encoding secreted protein NOV16m.
 PN WO2004000997-A2.
 PD 31-DEC-2003.
 PA (CURA-) CURAGEN CORP.
 Query Match 2.4%; Score 76.6; DB 12; Length 1894;
 Best Local Similarity 51.7%; Pred. No. 2.5e-09;
 RESULT 1231
 ID ABS64379 standard; DNA; 1896 BP.
 DE Human semaphorin-like gene #1.
 PN WO200264791-A2.
 PD 22-AUG-2002.
 PA (CURA-) CURAGEN CORP.
 Query Match 2.4%; Score 76.6; DB 6; Length 1896;
 Best Local Similarity 51.7%; Pred. No. 2.5e-09;
 RESULT 1232
 ID ADJ34328 standard; cDNA; 1950 BP.
 DE Human cDNA encoding secreted protein NOV16l.
 PN WO2004000997-A2.
 PD 31-DEC-2003.
 PA (CURA-) CURAGEN CORP.
 Query Match 2.4%; Score 76.6; DB 12; Length 1950;
 Best Local Similarity 51.7%; Pred. No. 2.5e-09;
 RESULT 1233
 ID AAD38696 standard; cDNA; 2014 BP.
 DE Human LP221 secreted protein encoding cDNA.

PN WO200226801-A2.
 PD 04-APR-2002.
 PA (ELIL) LILLY & CO ELI.
 Query Match 2.4%; Score 76.6; DB 6; Length 2014;
 Best Local Similarity 51.7%; Pred. No. 2.6e-09;
 RESULT 1234
 ID ABS64381 standard; DNA; 2191 BP.
 DE Human semaphorin-like gene #2.
 PN WO200264791-A2.
 PD 22-AUG-2002.
 PA (CURA-) CURAGEN CORP.
 Query Match 2.4%; Score 76.6; DB 6; Length 2191;
 Best Local Similarity 51.7%; Pred. No. 2.7e-09;
 RESULT 1235
 ID ADJ34318 standard; cDNA; 2191 BP.
 DE Human cDNA encoding secreted protein NOV16g.
 PN WO2004000997-A2.
 PD 31-DEC-2003.
 PA (CURA-) CURAGEN CORP.
 Query Match 2.4%; Score 76.6; DB 12; Length 2191;
 Best Local Similarity 51.7%; Pred. No. 2.7e-09;
 RESULT 1236
 ID ABS64383 standard; DNA; 2359 BP.
 DE Human semaphorin-like gene #4.
 PN WO200264791-A2.
 PD 22-AUG-2002.
 PA (CURA-) CURAGEN CORP.
 Query Match 2.4%; Score 76.6; DB 6; Length 2359;
 Best Local Similarity 51.7%; Pred. No. 2.8e-09;
 RESULT 1237
 ID ADJ34322 standard; cDNA; 2359 BP.
 DE Human cDNA encoding secreted protein NOV16i.
 PN WO2004000997-A2.
 PD 31-DEC-2003.
 PA (CURA-) CURAGEN CORP.
 Query Match 2.4%; Score 76.6; DB 12; Length 2359;
 Best Local Similarity 51.7%; Pred. No. 2.8e-09;
 RESULT 1238
 ID ABS64382 standard; DNA; 3196 BP.
 DE Human semaphorin-like gene #3.
 PN WO200264791-A2.
 PD 22-AUG-2002.
 PA (CURA-) CURAGEN CORP.
 Query Match 2.4%; Score 76.6; DB 6; Length 3196;
 Best Local Similarity 51.7%; Pred. No. 3.2e-09;
 RESULT 1239
 ID ADJ34320 standard; cDNA; 3196 BP.
 DE Human cDNA encoding secreted protein NOV16h.
 PN WO2004000997-A2.
 PD 31-DEC-2003.
 PA (CURA-) CURAGEN CORP.
 Query Match 2.4%; Score 76.6; DB 12; Length 3196;
 Best Local Similarity 51.7%; Pred. No. 3.2e-09;
 RESULT 1240
 ID ABS64380 standard; DNA; 3205 BP.
 DE Human semaphorin 6A1 like gene.
 PN WO200264791-A2.

PD 22-AUG-2002.
 PA (CURA-) CURAGEN CORP.
 Query Match 2.4%; Score 76.6; DB 6; Length 3205;
 Best Local Similarity 51.7%; Pred. No. 3.2e-09;
 RESULT 1241
 ID ADJ34310 standard; cDNA; 3205 BP.
 DE Human cDNA encoding secreted protein NOV16c.
 PN WO2004000997-A2.
 PD 31-DEC-2003.
 PA (CURA-) CURAGEN CORP.
 Query Match 2.4%; Score 76.6; DB 12; Length 3205;
 Best Local Similarity 51.7%; Pred. No. 3.2e-09;
 RESULT 1242
 ID ADJ34326 standard; cDNA; 3231 BP.
 DE Human cDNA encoding secreted protein NOV16k.
 PN WO2004000997-A2.
 PD 31-DEC-2003.
 PA (CURA-) CURAGEN CORP.
 Query Match 2.4%; Score 76.6; DB 12; Length 3231;
 Best Local Similarity 51.7%; Pred. No. 3.3e-09;
 RESULT 1243
 ID ABS64384 standard; DNA; 3364 BP.
 DE Human semaphorin-like gene #5.
 PN WO200264791-A2.
 PD 22-AUG-2002.
 PA (CURA-) CURAGEN CORP.
 Query Match 2.4%; Score 76.6; DB 6; Length 3364;
 Best Local Similarity 51.7%; Pred. No. 3.3e-09;
 RESULT 1244
 ID ADJ34324 standard; cDNA; 3364 BP.
 DE Human cDNA encoding secreted protein NOV16j.
 PN WO2004000997-A2.
 PD 31-DEC-2003.
 PA (CURA-) CURAGEN CORP.
 Query Match 2.4%; Score 76.6; DB 12; Length 3364;
 Best Local Similarity 51.7%; Pred. No. 3.3e-09;
 RESULT 1245
 ID ABA00055 standard; cDNA; 4234 BP.
 DE CADHP-2 coding sequence, Incyte ID No: 7596315CB1.
 PN WO200259312-A2.
 PD 01-AUG-2002.
 PA (INCY-) INCYTE GENOMICS INC.
 Query Match 2.4%; Score 76.6; DB 6; Length 4234;
 Best Local Similarity 51.7%; Pred. No. 3.7e-09;
 RESULT 1246
 ID ABX34714 standard; cDNA; 6645 BP.
 DE Human mddt cDNA SEQ ID 275.
 PN WO200279449-A2.
 PD 10-OCT-2002.
 PA (INCY-) INCYTE GENOMICS INC.
 Query Match 2.4%; Score 76.6; DB 8; Length 6645;
 Best Local Similarity 51.7%; Pred. No. 4.7e-09;
 RESULT 1247
 ID AAF90250 standard; DNA; 2340 BP.
 DE Nucleotide sequence of a semaphorin polypeptide designated ZSMF-16.
 PN WO200140278-A2.
 PD 07-JUN-2001.

PA (ZYMO) ZYMOGENETICS INC.
 Query Match 2.4%; Score 76.2; DB 4; Length 2340;
 Best Local Similarity 51.7%; Pred. No. 3.5e-09;

RESULT 1248
 ID ABA97362 standard; cDNA; 2340 BP.
 DE Human ZSMF-16 encoding sequence.
 PN US2001049432-A1.
 PD 06-DEC-2001.
 PA (HOLL/) HOLLOWAY J L.
 PA (FOLE/) FOLEY K P.
 Query Match 2.4%; Score 76.2; DB 6; Length 2340;
 Best Local Similarity 51.7%; Pred. No. 3.5e-09;

RESULT 1249
 ID ADJ34332 standard; cDNA; 1894 BP.
 DE Human cDNA encoding secreted protein NOV16n.
 PN WO2004000997-A2.
 PD 31-DEC-2003.
 PA (CURA-) CURAGEN CORP.
 Query Match 2.4%; Score 75; DB 12; Length 1894;
 Best Local Similarity 51.4%; Pred. No. 6.6e-09;

RESULT 1250
 ID ABL50334 standard; cDNA; 2132 BP.
 DE Human cancer cell growth inhibiting protein PP4377 cDNA SEQ ID NO:6.
 PN CN1324820-A.
 PD 05-DEC-2001.
 PA (SHAN-) SHANGHAI CITY INST ONCOLOGY.
 Query Match 2.3%; Score 72.4; DB 6; Length 2132;
 Best Local Similarity 57.4%; Pred. No. 3.5e-08;

RESULT 1251
 ID ACA64866 standard; DNA; 8056 BP.
 DE Human SEMA5A DNA corresponding to U52840.
 PN DE10127572-A1.
 PD 05-DEC-2002.
 PA (PATH-) PATHOARRAY GMBH.
 Query Match 2.3%; Score 71.4; DB 8; Length 8056;
 Best Local Similarity 52.5%; Pred. No. 1.2e-07;

RESULT 1252
 ID ACA64846 standard; DNA; 8056 BP.
 DE Human SEMA5A DNA corresponding to NM_003966.
 PN DE10127572-A1.
 PD 05-DEC-2002.
 PA (PATH-) PATHOARRAY GMBH.
 Query Match 2.3%; Score 71.4; DB 8; Length 8056;
 Best Local Similarity 52.5%; Pred. No. 1.2e-07;

RESULT 1253
 ID ADD14721 standard; cDNA; 8056 BP.
 DE Human src biomarker polynucleotide SEQ ID NO:115.
 PN WO2003062395-A2.
 PD 31-JUL-2003.
 PA (BRIM) BRISTOL-MYERS SQUIBB CO.
 Query Match 2.3%; Score 71.4; DB 10; Length 8056;
 Best Local Similarity 52.5%; Pred. No. 1.2e-07;

RESULT 1254
 ID ADQ21453 standard; DNA; 8056 BP.
 DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 4273.
 PN WO2004048938-A2.
 PD 10-JUN-2004.

PA (PROT-) PROTEIN DESIGN LABS INC.
 Query Match 2.3%; Score 71.4; DB 12; Length 8056;
 Best Local Similarity 52.5%; Pred. No. 1.2e-07;
 RESULT 1255
 ID ADQ25299 standard; DNA; 8214 BP.
 DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 8119.
 PN WO2004048938-A2.
 PD 10-JUN-2004.
 PA (PROT-) PROTEIN DESIGN LABS INC.
 Query Match 2.3%; Score 71.4; DB 12; Length 8214;
 Best Local Similarity 52.5%; Pred. No. 1.3e-07;
 RESULT 1256
 ID ABT32087 standard; DNA; 928 BP.
 DE NOVX DNA sequence SEQ ID No 13.
 PN WO2003004618-A2.
 PD 16-JAN-2003.
 PA (CURA-) CURAGEN CORP.
 Query Match 2.3%; Score 71.2; DB 8; Length 928;
 Best Local Similarity 51.6%; Pred. No. 4.8e-08;
 RESULT 1257
 ID ABA04080 standard; cDNA; 1194 BP.
 DE Human semaphorin G-like NHP encoding cDNA SEQ ID NO:36.
 PN WO200188133-A2.
 PD 22-NOV-2001.
 PA (LEXI-) LEXICON GENETICS INC.
 Query Match 2.3%; Score 71.2; DB 6; Length 1194;
 Best Local Similarity 50.9%; Pred. No. 5.4e-08;
 RESULT 1258
 ID ABL20385 standard; DNA; 2661 BP.
 DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 12628.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Query Match 2.2%; Score 69.8; DB 4; Length 2661;
 Best Local Similarity 57.6%; Pred. No. 1.9e-07;
 RESULT 1259
 ID AAQ87445 standard; cDNA; 2670 BP.
 DE Drosophila semaphorin II cDNA.
 PN WO9507706-A1.
 PD 23-MAR-1995.
 PA (REGC) UNIV CALIFORNIA.
 Query Match 2.2%; Score 69.8; DB 2; Length 2670;
 Best Local Similarity 57.6%; Pred. No. 1.9e-07;
 RESULT 1260
 ID ABL07999 standard; cDNA; 2746 BP.
 DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 18479.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Query Match 2.2%; Score 69.8; DB 4; Length 2746;
 Best Local Similarity 57.6%; Pred. No. 1.9e-07;
 RESULT 1261
 ID ABL07998 standard; cDNA; 18445 BP.
 DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 18476.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.

Query Match 2.2%; Score 69.8; DB 4; Length 18445;
 Best Local Similarity 57.6%; Pred. No. 5e-07;
 RESULT 1262
 ID ABL20384 standard; DNA; 18459 BP.
 DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 12625.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Query Match 2.2%; Score 69.8; DB 4; Length 18459;
 Best Local Similarity 57.6%; Pred. No. 5e-07;
 RESULT 1263
 ID ABT32088 standard; DNA; 777 BP.
 DE NOVX DNA sequence SEQ ID No 15.
 PN WO2003004618-A2.
 PD 16-JAN-2003.
 PA (CURA-) CURAGEN CORP.
 Query Match 2.2%; Score 68; DB 8; Length 777;
 Best Local Similarity 51.0%; Pred. No. 3.1e-07;
 RESULT 1264
 ID AAS13845 standard; cDNA; 1755 BP.
 DE DNA encoding novel human extracellular matrix (ECM) protein #3.
 PN WO200179253-A1.
 PD 25-OCT-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 2.1%; Score 66.6; DB 4; Length 1755;
 Best Local Similarity 46.9%; Pred. No. 1.1e-06;
 RESULT 1265
 ID ABL07567 standard; cDNA; 1851 BP.
 DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 17183.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Query Match 2.1%; Score 65.8; DB 4; Length 1851;
 Best Local Similarity 53.8%; Pred. No. 1.9e-06;
 RESULT 1266
 ID ABA04071 standard; cDNA; 648 BP.
 DE Human semaphorin G-like NHP encoding cDNA SEQ ID NO:18.
 PN WO200188133-A2.
 PD 22-NOV-2001.
 PA (LEXI-) LEXICON GENETICS INC.
 Query Match 2.1%; Score 65.2; DB 6; Length 648;
 Best Local Similarity 50.2%; Pred. No. 1.6e-06;
 RESULT 1267
 ID ABL11115 standard; cDNA; 4254 BP.
 DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 27827.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Query Match 2.0%; Score 64.2; DB 4; Length 4254;
 Best Local Similarity 50.1%; Pred. No. 7.5e-06;
 RESULT 1268
 ID ABL11114 standard; cDNA; 12646 BP.
 DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 27824.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Query Match 2.0%; Score 64.2; DB 4; Length 12646;

Best Local Similarity 50.1%; Pred. No. 1.3e-05;
 RESULT 1269
 ID AAX75767 standard; DNA; 2530 BP.
 DE Human semaphorin III DNA.
 PN WO9845322-A2.
 PD 15-OCT-1998.
 PA (ROYA-) ROYAL NETHERLANDS ACAD ARTS & SCI.
 PA (UYRO-) UNIV ROTTERDAM ERASMUS.
 PA (UYUT-) RIJKSUNIV UTRECHT.
 Query Match 2.0%; Score 63.8; DB 2; Length 2530;
 Best Local Similarity 47.0%; Pred. No. 7.4e-06;
 RESULT 1270
 ID ABS76512 standard; cDNA; 2530 BP.
 DE cDNA encoding human ovarian cancer marker M473.
 PN WO200271928-A2.
 PD 19-SEP-2002.
 PA (MILL-) MILLENNIUM PHARM INC.
 Query Match 2.0%; Score 63.8; DB 6; Length 2530;
 Best Local Similarity 47.0%; Pred. No. 7.4e-06;
 RESULT 1271
 ID ADD08933 standard; cDNA; 2530 BP.
 DE Human semaphorin 3A encoding cDNA SEQ ID NO:9.
 PN WO2003029814-A2.
 PD 10-APR-2003.
 PA (LUDW-) LUDWIG INST CANCER RES.
 PA (LICN) LICENTIA LTD.
 Query Match 2.0%; Score 63.8; DB 10; Length 2530;
 Best Local Similarity 47.0%; Pred. No. 7.4e-06;
 RESULT 1272
 ID ADN95334 standard; DNA; 2530 BP.
 DE Human BEC/LEC-related gene sequence SeqID256.
 PN WO2003080640-A1.
 PD 02-OCT-2003.
 PA (LUDW-) LUDWIG INST CANCER RES.
 PA (LICN) LICENTIA LTD.
 Query Match 2.0%; Score 63.8; DB 11; Length 2530;
 Best Local Similarity 47.0%; Pred. No. 7.4e-06;
 RESULT 1273
 ID ADQ19750 standard; DNA; 2530 BP.
 DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 2569.
 PN WO2004048938-A2.
 PD 10-JUN-2004.
 PA (PROT-) PROTEIN DESIGN LABS INC.
 Query Match 2.0%; Score 63.8; DB 12; Length 2530;
 Best Local Similarity 47.0%; Pred. No. 7.4e-06;
 RESULT 1274
 ID AAQ87442 standard; cDNA; 2601 BP.
 DE Human semaphorin III cDNA.
 PN WO9507706-A1.
 PD 23-MAR-1995.
 PA (REGC) UNIV CALIFORNIA.
 Query Match 2.0%; Score 63.8; DB 2; Length 2601;
 Best Local Similarity 47.0%; Pred. No. 7.5e-06;
 RESULT 1275
 ID AAH47049 standard; DNA; 2709 BP.
 DE Semaphorin D cDNA sequence.
 PN WO200155455-A2.

PD 02-AUG-2001.
 PA (MILL-) MILLENNIUM PHARM INC.
 PA (JINS/) JIN S.
 Query Match 2.0%; Score 63.8; DB 4; Length 2709;
 Best Local Similarity 47.0%; Pred. No. 7.7e-06;
 RESULT 1276
 ID ADE25679 standard; cDNA; 2848 BP.
 DE Human cDNA differentially expressed in foam cells #83.
 PN US2003194721-A1.
 PD 16-OCT-2003.
 PA (INCY-) INCYTE GENOMICS INC.
 Query Match 2.0%; Score 63.8; DB 10; Length 2848;
 Best Local Similarity 47.0%; Pred. No. 7.9e-06;
 RESULT 1277
 ID ADQ23894 standard; DNA; 3023 BP.
 DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 6714.
 PN WO2004048938-A2.
 PD 10-JUN-2004.
 PA (PROT-) PROTEIN DESIGN LABS INC.
 Query Match 2.0%; Score 63.8; DB 12; Length 3023;
 Best Local Similarity 47.0%; Pred. No. 8.1e-06;
 RESULT 1278
 ID AAS68806 standard; cDNA; 889 BP.
 DE DNA encoding novel human diagnostic protein #4610.
 PN WO200175067-A2.
 PD 11-OCT-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match 2.0%; Score 63.2; DB 5; Length 889;
 Best Local Similarity 52.2%; Pred. No. 6.4e-06;
 RESULT 1279
 ID AAS66467 standard; cDNA; 2145 BP.
 DE DNA encoding novel human diagnostic protein #2271.
 PN WO200175067-A2.
 PD 11-OCT-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match 2.0%; Score 62; DB 5; Length 2145;
 Best Local Similarity 70.0%; Pred. No. 2.1e-05;
 RESULT 1280
 ID AAQ87441 standard; cDNA; 2854 BP.
 DE Grasshopper semaphorin I cDNA.
 PN WO9507706-A1.
 PD 23-MAR-1995.
 PA (REGC) UNIV CALIFORNIA.
 Query Match 2.0%; Score 62; DB 2; Length 2854;
 Best Local Similarity 47.7%; Pred. No. 2.4e-05;
 RESULT 1281
 ID AAH08370 standard; cDNA; 662 BP.
 DE Human cDNA clone (5'-primer) SEQ ID NO:5205.
 PN EP1074617-A2.
 PD 07-FEB-2001.
 PA (HELI-) HELIX RES INST.
 Query Match 1.9%; Score 61.2; DB 4; Length 662;
 Best Local Similarity 52.1%; Pred. No. 1.9e-05;
 RESULT 1282
 ID ADA71938 standard; DNA; 2000 BP.
 DE Rice gene, SEQ ID 5263.
 PN WO2003000898-A1.

PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 1.9%; Score 60.8; DB 8; Length 2000;
Best Local Similarity 10.2%; Pred. No. 4.2e-05;
RESULT 1283
ID ABA08261 standard; cDNA; 828 BP.
DE Human semaphorin 4G homologue-encoding cDNA, SEQ ID NO:37.
PN WO200157188-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 1.9%; Score 60.6; DB 4; Length 828;
Best Local Similarity 51.7%; Pred. No. 3e-05;
RESULT 1284
ID ABN43096 standard; DNA; 60 BP.
DE Human spliced transcript detection oligonucleotide SEQ ID NO:15844.
PN WO200210449-A2.
PD 07-FEB-2002.
PA (COMP-) COMPUGEN INC.
Query Match 1.9%; Score 60; DB 6; Length 60;
Best Local Similarity 100.0%; Pred. No. 1.2e-05;
RESULT 1285
ID ABL07566 standard; cDNA; 7832 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 17180.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 1.9%; Score 59.8; DB 4; Length 7832;
Best Local Similarity 54.3%; Pred. No. 0.00015;
RESULT 1286
ID AAQ60748 standard; DNA; 265 BP.
DE Human brain Expressed Sequence Tag EST00865.
PN WO9316178-A2.
PD 19-AUG-1993.
PA (USSH) US DEPT HEALTH & HUMAN SERVICE.
Query Match 1.9%; Score 59; DB 2; Length 265;
Best Local Similarity 61.8%; Pred. No. 4.6e-05;
RESULT 1287
ID ABA04079 standard; cDNA; 351 BP.
DE Human semaphorin G-like NHP encoding cDNA SEQ ID NO:34.
PN WO200188133-A2.
PD 22-NOV-2001.
PA (LEXI-) LEXICON GENETICS INC.
Query Match 1.9%; Score 58.4; DB 6; Length 351;
Best Local Similarity 52.6%; Pred. No. 7.6e-05;
RESULT 1288
ID ADA02657 standard; DNA; 39780 BP.
DE Mouse Sema4d carcinoma associated gene, SEQ ID NO:1175.
PN WO2003057146-A2.
PD 17-JUL-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 1.8%; Score 58; DB 9; Length 39780;
Best Local Similarity 58.9%; Pred. No. 0.001;
RESULT 1289
ID ADB72395 standard; DNA; 39780 BP.
DE Mouse Sema4d gene.
PN WO2003008583-A2.
PD 30-JAN-2003.

PA (SAGR-) SAGRES DISCOVERY.
 Query Match 1.8%; Score 58; DB 10; Length 39780;
 Best Local Similarity 58.9%; Pred. No. 0.001;
 RESULT 1290
 ID ADE95905 standard; DNA; 39780 BP.
 DE Mouse Sema4d gene genomic DNA sequence.
 PN WO2003039484-A2.
 PD 15-MAY-2003.
 PA (SAGR-) SAGRES DISCOVERY.
 Query Match 1.8%; Score 58; DB 10; Length 39780;
 Best Local Similarity 58.9%; Pred. No. 0.001;
 RESULT 1291
 ID ADL35829 standard; DNA; 3552 BP.
 DE Human semaphorin III family (semaphorin3F) DNA.
 PN WO2004019893-A2.
 PD 11-MAR-2004.
 PA (RIGE-) RIGEL PHARM INC.
 Query Match 1.8%; Score 57.6; DB 12; Length 3552;
 Best Local Similarity 46.2%; Pred. No. 0.0004;
 RESULT 1292
 ID ADR52674 standard; DNA; 3552 BP.
 DE Drug therapy altered expressed gene #25.
 PN WO2004072265-A2.
 PD 26-AUG-2004.
 PA (AMHP) WYETH.
 PA (BURC/) BURCZYNSKI M.
 PA (TWIN/) TWINE N.
 PA (DORN/) DORNER A J.
 PA (TREP/) TREPICCHIO W L.
 Query Match 1.8%; Score 57.6; DB 13; Length 3552;
 Best Local Similarity 46.2%; Pred. No. 0.0004;
 RESULT 1293
 ID ACH12839 standard; cDNA; 495 BP.
 DE Human adult brain cDNA #51.
 PN US2003073623-A1.
 PD 17-APR-2003.
 PA (DRMA/) DRMANAC R T.
 PA (LABA/) LABAT I.
 PA (STAC/) STACHE-CRAIN B.
 PA (DICK/) DICKSON M C.
 PA (JONE/) JONES L W.
 Query Match 1.8%; Score 57.2; DB 9; Length 495;
 Best Local Similarity 55.2%; Pred. No. 0.00019;
 RESULT 1294
 ID ADA02660 standard; DNA; 48244 BP.
 DE Human SEMA4D carcinoma associated gene, SEQ ID NO:1178.
 PN WO2003057146-A2.
 PD 17-JUL-2003.
 PA (SAGR-) SAGRES DISCOVERY.
 Query Match 1.8%; Score 56.6; DB 9; Length 48244;
 Best Local Similarity 59.7%; Pred. No. 0.0027;
 RESULT 1295
 ID ADB72398 standard; DNA; 48244 BP.
 DE Human SEMA4D gene.
 PN WO2003008583-A2.
 PD 30-JAN-2003.
 PA (SAGR-) SAGRES DISCOVERY.

Query Match 1.8%; Score 56.6; DB 10; Length 48244;
Best Local Similarity 59.7%; Pred. No. 0.0027;

RESULT 1296

ID ADE95908 standard; DNA; 48244 BP.
DE Human SEMA4D gene genomic DNA sequence.
PN WO2003039484-A2.
PD 15-MAY-2003.
PA (SAGR-) SAGRES DISCOVERY.

Query Match 1.8%; Score 56.6; DB 10; Length 48244;
Best Local Similarity 59.7%; Pred. No. 0.0027;

RESULT 1297

ID ACN42421 standard; cDNA; 3486 BP.
DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:1296.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.

Query Match 1.8%; Score 56.2; DB 13; Length 3486;
Best Local Similarity 46.2%; Pred. No. 0.00093;

RESULT 1298

ID ACN42420 standard; cDNA; 3505 BP.
DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:1295.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.

Query Match 1.8%; Score 56.2; DB 13; Length 3505;
Best Local Similarity 46.2%; Pred. No. 0.00093;

RESULT 1299

ID ABN77998 standard; cDNA; 273 BP.
DE Human ORF2945 cDNA, SEQ ID NO:5889.
PN WO200190366-A2.
PD 29-NOV-2001.
PA (CURA-) CURAGEN CORP.

Query Match 1.8%; Score 55.6; DB 6; Length 273;
Best Local Similarity 71.6%; Pred. No. 0.00038;

RESULT 1300

ID ADR67092 standard; DNA; 10385 BP.
DE Human cancer associated gene genomic sequence SEQ ID NO:138.
PN WO2004074321-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.

Query Match 1.8%; Score 55.6; DB 13; Length 10385;
Best Local Similarity 71.6%; Pred. No. 0.0023;

RESULT 1301

ID ADA71938 standard; DNA; 2000 BP.
DE Rice gene, SEQ ID 5263.
PN WO2003000898-A1.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.

Query Match 1.7%; Score 54.4; DB 8; Length 2000;
Best Local Similarity 10.3%; Pred. No. 0.0021;

RESULT 1302

ID ADA41596 standard; DNA; 4410 BP.
DE Human secreted protein related DNA.
PN WO2002102993-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.

Query Match 1.7%; Score 53; DB 8; Length 4410;

Best Local Similarity 65.8%; Pred. No. 0.0074;
 RESULT 1303
 ID ADA57738 standard; DNA; 4410 BP.
 DE BAC fragment containing human secreted protein gene #412.
 PN WO2002102994-A2.
 PD 27-DEC-2002.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 1.7%; Score 53; DB 10; Length 4410;
 Best Local Similarity 65.8%; Pred. No. 0.0074;
 RESULT 1304
 ID ADE09669 standard; DNA; 438 BP.
 DE Novel DNA-related contig nucleotide sequence #391.
 PN WO2003054152-A2.
 PD 03-JUL-2003.
 PA (HYSE-) HYSEQ INC.
 Query Match 1.7%; Score 52.6; DB 10; Length 438;
 Best Local Similarity 49.1%; Pred. No. 0.003;
 RESULT 1305
 ID AAV35367 standard; cDNA; 2898 BP.
 DE Human semaphorin encoding cDNA.
 PN WO9822504-A1.
 PD 28-MAY-1998.
 PA (SUMU) SUMITOMO PHARM CO LTD.
 Query Match 1.7%; Score 52.6; DB 2; Length 2898;
 Best Local Similarity 57.7%; Pred. No. 0.0077;
 RESULT 1306
 ID ADI79371 standard; cDNA; 3982 BP.
 DE Mouse Sema3E nucleotide sequence SEQ ID NO:9.
 PN WO2004006898-A2.
 PD 22-JAN-2004.
 PA (SEMA-) SEMA APS.
 Query Match 1.7%; Score 52.6; DB 12; Length 3982;
 Best Local Similarity 57.7%; Pred. No. 0.009;
 RESULT 1307
 ID AAZ28469 standard; DNA; 4460 BP.
 DE Mouse semaphorin H (Sema H) polynucleotide sequence.
 PN WO9947671-A2.
 PD 23-SEP-1999.
 PA (LUKA/) LUKANIDIN E M.
 PA (CHRI/) CHRISTENSEN C R L.
 Query Match 1.7%; Score 52.6; DB 2; Length 4460;
 Best Local Similarity 57.7%; Pred. No. 0.0095;
 RESULT 1308
 ID AAS28805 standard; cDNA; 445 BP.
 DE Human immunoglobulin encoding cDNA SEQ ID No 51.
 PN WO200155315-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 1.7%; Score 52.4; DB 4; Length 445;
 Best Local Similarity 53.4%; Pred. No. 0.0034;
 RESULT 1309
 ID ABA06719 standard; cDNA; 445 BP.
 DE Human cDNA SEQ ID NO: 385.
 PN WO200154474-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 1.7%; Score 52.4; DB 4; Length 445;

Best Local Similarity 53.4%; Pred. No. 0.0034;
 RESULT 1310
 ID ABV84056 standard; cDNA; 445 BP.
 DE Human polynucleotide SEQ ID NO 385.
 PN US2002090672-A1.
 PD 11-JUL-2002.
 PA (ROSE/) ROSEN C A.
 PA (RUBE/) RUBEN S M.
 PA (BARA/) BARASH S C.
 Query Match 1.7%; Score 52.4; DB 6; Length 445;
 Best Local Similarity 53.4%; Pred. No. 0.0034;
 RESULT 1311
 ID ADB31530 standard; cDNA; 445 BP.
 DE Human cDNA encoding a novel protein SEQ ID NO 51.
 PN US2003077606-A1.
 PD 24-APR-2003.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 1.7%; Score 52.4; DB 10; Length 445;
 Best Local Similarity 53.4%; Pred. No. 0.0034;
 RESULT 1312
 ID ABA06535 standard; cDNA; 2514 BP.
 DE Human cDNA SEQ ID NO: 201.
 PN WO200154474-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 1.7%; Score 52.4; DB 4; Length 2514;
 Best Local Similarity 53.4%; Pred. No. 0.0081;
 RESULT 1313
 ID ABV83872 standard; cDNA; 2514 BP.
 DE Human polynucleotide SEQ ID NO 201.
 PN US2002090672-A1.
 PD 11-JUL-2002.
 PA (ROSE/) ROSEN C A.
 PA (RUBE/) RUBEN S M.
 PA (BARA/) BARASH S C.
 Query Match 1.7%; Score 52.4; DB 6; Length 2514;
 Best Local Similarity 53.4%; Pred. No. 0.0081;
 RESULT 1314
 ID ABK36165 standard; cDNA; 3054 BP.
 DE cDNA sequence #556 encoding novel human secreted protein.
 PN WO200177289-A2.
 PD 18-OCT-2001.
 PA (GEMY) GENETICS INST INC.
 Query Match 1.7%; Score 52.4; DB 6; Length 3054;
 Best Local Similarity 46.0%; Pred. No. 0.0089;
 RESULT 1315
 ID ADR67089 standard; DNA; 10241 BP.
 DE Mouse cancer associated gene genomic sequence SEQ ID NO:135.
 PN WO2004074321-A2.
 PD 02-SEP-2004.
 PA (SAGR-) SAGRES DISCOVERY INC.
 Query Match 1.7%; Score 52.4; DB 13; Length 10241;
 Best Local Similarity 69.6%; Pred. No. 0.016;
 RESULT 1316
 ID ABA59349 standard; DNA; 443 BP.
 DE Human foetal liver single exon nucleic acid probe #7654.
 PN WO200157277-A2.

PD 09-AUG-2001.

PA (MOLE-) MOLECULAR DYNAMICS INC.

Query Match 1.7%; Score 52.2; DB 4; Length 443;
Best Local Similarity 54.5%; Pred. No. 0.0039;

RESULT 1317

ID AAI39149 standard; DNA; 443 BP.

DE Probe #7835 used to measure gene expression in human placenta sample.

PN WO200157272-A2.

PD 09-AUG-2001.

PA (MOLE-) MOLECULAR DYNAMICS INC.

Query Match 1.7%; Score 52.2; DB 4; Length 443;
Best Local Similarity 54.5%; Pred. No. 0.0039;

RESULT 1318

ID ABA28049 standard; DNA; 443 BP.

DE Probe #6515 for gene expression analysis in human heart cell sample.

PN WO200157274-A2.

PD 09-AUG-2001.

PA (MOLE-) MOLECULAR DYNAMICS INC.

Query Match 1.7%; Score 52.2; DB 4; Length 443;
Best Local Similarity 54.5%; Pred. No. 0.0039;

RESULT 1319

ID AAK33363 standard; DNA; 443 BP.

DE Human bone marrow expressed single exon probe SEQ ID NO: 7920.

PN WO200157276-A2.

PD 09-AUG-2001.

PA (MOLE-) MOLECULAR DYNAMICS INC.

Query Match 1.7%; Score 52.2; DB 4; Length 443;
Best Local Similarity 54.5%; Pred. No. 0.0039;

RESULT 1320

ID AAK07566 standard; DNA; 443 BP.

DE Human brain expressed single exon probe SEQ ID NO: 7557.

PN WO200157275-A2.

PD 09-AUG-2001.

PA (MOLE-) MOLECULAR DYNAMICS INC.

Query Match 1.7%; Score 52.2; DB 4; Length 443;
Best Local Similarity 54.5%; Pred. No. 0.0039;

RESULT 1321

ID ABS33117 standard; DNA; 443 BP.

DE Human liver single exon probe, SEQ ID No 8107.

PN WO200157273-A2.

PD 09-AUG-2001.

PA (MOLE-) MOLECULAR DYNAMICS INC.

Query Match 1.7%; Score 52.2; DB 4; Length 443;
Best Local Similarity 54.5%; Pred. No. 0.0039;

RESULT 1322

ID ABS08198 standard; DNA; 443 BP.

DE Human genome-derived single exon probe from lung SEQ ID No 8189.

PN WO200186003-A2.

PD 15-NOV-2001.

PA (MOLE-) MOLECULAR DYNAMICS INC.

Query Match 1.7%; Score 52.2; DB 6; Length 443;
Best Local Similarity 54.5%; Pred. No. 0.0039;

RESULT 1323

ID ABL09787 standard; cDNA; 4340 BP.

DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 23843.

PN WO200171042-A2.

PD 27-SEP-2001.

PA (PEKE) PE CORP NY.

Query Match 1.6%; Score 51.6; DB 4; Length 4340;
Best Local Similarity 53.2%; Pred. No. 0.017;

RESULT 1324

ID ABA71861 standard; DNA; 274 BP.

DE Human foetal liver single exon nucleic acid probe #20166.

PN WO200157277-A2.

PD 09-AUG-2001.

PA (MOLE-) MOLECULAR DYNAMICS INC.

Query Match 1.6%; Score 51.2; DB 4; Length 274;
Best Local Similarity 58.7%; Pred. No. 0.0056;

RESULT 1325

ID AAI52204 standard; DNA; 274 BP.

DE Probe #20890 used to measure gene expression in human placenta sample.

PN WO200157272-A2.

PD 09-AUG-2001.

PA (MOLE-) MOLECULAR DYNAMICS INC.

Query Match 1.6%; Score 51.2; DB 4; Length 274;
Best Local Similarity 58.7%; Pred. No. 0.0056;

RESULT 1326

ID ABA37908 standard; DNA; 274 BP.

DE Probe #16374 for gene expression analysis in human heart cell sample.

PN WO200157274-A2.

PD 09-AUG-2001.

PA (MOLE-) MOLECULAR DYNAMICS INC.

Query Match 1.6%; Score 51.2; DB 4; Length 274;
Best Local Similarity 58.7%; Pred. No. 0.0056;

RESULT 1327

ID AAK46306 standard; DNA; 274 BP.

DE Human bone marrow expressed single exon probe SEQ ID NO: 20863.

PN WO200157276-A2.

PD 09-AUG-2001.

PA (MOLE-) MOLECULAR DYNAMICS INC.

Query Match 1.6%; Score 51.2; DB 4; Length 274;
Best Local Similarity 58.7%; Pred. No. 0.0056;

RESULT 1328

ID AAK20236 standard; DNA; 274 BP.

DE Human brain expressed single exon probe SEQ ID NO: 20227.

PN WO200157275-A2.

PD 09-AUG-2001.

PA (MOLE-) MOLECULAR DYNAMICS INC.

Query Match 1.6%; Score 51.2; DB 4; Length 274;
Best Local Similarity 58.7%; Pred. No. 0.0056;

RESULT 1329

ID ABS46029 standard; DNA; 274 BP.

DE Human liver single exon probe, SEQ ID No 21019.

PN WO200157273-A2.

PD 09-AUG-2001.

PA (MOLE-) MOLECULAR DYNAMICS INC.

Query Match 1.6%; Score 51.2; DB 4; Length 274;
Best Local Similarity 58.7%; Pred. No. 0.0056;

RESULT 1330

ID ABS20620 standard; DNA; 274 BP.

DE Human genome-derived single exon probe ORF from lung SEQ ID No 20611.

PN WO200186003-A2.

PD 15-NOV-2001.

PA (MOLE-) MOLECULAR DYNAMICS INC.

Query Match 1.6%; Score 51.2; DB 6; Length 274;
Best Local Similarity 58.7%; Pred. No. 0.0056;

RESULT 1331

ID ADQ92072 standard; DNA; 505 BP.
DE Human autoantigen DNA fragment MPMGp800D24583.
PN WO2004058972-A1.
PD 15-JUL-2004.
PA (THIE/) THIESEN H.
PA (LORE/) LORENZ P.

Query Match 1.6%; Score 51; DB 12; Length 505;
Best Local Similarity 55.4%; Pred. No. 0.0086;

RESULT 1332

ID ADQ87202 standard; cDNA; 2516 BP.
DE Human tumour-associated antigenic target (TAT) cDNA sequence #4079.
PN WO2004060270-A2.
PD 22-JUL-2004.
PA (GETH) GENENTECH INC.
PA (WUTD/) WU T D.
PA (ZHOU/) ZHOU Y.

Query Match 1.6%; Score 51; DB 13; Length 2516;
Best Local Similarity 46.8%; Pred. No. 0.019;

RESULT 1333

ID ADD08941 standard; cDNA; 2719 BP.
DE Human semaphorin 3F encoding cDNA SEQ ID NO:17.
PN WO2003029814-A2.
PD 10-APR-2003.
PA (LUDW-) LUDWIG INST CANCER RES.
PA (LICN) LICENTIA LTD.

Query Match 1.6%; Score 51; DB 10; Length 2719;
Best Local Similarity 46.8%; Pred. No. 0.02;

RESULT 1334

ID ACN42422 standard; cDNA; 3248 BP.
DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:1297.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.

Query Match 1.6%; Score 51; DB 13; Length 3248;
Best Local Similarity 46.8%; Pred. No. 0.022;

RESULT 1335

ID ADP75180 standard; DNA; 304905 BP.
DE Human Endophilin 2 gene.
PN WO2003031594-A2.
PD 17-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.

Query Match 1.6%; Score 50.6; DB 11; Length 304905;
Best Local Similarity 67.4%; Pred. No. 0.27;

RESULT 1336

ID AAQ87446 standard; cDNA; 2504 BP.
DE Tribolium semaphorin I cDNA.
PN WO9507706-A1.
PD 23-MAR-1995.
PA (REGC) UNIV CALIFORNIA.

Query Match 1.6%; Score 50.2; DB 2; Length 2504;
Best Local Similarity 54.6%; Pred. No. 0.031;

RESULT 1337

ID ADP28048 standard; DNA; 1899 BP.
DE Human secreted protein encoding sequence SEQ ID #46.

PN WO2004035732-A2.
 PD 29-APR-2004.
 PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
 Query Match 1.6%; Score 49.4; DB 12; Length 1899;
 Best Local Similarity 54.0%; Pred. No. 0.044;
 RESULT 1338
 ID ADP28047 standard; DNA; 1929 BP.
 DE Human secreted protein encoding sequence SEQ ID #45.
 PN WO2004035732-A2.
 PD 29-APR-2004.
 PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
 Query Match 1.6%; Score 49.4; DB 12; Length 1929;
 Best Local Similarity 54.0%; Pred. No. 0.045;
 RESULT 1339
 ID ADP28049 standard; DNA; 1929 BP.
 DE Human secreted protein encoding sequence SEQ ID #47.
 PN WO2004035732-A2.
 PD 29-APR-2004.
 PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
 Query Match 1.6%; Score 49.4; DB 12; Length 1929;
 Best Local Similarity 54.0%; Pred. No. 0.045;
 RESULT 1340
 ID ADP28050 standard; DNA; 1929 BP.
 DE Human secreted protein encoding sequence SEQ ID #48.
 PN WO2004035732-A2.
 PD 29-APR-2004.
 PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
 Query Match 1.6%; Score 49.4; DB 12; Length 1929;
 Best Local Similarity 54.0%; Pred. No. 0.045;
 RESULT 1341
 ID AAX89112 standard; DNA; 2331 BP.
 DE Human brain tissue-derived polypeptide coding sequence (clone OM007).
 PN WO9933873-A1.
 PD 08-JUL-1999.
 PA (ONOEY) ONO PHARM CO LTD.
 Query Match 1.6%; Score 49.4; DB 2; Length 2331;
 Best Local Similarity 56.4%; Pred. No. 0.049;
 RESULT 1342
 ID AAA37109 standard; cDNA; 3871 BP.
 DE Human PRO1491 (UNQ760) cDNA sequence SEQ ID NO:309.
 PN WO200012708-A2.
 PD 09-MAR-2000.
 PA (GETH) GENENTECH INC.
 Query Match 1.6%; Score 49.4; DB 3; Length 3871;
 Best Local Similarity 56.4%; Pred. No. 0.063;
 RESULT 1343
 ID AAF54421 standard; DNA; 3871 BP.
 DE DNA encoding protein of the invention #86.
 PN WO200078961-A1.
 PD 28-DEC-2000.
 PA (GETH) GENENTECH INC.
 Query Match 1.6%; Score 49.4; DB 4; Length 3871;
 Best Local Similarity 56.4%; Pred. No. 0.063;
 RESULT 1344
 ID AAS46098 standard; cDNA; 3871 BP.
 DE Human DNA encoding PRO polypeptide sequence #174.
 PN WO200168848-A2.

PD 20-SEP-2001.
PA (GETH) GENENTECH INC.
Query Match 1.6%; Score 49.4; DB 4; Length 3871;
Best Local Similarity 56.4%; Pred. No. 0.063;
RESULT 1345
ID ACA89548 standard; cDNA; 3871 BP.
DE cDNA encoding human PRO polypeptide #174.
PN US2003036141-A1.
PD 20-FEB-2003.
Query Match 1.6%; Score 49.4; DB 8; Length 3871;
Best Local Similarity 56.4%; Pred. No. 0.063;
RESULT 1346
ID ACA73558 standard; cDNA; 3871 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #174.
PN US2003036146-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 1.6%; Score 49.4; DB 8; Length 3871;
Best Local Similarity 56.4%; Pred. No. 0.063;
RESULT 1347
ID ACA05873 standard; cDNA; 3871 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #174.
PN US2003036162-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 1.6%; Score 49.4; DB 8; Length 3871;
Best Local Similarity 56.4%; Pred. No. 0.063;
RESULT 1348
ID ACA66707 standard; cDNA; 3871 BP.
DE cDNA encoding human PRO protein #174.
PN US2003036137-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 1.6%; Score 49.4; DB 8; Length 3871;
Best Local Similarity 56.4%; Pred. No. 0.063;
RESULT 1349
ID ACF20282 standard; cDNA; 3871 BP.
DE Human secreted polypeptide PRO1491-encoding cDNA, SEQ ID NO:347.
PN US2003040063-A1.
PD 27-FEB-2003.
Query Match 1.6%; Score 49.4; DB 8; Length 3871;
Best Local Similarity 56.4%; Pred. No. 0.063;
RESULT 1350
ID ACF19668 standard; cDNA; 3871 BP.
DE Human secreted polypeptide PRO1491-encoding cDNA, SEQ ID NO:347.
PN US2003040064-A1.
PD 27-FEB-2003.
Query Match 1.6%; Score 49.4; DB 8; Length 3871;
Best Local Similarity 56.4%; Pred. No. 0.063;
RESULT 1351
ID ACD21956 standard; cDNA; 3871 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #174.
PN US2003027267-A1.
PD 06-FEB-2003.
Query Match 1.6%; Score 49.4; DB 8; Length 3871;
Best Local Similarity 56.4%; Pred. No. 0.063;
RESULT 1352

ID ACF13121 standard; cDNA; 3871 BP.
 DE Human secreted polypeptide PRO1491-encoding cDNA, SEQ ID NO:347.
 PN US2003036160-A1.
 PD 20-FEB-2003.
 Query Match 1.6%; Score 49.4; DB 8; Length 3871;
 Best Local Similarity 56.4%; Pred. No. 0.063;
 RESULT 1353
 ID ACD25224 standard; cDNA; 3871 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #174.
 PN US2003044925-A1.
 PD 06-MAR-2003.
 Query Match 1.6%; Score 49.4; DB 8; Length 3871;
 Best Local Similarity 56.4%; Pred. No. 0.063;
 RESULT 1354
 ID ACF00273 standard; cDNA; 3871 BP.
 DE Human secreted polypeptide PRO1491-encoding cDNA, SEQ ID NO:347.
 PN US2003054474-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 1.6%; Score 49.4; DB 8; Length 3871;
 Best Local Similarity 56.4%; Pred. No. 0.063;
 RESULT 1355
 ID ACA72330 standard; cDNA; 3871 BP.
 DE Novel human secreted and transmembrane protein PRO1491 cDNA.
 PN US2003032114-A1.
 PD 13-FEB-2003.
 Query Match 1.6%; Score 49.4; DB 8; Length 3871;
 Best Local Similarity 56.4%; Pred. No. 0.063;
 RESULT 1356
 ID ACD04854 standard; cDNA; 3871 BP.
 DE Novel human secreted and transmembrane protein PRO1491 cDNA.
 PN US2003032101-A1.
 PD 13-FEB-2003.
 Query Match 1.6%; Score 49.4; DB 8; Length 3871;
 Best Local Similarity 56.4%; Pred. No. 0.063;
 RESULT 1357
 ID ACD18315 standard; cDNA; 3871 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #174.
 PN US2003036124-A1.
 PD 20-FEB-2003.
 Query Match 1.6%; Score 49.4; DB 8; Length 3871;
 Best Local Similarity 56.4%; Pred. No. 0.063;
 RESULT 1358
 ID ACD08322 standard; cDNA; 3871 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #174.
 PN US2003040054-A1.
 PD 27-FEB-2003.
 Query Match 1.6%; Score 49.4; DB 8; Length 3871;
 Best Local Similarity 56.4%; Pred. No. 0.063;
 RESULT 1359
 ID ACA88756 standard; cDNA; 3871 BP.
 DE Novel human secreted and transmembrane protein PRO1491 cDNA.
 PN US2003036133-A1.
 PD 20-FEB-2003.
 Query Match 1.6%; Score 49.4; DB 8; Length 3871;
 Best Local Similarity 56.4%; Pred. No. 0.063;
 RESULT 1360

ID ACA70198 standard; cDNA; 3871 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #174.
 PN US2003036134-A1.
 PD 20-FEB-2003.
 Query Match 1.6%; Score 49.4; DB 8; Length 3871;
 Best Local Similarity 56.4%; Pred. No. 0.063;
 RESULT 1361
 ID ACD12420 standard; cDNA; 3871 BP.
 DE Novel human secreted and transmembrane protein PRO1491 cDNA.
 PN US2003022294-A1.
 PD 30-JAN-2003.
 Query Match 1.6%; Score 49.4; DB 8; Length 3871;
 Best Local Similarity 56.4%; Pred. No. 0.063;
 RESULT 1362
 ID ACC74335 standard; cDNA; 3871 BP.
 DE Human secreted polypeptide PRO1491-encoding cDNA, SEQ ID NO:347.
 PN US2003027275-A1.
 PD 06-FEB-2003.
 Query Match 1.6%; Score 49.4; DB 8; Length 3871;
 Best Local Similarity 56.4%; Pred. No. 0.063;
 RESULT 1363
 ID ACD15963 standard; cDNA; 3871 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #174.
 PN US2003027324-A1.
 PD 06-FEB-2003.
 Query Match 1.6%; Score 49.4; DB 8; Length 3871;
 Best Local Similarity 56.4%; Pred. No. 0.063;
 RESULT 1364
 ID ACD25531 standard; cDNA; 3871 BP.
 DE Novel human secreted and transmembrane protein PRO1491 cDNA.
 PN US2003036118-A1.
 PD 20-FEB-2003.
 PA (GETH) GENENTECH INC.
 Query Match 1.6%; Score 49.4; DB 8; Length 3871;
 Best Local Similarity 56.4%; Pred. No. 0.063;
 RESULT 1365
 ID ACD18008 standard; cDNA; 3871 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #174.
 PN US2003036123-A1.
 PD 20-FEB-2003.
 Query Match 1.6%; Score 49.4; DB 8; Length 3871;
 Best Local Similarity 56.4%; Pred. No. 0.063;
 RESULT 1366
 ID ACC88295 standard; cDNA; 3871 BP.
 DE Human secreted polypeptide PRO1491-encoding cDNA, SEQ ID NO:347.
 PN US2003036148-A1.
 PD 20-FEB-2003.
 Query Match 1.6%; Score 49.4; DB 8; Length 3871;
 Best Local Similarity 56.4%; Pred. No. 0.063;
 RESULT 1367
 ID ACD21649 standard; cDNA; 3871 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #174.
 PN US2003040060-A1.
 PD 27-FEB-2003.
 Query Match 1.6%; Score 49.4; DB 8; Length 3871;
 Best Local Similarity 56.4%; Pred. No. 0.063;
 RESULT 1368

ID ACD18716 standard; cDNA; 3871 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #174.
 PN US2003044916-A1.
 PD 06-MAR-2003.
 Query Match 1.6%; Score 49.4; DB 8; Length 3871;
 Best Local Similarity 56.4%; Pred. No. 0.063;
 RESULT 1369
 ID ABX98326 standard; cDNA; 3871 BP.
 DE Human cDNA encoding a secreted/transmembrane protein, SEQ ID 347.
 PN US2003036156-A1.
 PD 20-FEB-2003.
 Query Match 1.6%; Score 49.4; DB 8; Length 3871;
 Best Local Similarity 56.4%; Pred. No. 0.063;
 RESULT 1370
 ID ACD14077 standard; cDNA; 3871 BP.
 DE Human PRO polynucleotide #174.
 PN US2003032117-A1.
 PD 13-FEB-2003.
 Query Match 1.6%; Score 49.4; DB 8; Length 3871;
 Best Local Similarity 56.4%; Pred. No. 0.063;
 RESULT 1371
 ID ACD09857 standard; cDNA; 3871 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #174.
 PN US2003036128-A1.
 PD 20-FEB-2003.
 Query Match 1.6%; Score 49.4; DB 8; Length 3871;
 Best Local Similarity 56.4%; Pred. No. 0.063;
 RESULT 1372
 ID ACC88602 standard; cDNA; 3871 BP.
 DE Human secreted polypeptide PRO1491-encoding cDNA, SEQ ID NO:347.
 PN US2003027266-A1.
 PD 06-FEB-2003.
 Query Match 1.6%; Score 49.4; DB 8; Length 3871;
 Best Local Similarity 56.4%; Pred. No. 0.063;
 RESULT 1373
 ID ACD21342 standard; cDNA; 3871 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #174.
 PN US2003054483-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 1.6%; Score 49.4; DB 8; Length 3871;
 Best Local Similarity 56.4%; Pred. No. 0.063;
 RESULT 1374
 ID ABX75714 standard; cDNA; 3871 BP.
 DE Human cDNA encoding secreted/transmembrane protein, PRO1491.
 PN US2003022298-A1.
 PD 30-JAN-2003.
 Query Match 1.6%; Score 49.4; DB 8; Length 3871;
 Best Local Similarity 56.4%; Pred. No. 0.063;
 RESULT 1375
 ID ABX97917 standard; cDNA; 3871 BP.
 DE Human PRO polynucleotide #174.
 PN US2003032102-A1.
 PD 13-FEB-2003.
 Query Match 1.6%; Score 49.4; DB 8; Length 3871;
 Best Local Similarity 56.4%; Pred. No. 0.063;
 RESULT 1376

ID ACA97393 standard; cDNA; 3871 BP.
 DE Novel human secreted and transmembrane protein PRO1491 cDNA.
 PN US2003036117-A1.
 PD 20-FEB-2003.
 Query Match 1.6%; Score 49.4; DB 8; Length 3871;
 Best Local Similarity 56.4%; Pred. No. 0.063;
 RESULT 1377
 ID ACA57856 standard; cDNA; 3871 BP.
 DE Human PRO1491 cDNA.
 PN US2003036143-A1.
 PD 20-FEB-2003.
 Query Match 1.6%; Score 49.4; DB 8; Length 3871;
 Best Local Similarity 56.4%; Pred. No. 0.063;
 RESULT 1378
 ID ACD14384 standard; cDNA; 3871 BP.
 DE Human PRO polynucleotide #174.
 PN US2003032130-A1.
 PD 13-FEB-2003.
 Query Match 1.6%; Score 49.4; DB 8; Length 3871;
 Best Local Similarity 56.4%; Pred. No. 0.063;
 RESULT 1379
 ID ACC91167 standard; cDNA; 3871 BP.
 DE Human secreted polypeptide PRO1491-encoding cDNA, SEQ ID NO:347.
 PN US2003032138-A1.
 PD 13-FEB-2003.
 PA (GETH) GENENTECH INC.
 Query Match 1.6%; Score 49.4; DB 8; Length 3871;
 Best Local Similarity 56.4%; Pred. No. 0.063;
 RESULT 1380
 ID ACC88909 standard; cDNA; 3871 BP.
 DE Human secreted polypeptide PRO1491-encoding cDNA, SEQ ID NO:347.
 PN US2003036132-A1.
 PD 20-FEB-2003.
 Query Match 1.6%; Score 49.4; DB 8; Length 3871;
 Best Local Similarity 56.4%; Pred. No. 0.063;
 RESULT 1381
 ID ACD07106 standard; cDNA; 3871 BP.
 DE Human PRO polynucleotide #174.
 PN US2003008353-A1.
 PD 09-JAN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 1.6%; Score 49.4; DB 8; Length 3871;
 Best Local Similarity 56.4%; Pred. No. 0.063;
 RESULT 1382
 ID ACA67557 standard; cDNA; 3871 BP.
 DE Human PRO polynucleotide #174.
 PN US2003017542-A1.
 PD 23-JAN-2003.
 Query Match 1.6%; Score 49.4; DB 8; Length 3871;
 Best Local Similarity 56.4%; Pred. No. 0.063;
 RESULT 1383
 ID ACC81612 standard; cDNA; 3871 BP.
 DE Human secreted polypeptide PRO1491-encoding cDNA, SEQ ID NO:347.
 PN US2003032137-A1.
 PD 13-FEB-2003.
 Query Match 1.6%; Score 49.4; DB 8; Length 3871;
 Best Local Similarity 56.4%; Pred. No. 0.063;

RESULT 1384

ID ACC89216 standard; cDNA; 3871 BP.
DE Human secreted polypeptide PRO1491-encoding cDNA, SEQ ID NO:347.
PN US2003027269-A1.
PD 06-FEB-2003.

Query Match 1.6%; Score 49.4; DB 8; Length 3871;
Best Local Similarity 56.4%; Pred. No. 0.063;

RESULT 1385

ID ACC86572 standard; cDNA; 3871 BP.
DE Human secreted polypeptide PRO1491-encoding cDNA, SEQ ID NO:347.
PN US2003027268-A1.
PD 06-FEB-2003.

Query Match 1.6%; Score 49.4; DB 8; Length 3871;
Best Local Similarity 56.4%; Pred. No. 0.063;

RESULT 1386

ID ACC89830 standard; cDNA; 3871 BP.
DE Human secreted polypeptide PRO1491-encoding cDNA, SEQ ID NO:347.
PN US2003027274-A1.
PD 06-FEB-2003.

Query Match 1.6%; Score 49.4; DB 8; Length 3871;
Best Local Similarity 56.4%; Pred. No. 0.063;

RESULT 1387

ID ACC93009 standard; cDNA; 3871 BP.
DE Human secreted polypeptide PRO1491-encoding cDNA, SEQ ID NO:347.
PN US2003032135-A1.
PD 13-FEB-2003.

PA (GETH) GENENTECH INC.

Query Match 1.6%; Score 49.4; DB 8; Length 3871;
Best Local Similarity 56.4%; Pred. No. 0.063;

RESULT 1388

ID ACA72637 standard; cDNA; 3871 BP.
DE Human PRO polynucleotide #174.
PN US2003022295-A1.
PD 30-JAN-2003.

Query Match 1.6%; Score 49.4; DB 8; Length 3871;
Best Local Similarity 56.4%; Pred. No. 0.063;

RESULT 1389

ID ACA89155 standard; cDNA; 3871 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #174.
PN US2003022297-A1.
PD 30-JAN-2003.

Query Match 1.6%; Score 49.4; DB 8; Length 3871;
Best Local Similarity 56.4%; Pred. No. 0.063;

RESULT 1390

ID ACA69891 standard; cDNA; 3871 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #174.
PN US2003032105-A1.
PD 13-FEB-2003.

Query Match 1.6%; Score 49.4; DB 8; Length 3871;
Best Local Similarity 56.4%; Pred. No. 0.063;

RESULT 1391

ID ACA97034 standard; cDNA; 3871 BP.
DE Novel human secreted and transmembrane protein PRO1491 cDNA.
PN US2003032123-A1.
PD 13-FEB-2003.

Query Match 1.6%; Score 49.4; DB 8; Length 3871;
Best Local Similarity 56.4%; Pred. No. 0.063;

RESULT 1392

ID ACA91030 standard; cDNA; 3871 BP.
DE Novel human secreted and transmembrane protein PRO1491 cDNA.
PN US2003032108-A1.
PD 13-FEB-2003.

Query Match 1.6%; Score 49.4; DB 8; Length 3871;
Best Local Similarity 56.4%; Pred. No. 0.063;

RESULT 1393

ID ACA70812 standard; cDNA; 3871 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #174.
PN US2003032111-A1.
PD 13-FEB-2003.

Query Match 1.6%; Score 49.4; DB 8; Length 3871;
Best Local Similarity 56.4%; Pred. No. 0.063;

RESULT 1394

ID ACA95322 standard; cDNA; 3871 BP.
DE Novel human secreted and transmembrane protein PRO1491 cDNA.
PN US2003032119-A1.
PD 13-FEB-2003.

PA (GETH) GENENTECH INC.

Query Match 1.6%; Score 49.4; DB 8; Length 3871;
Best Local Similarity 56.4%; Pred. No. 0.063;

RESULT 1395

ID ACC86265 standard; cDNA; 3871 BP.
DE Human secreted polypeptide PRO1491-encoding cDNA, SEQ ID NO:347.
PN US2003027263-A1.
PD 06-FEB-2003.

Query Match 1.6%; Score 49.4; DB 8; Length 3871;
Best Local Similarity 56.4%; Pred. No. 0.063;

RESULT 1396

ID ACC90137 standard; cDNA; 3871 BP.
DE Human secreted polypeptide PRO1491-encoding cDNA, SEQ ID NO:347.
PN US2003027271-A1.
PD 06-FEB-2003.

Query Match 1.6%; Score 49.4; DB 8; Length 3871;
Best Local Similarity 56.4%; Pred. No. 0.063;

RESULT 1397

ID ACD12745 standard; cDNA; 3871 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #174.
PN US2003036125-A1.
PD 20-FEB-2003.

Query Match 1.6%; Score 49.4; DB 8; Length 3871;
Best Local Similarity 56.4%; Pred. No. 0.063;

RESULT 1398

ID ACF19975 standard; cDNA; 3871 BP.
DE Human secreted polypeptide PRO1491-encoding cDNA, SEQ ID NO:347.
PN US2003040068-A1.
PD 27-FEB-2003.

Query Match 1.6%; Score 49.4; DB 8; Length 3871;
Best Local Similarity 56.4%; Pred. No. 0.063;

RESULT 1399

ID ABX76919 standard; cDNA; 3871 BP.
DE Human PRO polynucleotide #174.
PN US2003027280-A1.
PD 06-FEB-2003.

Query Match 1.6%; Score 49.4; DB 8; Length 3871;
Best Local Similarity 56.4%; Pred. No. 0.063;

RESULT 1400

ID ACA73251 standard; cDNA; 3871 BP.
DE Novel human secreted and transmembrane protein PRO1491 cDNA.
PN US2003022300-A1.
PD 30-JAN-2003.

Query Match 1.6%; Score 49.4; DB 8; Length 3871;
Best Local Similarity 56.4%; Pred. No. 0.063;

RESULT 1401

ID ACA68794 standard; cDNA; 3871 BP.
DE Novel human secreted and transmembrane protein PRO1491 cDNA.
PN US2003036136-A1.
PD 20-FEB-2003.

Query Match 1.6%; Score 49.4; DB 8; Length 3871;
Best Local Similarity 56.4%; Pred. No. 0.063;

RESULT 1402

ID ACA74638 standard; cDNA; 3871 BP.
DE cDNA encoding human PRO polypeptide #174.
PN US2003036138-A1.
PD 20-FEB-2003.

Query Match 1.6%; Score 49.4; DB 8; Length 3871;
Best Local Similarity 56.4%; Pred. No. 0.063;

RESULT 1403

ID ACA70505 standard; cDNA; 3871 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #174.
PN US2003032109-A1.
PD 13-FEB-2003.

Query Match 1.6%; Score 49.4; DB 8; Length 3871;
Best Local Similarity 56.4%; Pred. No. 0.063;

RESULT 1404

ID ACD14691 standard; cDNA; 3871 BP.
DE Human PRO polynucleotide #174.
PN US2003040066-A1.
PD 27-FEB-2003.

Query Match 1.6%; Score 49.4; DB 8; Length 3871;
Best Local Similarity 56.4%; Pred. No. 0.063;

RESULT 1405

ID ACA68363 standard; cDNA; 3871 BP.
DE Novel human secreted and transmembrane protein PRO1491 cDNA.
PN US2003032104-A1.
PD 13-FEB-2003.

Query Match 1.6%; Score 49.4; DB 8; Length 3871;
Best Local Similarity 56.4%; Pred. No. 0.063;

RESULT 1406

ID ABX98828 standard; cDNA; 3871 BP.
DE Novel human secreted and transmembrane protein PRO1491 cDNA.
PN US2003036157-A1.
PD 20-FEB-2003.

Query Match 1.6%; Score 49.4; DB 8; Length 3871;
Best Local Similarity 56.4%; Pred. No. 0.063;

RESULT 1407

ID ACC81305 standard; cDNA; 3871 BP.
DE Human secreted polypeptide PRO1491-encoding cDNA, SEQ ID NO:347.
PN US2003032120-A1.
PD 13-FEB-2003.

Query Match 1.6%; Score 49.4; DB 8; Length 3871;
Best Local Similarity 56.4%; Pred. No. 0.063;

RESULT 1408

ID ACA95629 standard; cDNA; 3871 BP.
 DE Novel human secreted and transmembrane protein PRO1491 cDNA.
 PN US2003036155-A1.
 PD 20-FEB-2003.
 Query Match 1.6%; Score 49.4; DB 8; Length 3871;
 Best Local Similarity 56.4%; Pred. No. 0.063;
 RESULT 1409
 ID ACD04547 standard; cDNA; 3871 BP.
 DE Novel human secreted and transmembrane protein PRO1491 cDNA.
 PN US2003022296-A1.
 PD 30-JAN-2003.
 Query Match 1.6%; Score 49.4; DB 8; Length 3871;
 Best Local Similarity 56.4%; Pred. No. 0.063;
 RESULT 1410
 ID ACC87988 standard; cDNA; 3871 BP.
 DE Human secreted polypeptide PRO1491-encoding cDNA, SEQ ID NO:347.
 PN US2003027281-A1.
 PD 06-FEB-2003.
 PA (GETH) GENENTECH INC.
 Query Match 1.6%; Score 49.4; DB 8; Length 3871;
 Best Local Similarity 56.4%; Pred. No. 0.063;
 RESULT 1411
 ID ACF12650 standard; cDNA; 3871 BP.
 DE Human secreted polypeptide PRO1491-encoding cDNA, SEQ ID NO:347.
 PN US2003040058-A1.
 PD 27-FEB-2003.
 Query Match 1.6%; Score 49.4; DB 8; Length 3871;
 Best Local Similarity 56.4%; Pred. No. 0.063;
 RESULT 1412
 ID ACA96365 standard; cDNA; 3871 BP.
 DE Human PRO polynucleotide #174.
 PN US2003017540-A1.
 PD 23-JAN-2003.
 Query Match 1.6%; Score 49.4; DB 8; Length 3871;
 Best Local Similarity 56.4%; Pred. No. 0.063;
 RESULT 1413
 ID ACA65139 standard; cDNA; 3871 BP.
 DE Human PRO polynucleotide #174.
 PN US2003032106-A1.
 PD 13-FEB-2003.
 Query Match 1.6%; Score 49.4; DB 8; Length 3871;
 Best Local Similarity 56.4%; Pred. No. 0.063;
 RESULT 1414
 ID ACA73865 standard; cDNA; 3871 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #174.
 PN US2003032129-A1.
 PD 13-FEB-2003.
 Query Match 1.6%; Score 49.4; DB 8; Length 3871;
 Best Local Similarity 56.4%; Pred. No. 0.063;
 RESULT 1415
 ID ACA74277 standard; cDNA; 3871 BP.
 DE Novel human secreted and transmembrane protein PRO1491 cDNA.
 PN US2003032131-A1.
 PD 13-FEB-2003.
 Query Match 1.6%; Score 49.4; DB 8; Length 3871;
 Best Local Similarity 56.4%; Pred. No. 0.063;
 RESULT 1416

ID ACA96672 standard; cDNA; 3871 BP.
 DE Human PRO polynucleotide #174.
 PN US2003032103-A1.
 PD 13-FEB-2003.
 Query Match 1.6%; Score 49.4; DB 8; Length 3871;
 Best Local Similarity 56.4%; Pred. No. 0.063;
 RESULT 1417
 ID ACD10778 standard; cDNA; 3871 BP.
 DE cDNA encoding human PRO polypeptide #174.
 PN US2003032107-A1.
 PD 13-FEB-2003.
 Query Match 1.6%; Score 49.4; DB 8; Length 3871;
 Best Local Similarity 56.4%; Pred. No. 0.063;
 RESULT 1418
 ID ACC91474 standard; cDNA; 3871 BP.
 DE Human secreted polypeptide PRO1491-encoding cDNA, SEQ ID NO:347.
 PN US2003032139-A1.
 PD 13-FEB-2003.
 Query Match 1.6%; Score 49.4; DB 8; Length 3871;
 Best Local Similarity 56.4%; Pred. No. 0.063;
 RESULT 1419
 ID ACD02809 standard; cDNA; 3871 BP.
 DE cDNA encoding human PRO polypeptide #174.
 PN US2003022301-A1.
 PD 30-JAN-2003.
 Query Match 1.6%; Score 49.4; DB 8; Length 3871;
 Best Local Similarity 56.4%; Pred. No. 0.063;
 RESULT 1420
 ID ACC87374 standard; cDNA; 3871 BP.
 DE Human secreted polypeptide PRO1491-encoding cDNA, SEQ ID NO:347.
 PN US2003036165-A1.
 PD 20-FEB-2003.
 PA (GETH) GENENTECH INC.
 Query Match 1.6%; Score 49.4; DB 8; Length 3871;
 Best Local Similarity 56.4%; Pred. No. 0.063;
 RESULT 1421
 ID ACC85958 standard; cDNA; 3871 BP.
 DE Human secreted polypeptide PRO1491-encoding cDNA, SEQ ID NO:347.
 PN US2003027262-A1.
 PD 06-FEB-2003.
 Query Match 1.6%; Score 49.4; DB 8; Length 3871;
 Best Local Similarity 56.4%; Pred. No. 0.063;
 RESULT 1422
 ID ACA65446 standard; cDNA; 3871 BP.
 DE Human PRO polynucleotide #174.
 PN US2003032110-A1.
 PD 13-FEB-2003.
 Query Match 1.6%; Score 49.4; DB 8; Length 3871;
 Best Local Similarity 56.4%; Pred. No. 0.063;
 RESULT 1423
 ID ACA94263 standard; cDNA; 3871 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #174.
 PN US2003036142-A1.
 PD 20-FEB-2003.
 Query Match 1.6%; Score 49.4; DB 8; Length 3871;
 Best Local Similarity 56.4%; Pred. No. 0.063;
 RESULT 1424

ID ACA98007 standard; cDNA; 3871 BP.
 DE Human PRO polynucleotide #174.
 PN US2003036145-A1.
 PD 20-FEB-2003.
 Query Match 1.6%; Score 49.4; DB 8; Length 3871;
 Best Local Similarity 56.4%; Pred. No. 0.063;
 RESULT 1425
 ID ACA91509 standard; cDNA; 3871 BP.
 DE Novel human secreted and transmembrane protein PRO1491 cDNA.
 PN US2003036154-A1.
 PD 20-FEB-2003.
 Query Match 1.6%; Score 49.4; DB 8; Length 3871;
 Best Local Similarity 56.4%; Pred. No. 0.063;
 RESULT 1426
 ID ACA90723 standard; cDNA; 3871 BP.
 DE Novel human secreted and transmembrane protein PRO1491 cDNA.
 PN US2003036153-A1.
 PD 20-FEB-2003.
 Query Match 1.6%; Score 49.4; DB 8; Length 3871;
 Best Local Similarity 56.4%; Pred. No. 0.063;
 RESULT 1427
 ID ACD16270 standard; cDNA; 3871 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #174.
 PN US2003044931-A1.
 PD 06-MAR-2003.
 Query Match 1.6%; Score 49.4; DB 8; Length 3871;
 Best Local Similarity 56.4%; Pred. No. 0.063;
 RESULT 1428
 ID ACD17431 standard; cDNA; 3871 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #174.
 PN US2003036150-A1.
 PD 20-FEB-2003.
 Query Match 1.6%; Score 49.4; DB 8; Length 3871;
 Best Local Similarity 56.4%; Pred. No. 0.063;
 RESULT 1429
 ID ACC92088 standard; cDNA; 3871 BP.
 DE Human secreted polypeptide PRO1491-encoding cDNA, SEQ ID NO:347.
 PN US2003040069-A1.
 PD 27-FEB-2003.
 Query Match 1.6%; Score 49.4; DB 8; Length 3871;
 Best Local Similarity 56.4%; Pred. No. 0.063;
 RESULT 1430
 ID ACA74945 standard; cDNA; 3871 BP.
 DE cDNA encoding human PRO polypeptide #174.
 PN US2003022293-A1.
 PD 30-JAN-2003.
 Query Match 1.6%; Score 49.4; DB 8; Length 3871;
 Best Local Similarity 56.4%; Pred. No. 0.063;
 RESULT 1431
 ID ACA91816 standard; cDNA; 3871 BP.
 DE Human PRO polynucleotide #174.
 PN US2003032128-A1.
 PD 13-FEB-2003.
 Query Match 1.6%; Score 49.4; DB 8; Length 3871;
 Best Local Similarity 56.4%; Pred. No. 0.063;
 RESULT 1432
 ID ACA71460 standard; cDNA; 3871 BP.

DE Human secreted/transmembrane protein (PRO) cDNA #174.
PN US2003032116-A1.
PD 13-FEB-2003.
Query Match 1.6%; Score 49.4; DB 8; Length 3871;
Best Local Similarity 56.4%; Pred. No. 0.063;
RESULT 1433
ID ACC90860 standard; cDNA; 3871 BP.
DE Human secreted polypeptide PRO1491-encoding cDNA, SEQ ID NO:347.
PN US2003032122-A1.
PD 13-FEB-2003.
Query Match 1.6%; Score 49.4; DB 8; Length 3871;
Best Local Similarity 56.4%; Pred. No. 0.063;
RESULT 1434
ID ACA65870 standard; cDNA; 3871 BP.
DE cDNA encoding human PRO protein #174.
PN US2003036139-A1.
PD 20-FEB-2003.
Query Match 1.6%; Score 49.4; DB 8; Length 3871;
Best Local Similarity 56.4%; Pred. No. 0.063;
RESULT 1435
ID ACA95015 standard; cDNA; 3871 BP.
DE cDNA encoding human PRO polypeptide #174.
PN US2003017541-A1.
PD 23-JAN-2003.
Query Match 1.6%; Score 49.4; DB 8; Length 3871;
Best Local Similarity 56.4%; Pred. No. 0.063;
RESULT 1436
ID ACD16577 standard; cDNA; 3871 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #174.
PN US2003017543-A1.
PD 23-JAN-2003.
Query Match 1.6%; Score 49.4; DB 8; Length 3871;
Best Local Similarity 56.4%; Pred. No. 0.063;
RESULT 1437
ID ACD15656 standard; cDNA; 3871 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #174.
PN US2003036152-A1.
PD 20-FEB-2003.
Query Match 1.6%; Score 49.4; DB 8; Length 3871;
Best Local Similarity 56.4%; Pred. No. 0.063;
RESULT 1438
ID ABX16759 standard; cDNA; 3871 BP.
DE Human cDNA encoding secreted/transmembrane protein #174.
PN US2002127584-A1.
PD 12-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 1.6%; Score 49.4; DB 8; Length 3871;
Best Local Similarity 56.4%; Pred. No. 0.063;
RESULT 1439
ID ACA97700 standard; cDNA; 3871 BP.
DE Human PRO polynucleotide #174.
PN US2003032115-A1.
PD 13-FEB-2003.
Query Match 1.6%; Score 49.4; DB 9; Length 3871;
Best Local Similarity 56.4%; Pred. No. 0.063;
RESULT 1440
ID ACA99149 standard; cDNA; 3871 BP.

DE Novel human secreted and transmembrane protein PRO1491 cDNA.
PN US2003032140-A1.
PD 13-FEB-2003.
Query Match 1.6%; Score 49.4; DB 9; Length 3871;
Best Local Similarity 56.4%; Pred. No. 0.063;
RESULT 1441
ID ACC91781 standard; cDNA; 3871 BP.
DE Human secreted polypeptide PRO1491-encoding cDNA, SEQ ID NO:347.
PN US2003040076-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 1.6%; Score 49.4; DB 9; Length 3871;
Best Local Similarity 56.4%; Pred. No. 0.063;
RESULT 1442
ID ACD11192 standard; cDNA; 3871 BP.
DE Novel human secreted and transmembrane protein PRO1491 cDNA.
PN US2003008352-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 1.6%; Score 49.4; DB 9; Length 3871;
Best Local Similarity 56.4%; Pred. No. 0.063;
RESULT 1443
ID ACD15042 standard; cDNA; 3871 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #174.
PN US2003044922-A1.
PD 06-MAR-2003.
Query Match 1.6%; Score 49.4; DB 9; Length 3871;
Best Local Similarity 56.4%; Pred. No. 0.063;
RESULT 1444
ID ACD11806 standard; cDNA; 3871 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #174.
PN US2003032118-A1.
PD 13-FEB-2003.
Query Match 1.6%; Score 49.4; DB 9; Length 3871;
Best Local Similarity 56.4%; Pred. No. 0.063;
RESULT 1445
ID ACC95935 standard; cDNA; 3871 BP.
DE Human secreted polypeptide PRO1491-encoding cDNA, SEQ ID NO:347.
PN US2003036135-A1.
PD 20-FEB-2003.
Query Match 1.6%; Score 49.4; DB 9; Length 3871;
Best Local Similarity 56.4%; Pred. No. 0.063;
RESULT 1446
ID ACF16498 standard; cDNA; 3871 BP.
DE Human secreted polypeptide PRO1491-encoding cDNA, SEQ ID NO:347.
PN US2003054455-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 1.6%; Score 49.4; DB 9; Length 3871;
Best Local Similarity 56.4%; Pred. No. 0.063;
RESULT 1447
ID ACF02616 standard; cDNA; 3871 BP.
DE Human secreted polypeptide PRO1491-encoding cDNA, SEQ ID NO:347.
PN US2003049741-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 1.6%; Score 49.4; DB 9; Length 3871;

Best Local Similarity 56.4%; Pred. No. 0.063;
 RESULT 1448
 ID ACF02923 standard; cDNA; 3871 BP.
 DE Human secreted polypeptide PRO1491-encoding cDNA, SEQ ID NO:347.
 PN US2003049743-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 1.6%; Score 49.4; DB 9; Length 3871;
 Best Local Similarity 56.4%; Pred. No. 0.063;
 RESULT 1449
 ID ACF21510 standard; cDNA; 3871 BP.
 DE Human secreted polypeptide PRO1491-encoding cDNA, SEQ ID NO:347.
 PN US2003049769-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 1.6%; Score 49.4; DB 9; Length 3871;
 Best Local Similarity 56.4%; Pred. No. 0.063;
 RESULT 1450
 ID ACF10194 standard; cDNA; 3871 BP.
 DE Human secreted polypeptide PRO1491-encoding cDNA, SEQ ID NO:347.
 PN US2003068743-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 1.6%; Score 49.4; DB 9; Length 3871;
 Best Local Similarity 56.4%; Pred. No. 0.063;
 RESULT 1451
 ID ACF78087 standard; cDNA; 3871 BP.
 DE Human secreted polypeptide PRO1491-encoding cDNA, SEQ ID NO:347.
 PN US2003054479-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 1.6%; Score 49.4; DB 9; Length 3871;
 Best Local Similarity 56.4%; Pred. No. 0.063;
 RESULT 1452
 ID ACD46792 standard; cDNA; 3871 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #174.
 PN US2003068685-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 1.6%; Score 49.4; DB 9; Length 3871;
 Best Local Similarity 56.4%; Pred. No. 0.063;
 RESULT 1453
 ID ACD49555 standard; cDNA; 3871 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #174.
 PN US2003068725-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 1.6%; Score 49.4; DB 9; Length 3871;
 Best Local Similarity 56.4%; Pred. No. 0.063;
 RESULT 1454
 ID ACF28322 standard; cDNA; 3871 BP.
 DE Human secreted polypeptide PRO1491-encoding cDNA, SEQ ID NO:347.
 PN US2003068752-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 1.6%; Score 49.4; DB 9; Length 3871;
 Best Local Similarity 56.4%; Pred. No. 0.063;

RESULT 1455

ID ACD89012 standard; cDNA; 3871 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #174.
PN US2003068682-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 1.6%; Score 49.4; DB 9; Length 3871;
Best Local Similarity 56.4%; Pred. No. 0.063;

RESULT 1456

ID ACD84407 standard; cDNA; 3871 BP.
DE Human PRO polynucleotide #174.
PN US2003068701-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 1.6%; Score 49.4; DB 9; Length 3871;
Best Local Similarity 56.4%; Pred. No. 0.063;

RESULT 1457

ID ACD99181 standard; cDNA; 3871 BP.
DE cDNA encoding human PRO polypeptide #174.
PN US2003068755-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 1.6%; Score 49.4; DB 9; Length 3871;
Best Local Similarity 56.4%; Pred. No. 0.063;

RESULT 1458

ID ADA78099 standard; cDNA; 3871 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #174.
PN US2003073180-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 1.6%; Score 49.4; DB 9; Length 3871;
Best Local Similarity 56.4%; Pred. No. 0.063;

RESULT 1459

ID ACF48923 standard; cDNA; 3871 BP.
DE Human secreted polypeptide PRO1491-encoding cDNA, SEQ ID NO:347.
PN US2003104539-A1.
PD 05-JUN-2003.
Query Match 1.6%; Score 49.4; DB 9; Length 3871;
Best Local Similarity 56.4%; Pred. No. 0.063;

RESULT 1460

ID ACD09243 standard; cDNA; 3871 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #174.
PN US2003036131-A1.
PD 20-FEB-2003.
Query Match 1.6%; Score 49.4; DB 9; Length 3871;
Best Local Similarity 56.4%; Pred. No. 0.063;

RESULT 1461

ID ACF12036 standard; cDNA; 3871 BP.
DE Human secreted polypeptide PRO1491-encoding cDNA, SEQ ID NO:347.
PN US2003040075-A1.
PD 27-FEB-2003.
Query Match 1.6%; Score 49.4; DB 9; Length 3871;
Best Local Similarity 56.4%; Pred. No. 0.063;

RESULT 1462

ID ACF41270 standard; cDNA; 3871 BP.
DE Human secreted polypeptide PRO1491-encoding cDNA, SEQ ID NO:347.
PN US2003054459-A1.

PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 1.6%; Score 49.4; DB 9; Length 3871;
Best Local Similarity 56.4%; Pred. No. 0.063;
RESULT 1463
ID ACF15884 standard; cDNA; 3871 BP.
DE Human secreted polypeptide PRO1491-encoding cDNA, SEQ ID NO:347.
PN US2003044930-A1.
PD 06-MAR-2003.
Query Match 1.6%; Score 49.4; DB 9; Length 3871;
Best Local Similarity 56.4%; Pred. No. 0.063;
RESULT 1464
ID ACF16191 standard; cDNA; 3871 BP.
DE Human secreted polypeptide PRO1491-encoding cDNA, SEQ ID NO:347.
PN US2003040071-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 1.6%; Score 49.4; DB 9; Length 3871;
Best Local Similarity 56.4%; Pred. No. 0.063;
RESULT 1465
ID ACD32018 standard; cDNA; 3871 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #174.
PN US2003054471-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 1.6%; Score 49.4; DB 9; Length 3871;
Best Local Similarity 56.4%; Pred. No. 0.063;
RESULT 1466
ID ACF18826 standard; cDNA; 3871 BP.
DE Human secreted polypeptide PRO1491-encoding cDNA, SEQ ID NO:347.
PN US2003064452-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 1.6%; Score 49.4; DB 9; Length 3871;
Best Local Similarity 56.4%; Pred. No. 0.063;
RESULT 1467
ID ACF09273 standard; cDNA; 3871 BP.
DE Human secreted polypeptide PRO1491-encoding cDNA, SEQ ID NO:347.
PN US2003068705-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 1.6%; Score 49.4; DB 9; Length 3871;
Best Local Similarity 56.4%; Pred. No. 0.063;
RESULT 1468
ID ACF78394 standard; cDNA; 3871 BP.
DE Human secreted polypeptide PRO1491-encoding cDNA, SEQ ID NO:347.
PN US2003054473-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 1.6%; Score 49.4; DB 9; Length 3871;
Best Local Similarity 56.4%; Pred. No. 0.063;
RESULT 1469
ID ACF51993 standard; cDNA; 3871 BP.
DE Human secreted polypeptide PRO1491-encoding cDNA, SEQ ID NO:347.
PN US2003064440-A1.
PD 03-APR-2003.
Query Match 1.6%; Score 49.4; DB 9; Length 3871;

Best Local Similarity 56.4%; Pred. No. 0.063;

RESULT 1470

ID ACF26480 standard; cDNA; 3871 BP.

DE Human secreted polypeptide PRO1491-encoding cDNA, SEQ ID NO:347.

PN US2003068704-A1.

PD 10-APR-2003.

PA (GETH) GENENTECH INC.

Query Match 1.6%; Score 49.4; DB 9; Length 3871;

Best Local Similarity 56.4%; Pred. No. 0.063;

RESULT 1471

ID ACF24273 standard; cDNA; 3871 BP.

DE Human secreted polypeptide PRO1491-encoding cDNA, SEQ ID NO:347.

PN US2003068722-A1.

PD 10-APR-2003.

PA (GETH) GENENTECH INC.

Query Match 1.6%; Score 49.4; DB 9; Length 3871;

Best Local Similarity 56.4%; Pred. No. 0.063;

RESULT 1472

ID ACF63584 standard; cDNA; 3871 BP.

DE Human secreted polypeptide PRO1491-encoding cDNA, SEQ ID NO:347.

PN US2003073183-A1.

PD 17-APR-2003.

PA (GETH) GENENTECH INC.

Query Match 1.6%; Score 49.4; DB 9; Length 3871;

Best Local Similarity 56.4%; Pred. No. 0.063;

RESULT 1473

ID ACF50458 standard; cDNA; 3871 BP.

DE Human secreted polypeptide PRO1491-encoding cDNA, SEQ ID NO:347.

PN US2003104549-A1.

PD 05-JUN-2003.

PA (GETH) GENENTECH INC.

Query Match 1.6%; Score 49.4; DB 9; Length 3871;

Best Local Similarity 56.4%; Pred. No. 0.063;

RESULT 1474

ID ACH07929 standard; cDNA; 3871 BP.

DE Human secreted/transmembrane protein (PRO) cDNA #174.

PN US2003049749-A1.

PD 13-MAR-2003.

PA (GETH) GENENTECH INC.

Query Match 1.6%; Score 49.4; DB 9; Length 3871;

Best Local Similarity 56.4%; Pred. No. 0.063;

RESULT 1475

ID ACF13735 standard; cDNA; 3871 BP.

DE Human secreted polypeptide PRO1491-encoding cDNA, SEQ ID NO:347.

PN US2003064462-A1.

PD 03-APR-2003.

PA (GETH) GENENTECH INC.

Query Match 1.6%; Score 49.4; DB 9; Length 3871;

Best Local Similarity 56.4%; Pred. No. 0.063;

RESULT 1476

ID ACD41661 standard; cDNA; 3871 BP.

DE Human secreted/transmembrane protein (PRO) cDNA #174.

PN US2003065159-A1.

PD 03-APR-2003.

PA (GETH) GENENTECH INC.

Query Match 1.6%; Score 49.4; DB 9; Length 3871;

Best Local Similarity 56.4%; Pred. No. 0.063;

RESULT 1477

ID ACF32074 standard; cDNA; 3871 BP.
DE Human secreted polypeptide PRO1491-encoding cDNA, SEQ ID NO:347.
PN US2003064447-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 1.6%; Score 49.4; DB 9; Length 3871;
Best Local Similarity 56.4%; Pred. No. 0.063;

RESULT 1478

ID ACF23352 standard; cDNA; 3871 BP.
DE Human secreted polypeptide PRO1491-encoding cDNA, SEQ ID NO:347.
PN US2003073184-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 1.6%; Score 49.4; DB 9; Length 3871;
Best Local Similarity 56.4%; Pred. No. 0.063;

RESULT 1479

ID ACF40042 standard; cDNA; 3871 BP.
DE Human secreted polypeptide PRO1491-encoding cDNA, SEQ ID NO:347.
PN US2003064463-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 1.6%; Score 49.4; DB 9; Length 3871;
Best Local Similarity 56.4%; Pred. No. 0.063;

RESULT 1480

ID ACD45564 standard; cDNA; 3871 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #174.
PN US2003064451-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 1.6%; Score 49.4; DB 9; Length 3871;
Best Local Similarity 56.4%; Pred. No. 0.063;

RESULT 1481

ID ACF53221 standard; cDNA; 3871 BP.
DE Human secreted polypeptide PRO1491-encoding cDNA, SEQ ID NO:347.
PN US2003068721-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 1.6%; Score 49.4; DB 9; Length 3871;
Best Local Similarity 56.4%; Pred. No. 0.063;

RESULT 1482

ID ACF27401 standard; cDNA; 3871 BP.
DE Human secreted polypeptide PRO1491-encoding cDNA, SEQ ID NO:347.
PN US2003068699-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 1.6%; Score 49.4; DB 9; Length 3871;
Best Local Similarity 56.4%; Pred. No. 0.063;

RESULT 1483

ID ACF45239 standard; cDNA; 3871 BP.
DE Human secreted polypeptide PRO1491-encoding cDNA, SEQ ID NO:347.
PN US2003068707-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 1.6%; Score 49.4; DB 9; Length 3871;
Best Local Similarity 56.4%; Pred. No. 0.063;

RESULT 1484

ID ACF29857 standard; cDNA; 3871 BP.
 DE Human secreted polypeptide PRO1491-encoding cDNA, SEQ ID NO:347.
 PN US2003073175-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 1.6%; Score 49.4; DB 9; Length 3871;
 Best Local Similarity 56.4%; Pred. No. 0.063;
 RESULT 1485
 ID ACD89933 standard; cDNA; 3871 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #174.
 PN US2003068695-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 1.6%; Score 49.4; DB 9; Length 3871;
 Best Local Similarity 56.4%; Pred. No. 0.063;
 RESULT 1486
 ID ACD84714 standard; cDNA; 3871 BP.
 DE Human PRO polynucleotide #174.
 PN US2003068703-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 1.6%; Score 49.4; DB 9; Length 3871;
 Best Local Similarity 56.4%; Pred. No. 0.063;
 RESULT 1487
 ID ACD98874 standard; cDNA; 3871 BP.
 DE cDNA encoding human PRO polypeptide #174.
 PN US2003068732-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 1.6%; Score 49.4; DB 9; Length 3871;
 Best Local Similarity 56.4%; Pred. No. 0.063;
 RESULT 1488
 ID ACF77166 standard; cDNA; 3871 BP.
 DE Human secreted polypeptide PRO1491-encoding cDNA, SEQ ID NO:347.
 PN US2003082717-A1.
 PD 01-MAY-2003.
 Query Match 1.6%; Score 49.4; DB 9; Length 3871;
 Best Local Similarity 56.4%; Pred. No. 0.063;
 RESULT 1489
 ID ACF76859 standard; cDNA; 3871 BP.
 DE Human secreted polypeptide PRO1491-encoding cDNA, SEQ ID NO:347.
 PN US2003104548-A1.
 PD 05-JUN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 1.6%; Score 49.4; DB 9; Length 3871;
 Best Local Similarity 56.4%; Pred. No. 0.063;
 RESULT 1490
 ID ACF49844 standard; cDNA; 3871 BP.
 DE Human secreted polypeptide PRO1491-encoding cDNA, SEQ ID NO:347.
 PN US2003104542-A1.
 PD 05-JUN-2003.
 Query Match 1.6%; Score 49.4; DB 9; Length 3871;
 Best Local Similarity 56.4%; Pred. No. 0.063;
 RESULT 1491
 ID ACF50151 standard; cDNA; 3871 BP.
 DE Human secreted polypeptide PRO1491-encoding cDNA, SEQ ID NO:347.
 PN US2003104543-A1.

PD 05-JUN-2003.

Query Match 1.6%; Score 49.4; DB 9; Length 3871;
Best Local Similarity 56.4%; Pred. No. 0.063;

RESULT 1492

ID ACD09550 standard; cDNA; 3871 BP.

DE Human secreted/transmembrane protein (PRO) cDNA #174.

PN US2003036127-A1.

PD 20-FEB-2003.

Query Match 1.6%; Score 49.4; DB 9; Length 3871;
Best Local Similarity 56.4%; Pred. No. 0.063;

RESULT 1493

ID ACD08629 standard; cDNA; 3871 BP.

DE Human secreted/transmembrane protein (PRO) cDNA #174.

PN US2003040061-A1.

PD 27-FEB-2003.

Query Match 1.6%; Score 49.4; DB 9; Length 3871;
Best Local Similarity 56.4%; Pred. No. 0.063;

RESULT 1494

ID ACF12343 standard; cDNA; 3871 BP.

DE Human secreted polypeptide PRO1491-encoding cDNA, SEQ ID NO:347.

PN US2003036130-A1.

PD 20-FEB-2003.

Query Match 1.6%; Score 49.4; DB 9; Length 3871;
Best Local Similarity 56.4%; Pred. No. 0.063;

RESULT 1495

ID ACC94851 standard; cDNA; 3871 BP.

DE Human secreted polypeptide PRO1491-encoding cDNA, SEQ ID NO:347.

PN US2003054468-A1.

PD 20-MAR-2003.

PA (GETH) GENENTECH INC.

Query Match 1.6%; Score 49.4; DB 9; Length 3871;
Best Local Similarity 56.4%; Pred. No. 0.063;

RESULT 1496

ID ACD22570 standard; cDNA; 3871 BP.

DE Human secreted/transmembrane protein (PRO) cDNA #174.

PN US2003054470-A1.

PD 20-MAR-2003.

PA (GETH) GENENTECH INC.

Query Match 1.6%; Score 49.4; DB 9; Length 3871;
Best Local Similarity 56.4%; Pred. No. 0.063;

RESULT 1497

ID ACF15270 standard; cDNA; 3871 BP.

DE Human secreted polypeptide PRO1491-encoding cDNA, SEQ ID NO:347.

PN US2003044917-A1.

PD 06-MAR-2003.

Query Match 1.6%; Score 49.4; DB 9; Length 3871;
Best Local Similarity 56.4%; Pred. No. 0.063;

RESULT 1498

ID ACC97365 standard; cDNA; 3871 BP.

DE Human secreted polypeptide PRO1491-encoding cDNA, SEQ ID NO:347.

PN US2003044929-A1.

PD 06-MAR-2003.

Query Match 1.6%; Score 49.4; DB 9; Length 3871;
Best Local Similarity 56.4%; Pred. No. 0.063;

RESULT 1499

ID ACC92395 standard; cDNA; 3871 BP.

DE Human secreted polypeptide PRO1491-encoding cDNA, SEQ ID NO:347.

PN US2003059880-A1.

PD 27-MAR-2003.

PA (GETH) GENENTECH INC.

Query Match 1.6%; Score 49.4; DB 9; Length 3871;

Best Local Similarity 56.4%; Pred. No. 0.063;

RESULT 1500

ID ACF14042 standard; cDNA; 3871 BP.

DE Human secreted polypeptide PRO1491-encoding cDNA, SEQ ID NO:347.

PN US2003064465-A1.

PD 03-APR-2003.

PA (GETH) GENENTECH INC.

Query Match 1.6%; Score 49.4; DB 9; Length 3871;

Best Local Similarity 56.4%; Pred. No. 0.063;

OM nucleic - nucleic search, using sw model

Run on: February 15, 2005, 01:50:12 ; Search time 504 Seconds
 (without alignments)
 10204.003 Million cell updates/sec

Title: US-10-015-391A-276
 Perfect score: 3143
 Sequence: 1 gggctgaggcactgagagac.....aaatataaggcttaaaaaaa 3143

Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 1500 summaries

Database : Issued Patents_NA:*
 1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
 2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
 3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
 4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
 5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
 6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	3040.8	96.7	3104	4	US-09-578-063-17	Sequence 17, Appl
2	2283	72.6	2283	4	US-09-578-063-18	Sequence 18, Appl
3	1727.6	55.0	3046	4	US-09-578-063-71	Sequence 71, Appl
4	1727.6	55.0	3046	4	US-09-578-063-77	Sequence 77, Appl
5	230	7.3	2433	4	US-09-300-958A-24	Sequence 24, Appl
6	153.4	4.9	4157	4	US-08-556-422A-1	Sequence 1, Appli
7	126	4.0	3524	4	US-09-077-940A-3	Sequence 3, Appli
8	125.4	4.0	3692	4	US-09-077-940A-1	Sequence 1, Appli
9	121.4	3.9	2820	4	US-09-854-845-15	Sequence 15, Appl
10	121.4	3.9	2865	4	US-09-854-845-13	Sequence 13, Appl
11	121.4	3.9	3105	4	US-09-854-845-5	Sequence 5, Appli

12	121.4	3.9	3150	4	US-09-854-845-1	Sequence 1, Appli
13	121.4	3.9	3237	4	US-09-854-845-7	Sequence 7, Appli
14	121.4	3.9	3282	4	US-09-854-845-3	Sequence 3, Appli
15	121.4	3.9	3411	4	US-09-854-845-11	Sequence 11, Appl
16	121.4	3.9	3456	4	US-09-854-845-9	Sequence 9, Appli
17	121.4	3.9	4074	4	US-09-854-845-17	Sequence 17, Appl
18	105.4	3.4	2094	4	US-09-854-845-24	Sequence 24, Appl
19	105.4	3.4	2517	4	US-09-854-845-28	Sequence 28, Appl
20	105.4	3.4	2598	4	US-09-854-845-32	Sequence 32, Appl
21	105.4	3.4	2951	4	US-09-854-845-50	Sequence 50, Appl
22	102.4	3.3	2109	4	US-09-854-845-22	Sequence 22, Appl
23	102.4	3.3	2532	4	US-09-854-845-26	Sequence 26, Appl
24	102.4	3.3	2575	4	US-09-774-528-40	Sequence 40, Appl
25	102.4	3.3	2613	4	US-09-854-845-30	Sequence 30, Appl
26	102	3.2	1890	4	US-09-520-781-29	Sequence 29, Appl
27	102	3.2	2278	4	US-09-976-594-1002	Sequence 1002, Ap
28	102	3.2	3333	4	US-09-520-781-5	Sequence 5, Appli
29	102	3.2	3498	4	US-09-520-781-3	Sequence 3, Appli
30	102	3.2	4280	4	US-09-774-528-330	Sequence 330, App
31	98.6	3.1	1797	4	US-09-854-845-40	Sequence 40, Appl
32	98.6	3.1	2220	4	US-09-854-845-44	Sequence 44, Appl
33	98.6	3.1	2301	4	US-09-854-845-48	Sequence 48, Appl
34	98.6	3.1	2790	4	US-09-254-594-5	Sequence 5, Appli
35	98.6	3.1	3432	4	US-09-254-594-4	Sequence 4, Appli
36	95.6	3.0	1812	4	US-09-854-845-38	Sequence 38, Appl
37	95.6	3.0	2235	4	US-09-854-845-42	Sequence 42, Appl
38	95.6	3.0	2316	4	US-09-854-845-46	Sequence 46, Appl
39	89.8	2.9	2787	4	US-09-254-594-2	Sequence 2, Appli
40	89.8	2.9	3195	4	US-09-254-594-1	Sequence 1, Appli
41	84.2	2.7	4286	4	US-09-976-594-632	Sequence 632, App
42	79.6	2.5	2349	4	US-09-813-290-3	Sequence 3, Appli
43	79.6	2.5	2628	4	US-09-813-290-1	Sequence 1, Appli
44	79.6	2.5	3568	4	US-09-813-290-5	Sequence 5, Appli
45	78.6	2.5	3560	1	US-08-121-713D-59	Sequence 59, Appl
46	78.6	2.5	3560	1	US-08-835-268-59	Sequence 59, Appl
47	78.6	2.5	3560	2	US-09-060-692-59	Sequence 59, Appl
48	78.6	2.5	3560	3	US-08-833-391-59	Sequence 59, Appl
49	78.6	2.5	3560	3	US-09-060-610-59	Sequence 59, Appl
50	78.6	2.5	3560	5	PCT-US94-10151A-59	Sequence 59, Appl
51	78.2	2.5	1923	4	US-09-653-274-12	Sequence 12, Appl
52	78.2	2.5	1923	4	US-10-461-791-12	Sequence 12, Appl
53	78.2	2.5	3261	4	US-09-653-274-5	Sequence 5, Appli
54	78.2	2.5	3261	4	US-10-461-791-5	Sequence 5, Appli
55	78.2	2.5	3694	4	US-09-653-274-3	Sequence 3, Appli
56	78.2	2.5	3694	4	US-10-461-791-3	Sequence 3, Appli
57	78	2.5	1491	4	US-09-854-845-20	Sequence 20, Appl
58	71.2	2.3	1194	4	US-09-854-845-36	Sequence 36, Appl
59	69.8	2.2	2670	1	US-08-121-713D-61	Sequence 61, Appl
60	69.8	2.2	2670	1	US-08-835-268-61	Sequence 61, Appl
61	69.8	2.2	2670	2	US-09-060-692-61	Sequence 61, Appl
62	69.8	2.2	2670	3	US-08-833-391-61	Sequence 61, Appl
63	69.8	2.2	2670	3	US-09-060-610-61	Sequence 61, Appl
64	69.8	2.2	2670	5	PCT-US94-10151A-61	Sequence 61, Appl
65	65.2	2.1	648	4	US-09-854-845-18	Sequence 18, Appl
66	63.8	2.0	2601	1	US-08-121-713D-53	Sequence 53, Appl
67	63.8	2.0	2601	1	US-08-835-268-53	Sequence 53, Appl
68	63.8	2.0	2601	2	US-09-060-692-53	Sequence 53, Appl

	69	63.8	2.0	2601	3	US-08-833-391-53	Sequence 53, Appl
	70	63.8	2.0	2601	3	US-09-060-610-53	Sequence 53, Appl
	71	63.8	2.0	2601	5	PCT-US94-10151A-53	Sequence 53, Appl
	72	62.6	2.0	7218	1	US-08-232-463-14	Sequence 14, Appl
	73	62	2.0	2854	1	US-08-121-713D-57	Sequence 57, Appl
	74	62	2.0	2854	1	US-08-835-268-57	Sequence 57, Appl
	75	62	2.0	2854	2	US-09-060-692-57	Sequence 57, Appl
	76	62	2.0	2854	3	US-08-833-391-57	Sequence 57, Appl
	77	62	2.0	2854	3	US-09-060-610-57	Sequence 57, Appl
	78	62	2.0	2854	5	PCT-US94-10151A-57	Sequence 57, Appl
	79	58.4	1.9	351	4	US-09-854-845-34	Sequence 34, Appl
c	80	54.2	1.7	1654	4	US-09-270-767-1815	Sequence 1815, Ap
c	81	54.2	1.7	1654	4	US-09-270-767-17097	Sequence 17097, A
	82	53.2	1.7	1224	4	US-09-270-767-292	Sequence 292, App
	83	53.2	1.7	1224	4	US-09-270-767-15574	Sequence 15574, A
	84	52.6	1.7	2898	3	US-09-308-179B-2	Sequence 2, Appli
	85	50.2	1.6	2504	1	US-08-121-713D-63	Sequence 63, Appl
	86	50.2	1.6	2504	1	US-08-835-268-63	Sequence 63, Appl
	87	50.2	1.6	2504	2	US-09-060-692-63	Sequence 63, Appl
	88	50.2	1.6	2504	3	US-08-833-391-63	Sequence 63, Appl
	89	50.2	1.6	2504	3	US-09-060-610-63	Sequence 63, Appl
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	91	48.4	1.5	2001	4	US-09-689-012-1	Sequence 1, Appli
	92	48.4	1.5	2010	3	US-09-240-410-1	Sequence 1, Appli
	93	48.4	1.5	2498	3	US-09-041-236-1	Sequence 1, Appli
	94	48.4	1.5	2498	4	US-09-771-467C-1	Sequence 1, Appli
	95	47.6	1.5	1481	1	US-08-136-922-1	Sequence 1, Appli
	96	46.2	1.5	540	3	US-08-149-101A-2	Sequence 2, Appli
	97	46.2	1.5	540	5	PCT-US94-12873-2	Sequence 2, Appli
	98	46.2	1.5	561	6	5187077-28	Patent No. 5187077
	99	46.2	1.5	561	6	5427925-26	Patent No. 5427925
	100	46.2	1.5	561	6	5187077-28	Patent No. 5187077
	101	46.2	1.5	561	6	5427925-26	Patent No. 5427925
	102	46.2	1.5	655	2	US-08-378-617A-31	Sequence 31, Appl
	103	46.2	1.5	1297	6	5187077-23	Patent No. 5187077
	104	46.2	1.5	1297	6	5427925-21	Patent No. 5427925
	105	46.2	1.5	1297	6	5187077-23	Patent No. 5187077
	106	46.2	1.5	1297	6	5427925-21	Patent No. 5427925
	107	46.2	1.5	3867	4	US-09-949-016-4978	Sequence 4978, Ap
	108	46.2	1.5	3868	4	US-09-949-016-337	Sequence 337, App
	109	46.2	1.5	10303	4	US-09-949-016-12079	Sequence 12079, A
	110	46.2	1.5	10304	4	US-09-949-016-16720	Sequence 16720, A
	111	44.8	1.4	300	4	US-09-513-999C-419	Sequence 419, App
	112	43.6	1.4	1038	4	US-09-252-991A-15806	Sequence 15806, A
c	113	43.6	1.4	1584	4	US-09-252-991A-15886	Sequence 15886, A
	114	43.6	1.4	1758	4	US-09-252-991A-15835	Sequence 15835, A
c	115	43.6	1.4	1911	4	US-09-252-991A-15858	Sequence 15858, A
	116	42.4	1.3	900	4	US-09-902-540-9504	Sequence 9504, Ap
c	117	42.4	1.3	1539	3	US-09-286-904-1	Sequence 1, Appli
c	118	42.4	1.3	1539	3	US-09-640-101-1	Sequence 1, Appli
	119	42.4	1.3	10992	4	US-09-902-540-1081	Sequence 1081, Ap
	120	42.2	1.3	651	4	US-09-252-991A-11750	Sequence 11750, A
	121	42.2	1.3	765	4	US-09-252-991A-11829	Sequence 11829, A
c	122	42.2	1.3	906	4	US-09-252-991A-11617	Sequence 11617, A
c	123	42.2	1.3	1002	4	US-09-252-991A-11561	Sequence 11561, A
	124	42.2	1.3	1487	4	US-09-949-016-4403	Sequence 4403, Ap
	125	42.2	1.3	1629	3	US-09-247-155-71	Sequence 71, Appl

126	42.2	1.3	1965	3	US-09-178-252-26	Sequence 26, Appl
127	42.2	1.3	1965	4	US-09-826-660-26	Sequence 26, Appl
128	42.2	1.3	22980	4	US-09-949-016-16145	Sequence 16145, A
129	41.8	1.3	5177	4	US-09-814-915A-79	Sequence 79, Appl
130	41.4	1.3	357	3	US-08-556-978B-83	Sequence 83, Appl
131	41.2	1.3	430	4	US-09-621-976-16656	Sequence 16656, A
132	41	1.3	334	4	US-09-513-999C-613	Sequence 613, App
133	41	1.3	505	4	US-09-621-976-15639	Sequence 15639, A
134	41	1.3	512	4	US-09-621-976-1339	Sequence 1339, Ap
135	40.6	1.3	4403765	3	US-09-103-840A-2	Sequence 2, Appli
136	40.6	1.3	4411529	3	US-09-103-840A-1	Sequence 1, Appli
137	40.4	1.3	411	4	US-09-902-540-5872	Sequence 5872, Ap
c 138	40.4	1.3	645	4	US-09-252-991A-5596	Sequence 5596, Ap
c 139	40.4	1.3	854	4	US-09-902-540-153	Sequence 153, App
140	40.4	1.3	1185	4	US-09-252-991A-5635	Sequence 5635, Ap
c 141	40.4	1.3	55031	4	US-09-949-016-17389	Sequence 17389, A
142	40.2	1.3	1194	4	US-09-489-039A-3387	Sequence 3387, Ap
c 143	40.2	1.3	1899	4	US-09-902-540-4564	Sequence 4564, Ap
144	40.2	1.3	2592	4	US-09-902-540-2500	Sequence 2500, Ap
c 145	40.2	1.3	16833	4	US-09-902-540-1112	Sequence 1112, Ap
c 146	40.2	1.3	24905	4	US-09-902-540-1225	Sequence 1225, Ap
c 147	40	1.3	601	4	US-09-949-016-26287	Sequence 26287, A
c 148	40	1.3	601	4	US-09-949-016-169811	Sequence 169811,
c 149	40	1.3	798	4	US-09-252-991A-10601	Sequence 10601, A
150	40	1.3	1707	4	US-09-252-991A-10468	Sequence 10468, A
151	40	1.3	1824	4	US-09-252-991A-10254	Sequence 10254, A
152	40	1.3	67386	4	US-09-949-016-16519	Sequence 16519, A
c 153	39.6	1.3	601	4	US-09-949-016-26286	Sequence 26286, A
c 154	39.6	1.3	601	4	US-09-949-016-169810	Sequence 169810,
155	39.6	1.3	2358	4	US-09-949-016-1246	Sequence 1246, Ap
156	39.6	1.3	16013	4	US-09-949-016-12988	Sequence 12988, A
157	39.2	1.2	364	4	US-09-621-976-17202	Sequence 17202, A
158	39.2	1.2	1361	4	US-09-614-912-37	Sequence 37, Appl
159	39.2	1.2	1888	4	US-09-599-360B-38	Sequence 38, Appl
160	39.2	1.2	55216	4	US-09-716-865-23	Sequence 23, Appl
c 161	39.2	1.2	55216	4	US-09-716-865-23	Sequence 23, Appl
162	39	1.2	305	4	US-09-513-999C-2219	Sequence 2219, Ap
163	39	1.2	472	4	US-09-621-976-16397	Sequence 16397, A
164	39	1.2	837	4	US-09-902-540-4676	Sequence 4676, Ap
165	39	1.2	931	4	US-09-902-540-4292	Sequence 4292, Ap
166	39	1.2	1222	1	US-08-195-744-3	Sequence 3, Appli
167	39	1.2	1222	2	US-08-788-279-3	Sequence 3, Appli
c 168	39	1.2	1230	4	US-09-252-991A-16191	Sequence 16191, A
169	39	1.2	1645	4	US-09-949-016-3832	Sequence 3832, Ap
170	39	1.2	1692	4	US-09-902-540-4219	Sequence 4219, Ap
171	39	1.2	1812	4	US-09-252-991A-16295	Sequence 16295, A
c 172	39	1.2	2019	4	US-09-252-991A-15983	Sequence 15983, A
173	39	1.2	4097	3	US-09-123-708-5	Sequence 5, Appli
174	39	1.2	4097	3	US-09-123-624-5	Sequence 5, Appli
175	39	1.2	4791	3	US-08-949-155-49	Sequence 49, Appl
176	39	1.2	4791	3	US-09-819-964-49	Sequence 49, Appl
177	39	1.2	20250	4	US-09-902-540-1213	Sequence 1213, Ap
c 178	39	1.2	24754	4	US-09-902-540-1230	Sequence 1230, Ap
179	39	1.2	26289	4	US-09-902-540-1210	Sequence 1210, Ap
c 180	39	1.2	34094	4	US-09-292-034-1	Sequence 1, Appli
181	38.6	1.2	870	4	US-09-902-540-5914	Sequence 5914, Ap
182	38.6	1.2	1289	4	US-09-902-540-175	Sequence 175, App

183	38.6	1.2	4843	3	US-08-986-485-1	Sequence 1, Appli
184	38.6	1.2	87648	4	US-09-949-016-13655	Sequence 13655, A
185	38.4	1.2	756	4	US-09-902-540-7453	Sequence 7453, Ap
c 186	38.4	1.2	858	4	US-09-902-540-72	Sequence 72, Appl
c 187	38.4	1.2	4063	4	US-09-902-540-595	Sequence 595, App
188	38.2	1.2	675	3	US-08-949-155-1	Sequence 1, Appli
189	38.2	1.2	675	3	US-09-819-964-1	Sequence 1, Appli
c 190	38.2	1.2	957	4	US-09-252-991A-10748	Sequence 10748, A
c 191	38.2	1.2	2862	4	US-09-252-991A-10659	Sequence 10659, A
c 192	38.2	1.2	2883	4	US-09-902-540-480	Sequence 480, App
193	38.2	1.2	2910	4	US-09-252-991A-10414	Sequence 10414, A
194	38.2	1.2	3111	4	US-09-252-991A-10504	Sequence 10504, A
195	38	1.2	601	4	US-09-949-016-61845	Sequence 61845, A
196	38	1.2	4521	4	US-09-902-540-3633	Sequence 3633, Ap
c 197	38	1.2	10585	4	US-09-949-016-12099	Sequence 12099, A
c 198	38	1.2	10586	4	US-09-949-016-17564	Sequence 17564, A
199	38	1.2	15778	4	US-09-949-016-13538	Sequence 13538, A
200	38	1.2	19269	4	US-09-902-540-1175	Sequence 1175, Ap
201	37.8	1.2	837	4	US-09-834-759-512	Sequence 512, App
202	37.8	1.2	837	4	US-09-834-759-513	Sequence 513, App
203	37.8	1.2	1047	4	US-09-252-991A-9034	Sequence 9034, Ap
204	37.8	1.2	1220	4	US-09-692-081-3	Sequence 3, Appli
205	37.8	1.2	1342	4	US-09-489-847-89	Sequence 89, Appl
c 206	37.8	1.2	1464	4	US-09-252-991A-8971	Sequence 8971, Ap
207	37.8	1.2	1494	4	US-09-252-991A-9117	Sequence 9117, Ap
c 208	37.8	1.2	89268	4	US-09-949-016-12025	Sequence 12025, A
c 209	37.8	1.2	90544	4	US-09-949-016-13302	Sequence 13302, A
c 210	37.6	1.2	4435	4	US-09-949-016-3780	Sequence 3780, Ap
c 211	37.6	1.2	4440	4	US-09-913-954-1	Sequence 1, Appli
c 212	37.6	1.2	22294	4	US-09-949-016-15522	Sequence 15522, A
213	37.4	1.2	792	4	US-09-252-991A-11705	Sequence 11705, A
214	37.4	1.2	876	4	US-09-252-991A-11783	Sequence 11783, A
c 215	37.4	1.2	975	4	US-09-252-991A-11651	Sequence 11651, A
216	37.4	1.2	1728	4	US-09-252-991A-9757	Sequence 9757, Ap
217	37.4	1.2	1803	4	US-09-252-991A-7559	Sequence 7559, Ap
c 218	37.4	1.2	1824	4	US-09-252-991A-10076	Sequence 10076, A
c 219	37.4	1.2	2007	4	US-09-252-991A-10141	Sequence 10141, A
220	37.4	1.2	2178	4	US-09-902-540-7409	Sequence 7409, Ap
221	37.4	1.2	2787	4	US-09-252-991A-7629	Sequence 7629, Ap
c 222	37.4	1.2	3135	4	US-09-252-991A-7924	Sequence 7924, Ap
c 223	37.4	1.2	6119	4	US-09-902-540-713	Sequence 713, App
c 224	37.4	1.2	41815	4	US-09-949-016-17447	Sequence 17447, A
225	37.2	1.2	1293	4	US-09-902-540-7230	Sequence 7230, Ap
226	37.2	1.2	4486	4	US-09-902-540-677	Sequence 677, App
227	37.2	1.2	50341	1	US-08-247-901C-1	Sequence 1, Appli
228	37.2	1.2	50341	2	US-09-075-904-1	Sequence 1, Appli
229	37.2	1.2	52297	3	US-09-426-436-1	Sequence 1, Appli
230	37.2	1.2	52297	3	US-08-705-557-1	Sequence 1, Appli
231	37	1.2	537	4	US-09-902-540-3308	Sequence 3308, Ap
c 232	37	1.2	832	4	US-09-621-976-2813	Sequence 2813, Ap
233	37	1.2	1249	3	US-09-333-208-1	Sequence 1, Appli
234	37	1.2	1249	3	US-09-333-254-1	Sequence 1, Appli
235	37	1.2	1249	3	US-09-183-270-1	Sequence 1, Appli
236	37	1.2	1286	4	US-09-489-847-124	Sequence 124, App
237	37	1.2	1288	4	US-09-205-258-125	Sequence 125, App
238	37	1.2	1371	4	US-09-902-540-9043	Sequence 9043, Ap
c 239	37	1.2	11295	4	US-09-902-540-967	Sequence 967, App

240	37	1.2	15351	4	US-09-902-540-1154	Sequence 1154, Ap
c 241	37	1.2	28374	4	US-09-949-016-17508	Sequence 17508, A
c 242	36.8	1.2	289	3	US-09-007-005-17	Sequence 17, Appl
c 243	36.8	1.2	289	3	US-09-244-796-17	Sequence 17, Appl
c 244	36.8	1.2	420	4	US-09-471-276-797	Sequence 797, App
245	36.8	1.2	465	4	US-09-902-540-4894	Sequence 4894, Ap
246	36.8	1.2	660	4	US-09-902-540-6872	Sequence 6872, Ap
247	36.8	1.2	707	3	US-08-998-416-940	Sequence 940, App
248	36.8	1.2	948	4	US-09-902-540-8588	Sequence 8588, Ap
249	36.8	1.2	1173	4	US-09-902-540-7901	Sequence 7901, Ap
250	36.8	1.2	1192	4	US-09-692-081-1	Sequence 1, Appli
251	36.8	1.2	1410	4	US-09-620-312D-1005	Sequence 1005, Ap
252	36.8	1.2	1644	4	US-09-902-540-4613	Sequence 4613, Ap
253	36.8	1.2	1888	4	US-09-949-016-3772	Sequence 3772, Ap
254	36.8	1.2	2771	4	US-09-016-434-1101	Sequence 1101, Ap
c 255	36.8	1.2	4019	4	US-09-902-540-583	Sequence 583, App
256	36.8	1.2	4941	4	US-09-902-540-7814	Sequence 7814, Ap
c 257	36.8	1.2	6603	4	US-09-902-540-796	Sequence 796, App
c 258	36.8	1.2	7650	4	US-09-902-540-779	Sequence 779, App
259	36.8	1.2	9499	4	US-09-949-016-15514	Sequence 15514, A
c 260	36.8	1.2	12955	4	US-09-902-540-1068	Sequence 1068, Ap
c 261	36.8	1.2	27490	4	US-09-902-540-1227	Sequence 1227, Ap
262	36.8	1.2	28493	4	US-09-902-540-1241	Sequence 1241, Ap
c 263	36.8	1.2	87617	4	US-09-949-016-16551	Sequence 16551, A
264	36.6	1.2	555	4	US-09-902-540-8998	Sequence 8998, Ap
c 265	36.6	1.2	601	4	US-09-949-001-403	Sequence 403, App
266	36.6	1.2	1294	4	US-10-151-832-4	Sequence 4, Appli
267	36.6	1.2	10692	4	US-09-902-540-960	Sequence 960, App
268	36.6	1.2	30922	4	US-09-949-016-16700	Sequence 16700, A
269	36.4	1.2	399	4	US-09-621-976-8976	Sequence 8976, Ap
270	36.4	1.2	601	4	US-09-949-016-46540	Sequence 46540, A
271	36.4	1.2	601	4	US-09-949-016-113556	Sequence 113556,
272	36.4	1.2	186734	4	US-09-949-016-14870	Sequence 14870, A
273	36.4	1.2	193689	4	US-09-949-016-12350	Sequence 12350, A
274	36.4	1.2	193689	4	US-09-949-016-13088	Sequence 13088, A
c 275	36.4	1.2	247299	4	US-09-949-016-17590	Sequence 17590, A
c 276	36.4	1.2	4403765	3	US-09-103-840A-2	Sequence 2, Appli
c 277	36.4	1.2	4411529	3	US-09-103-840A-1	Sequence 1, Appli
278	36.2	1.2	399	4	US-09-902-540-8378	Sequence 8378, Ap
c 279	36.2	1.2	601	4	US-09-949-016-175071	Sequence 175071,
280	36.2	1.2	963	4	US-09-252-991A-6624	Sequence 6624, Ap
281	36.2	1.2	1047	4	US-09-252-991A-6577	Sequence 6577, Ap
c 282	36.2	1.2	1364	1	US-08-306-691B-50	Sequence 50, Appl
c 283	36.2	1.2	1364	4	US-09-023-655-1372	Sequence 1372, Ap
c 284	36.2	1.2	1364	5	PCT-US93-06251-65	Sequence 65, Appl
c 285	36.2	1.2	1437	4	US-09-252-991A-6640	Sequence 6640, Ap
286	36.2	1.2	3256	4	US-09-719-085A-3	Sequence 3, Appli
c 287	36.2	1.2	7035	4	US-09-902-540-878	Sequence 878, App
288	36.2	1.2	360470	4	US-09-949-016-13173	Sequence 13173, A
289	36	1.1	330	4	US-09-252-991A-9667	Sequence 9667, Ap
c 290	36	1.1	462	4	US-09-252-991A-9543	Sequence 9543, Ap
c 291	36	1.1	474	4	US-09-252-991A-14040	Sequence 14040, A
292	36	1.1	561	4	US-09-252-991A-9743	Sequence 9743, Ap
c 293	36	1.1	601	4	US-09-949-016-70548	Sequence 70548, A
294	36	1.1	801	4	US-09-252-991A-1264	Sequence 1264, Ap
295	36	1.1	1035	4	US-09-252-991A-14224	Sequence 14224, A
c 296	36	1.1	1230	4	US-09-252-991A-1339	Sequence 1339, Ap

c 297	36	1.1	1233	4	US-09-252-991A-13999	Sequence 13999, A
298	36	1.1	1722	4	US-09-902-540-4876	Sequence 4876, Ap
299	36	1.1	1794	4	US-09-252-991A-8647	Sequence 8647, Ap
c 300	36	1.1	1869	4	US-09-252-991A-1298	Sequence 1298, Ap
301	36	1.1	1911	4	US-09-252-991A-14136	Sequence 14136, A
c 302	36	1.1	2274	4	US-09-252-991A-15970	Sequence 15970, A
303	36	1.1	2298	4	US-09-252-991A-1176	Sequence 1176, Ap
304	36	1.1	2385	1	US-08-393-333-1	Sequence 1, Appli
305	36	1.1	2782	4	US-09-963-137-158	Sequence 158, App
306	36	1.1	2782	4	US-09-949-016-968	Sequence 968, App
307	36	1.1	2783	4	US-09-949-016-5541	Sequence 5541, Ap
308	36	1.1	3120	4	US-09-417-197-54	Sequence 54, Appl
309	36	1.1	3138	4	US-09-417-197-78	Sequence 78, Appl
310	36	1.1	3675	4	US-09-252-991A-16309	Sequence 16309, A
311	36	1.1	3714	3	US-09-087-465-9	Sequence 9, Appli
312	36	1.1	3714	4	US-09-023-655-1470	Sequence 1470, Ap
313	36	1.1	4279	4	US-09-814-915A-97	Sequence 97, Appl
314	36	1.1	4281	4	US-09-949-016-5539	Sequence 5539, Ap
315	36	1.1	28378	4	US-09-949-016-17281	Sequence 17281, A
316	36	1.1	28509	4	US-09-902-540-1240	Sequence 1240, Ap
317	36	1.1	78720	4	US-09-949-016-12710	Sequence 12710, A
318	36	1.1	78720	4	US-09-949-016-17283	Sequence 17283, A
c 319	36	1.1	126200	4	US-09-949-016-11824	Sequence 11824, A
c 320	36	1.1	126200	4	US-09-949-016-13193	Sequence 13193, A
c 321	36	1.1	222452	4	US-09-949-016-12968	Sequence 12968, A
322	35.8	1.1	601	4	US-09-949-016-204613	Sequence 204613,
323	35.8	1.1	1831	1	US-10-095-946-7	Sequence 7, Appli
324	35.8	1.1	1831	3	US-09-183-959-7	Sequence 7, Appli
325	35.8	1.1	1831	4	US-09-535-315-7	Sequence 7, Appli
326	35.8	1.1	1841	4	US-09-347-650-5	Sequence 5, Appli
327	35.8	1.1	2088	1	US-08-331-394-1	Sequence 1, Appli
328	35.8	1.1	2088	1	US-08-250-858-1	Sequence 1, Appli
329	35.8	1.1	2088	1	US-08-446-915-1	Sequence 1, Appli
330	35.8	1.1	2088	2	US-08-744-139-1	Sequence 1, Appli
331	35.8	1.1	2088	4	US-08-779-599-1	Sequence 1, Appli
332	35.8	1.1	2088	5	PCT-US95-06639-1	Sequence 1, Appli
333	35.8	1.1	3292	3	US-09-320-878-22	Sequence 22, Appl
334	35.8	1.1	3292	4	US-09-141-908-15	Sequence 15, Appl
335	35.8	1.1	3292	4	US-09-657-440-22	Sequence 22, Appl
c 336	35.8	1.1	3723	4	US-09-904-065-3	Sequence 3, Appli
337	35.8	1.1	4089	1	US-07-908-245-1	Sequence 1, Appli
338	35.8	1.1	13711	4	US-09-949-016-11798	Sequence 11798, A
339	35.8	1.1	15702	4	US-09-949-016-15518	Sequence 15518, A
c 340	35.8	1.1	41170	4	US-09-902-540-1267	Sequence 1267, Ap
c 341	35.8	1.1	154746	4	US-09-827-688-8	Sequence 8, Appli
c 342	35.6	1.1	601	4	US-09-949-016-26288	Sequence 26288, A
c 343	35.6	1.1	601	4	US-09-949-016-26289	Sequence 26289, A
c 344	35.6	1.1	601	4	US-09-949-016-169812	Sequence 169812,
c 345	35.6	1.1	601	4	US-09-949-016-169813	Sequence 169813,
c 346	35.6	1.1	798	4	US-09-252-991A-11152	Sequence 11152, A
c 347	35.6	1.1	954	4	US-09-252-991A-14555	Sequence 14555, A
c 348	35.6	1.1	1473	4	US-09-252-991A-14687	Sequence 14687, A
c 349	35.6	1.1	1473	4	US-09-902-540-5372	Sequence 5372, Ap
350	35.6	1.1	1491	4	US-09-252-991A-15068	Sequence 15068, A
c 351	35.6	1.1	2205	4	US-09-252-991A-11217	Sequence 11217, A
352	35.6	1.1	2454	4	US-09-252-991A-11038	Sequence 11038, A
353	35.6	1.1	4084	4	US-09-902-540-697	Sequence 697, App

354	35.6	1.1	34662	4	US-09-902-540-1261	Sequence 1261, Ap
355	35.6	1.1	175236	4	US-09-949-016-14353	Sequence 14353, A
c 356	35.4	1.1	505	4	US-09-621-976-15639	Sequence 15639, A
c 357	35.4	1.1	594	4	US-09-252-991A-9966	Sequence 9966, Ap
358	35.4	1.1	1350	4	US-09-252-991A-10184	Sequence 10184, A
359	35.4	1.1	2823	4	US-09-919-497-7	Sequence 7, Appli
360	35.4	1.1	3358	3	US-09-248-571-2	Sequence 2, Appli
361	35.4	1.1	3358	3	US-09-553-736-2	Sequence 2, Appli
362	35.4	1.1	3639	4	US-09-252-991A-10045	Sequence 10045, A
c 363	35.4	1.1	3717	4	US-09-252-991A-9792	Sequence 9792, Ap
c 364	35.4	1.1	312957	4	US-09-949-001-31	Sequence 31, Appl
c 365	35.4	1.1	312972	4	US-09-949-001-34	Sequence 34, Appl
366	35.2	1.1	357	4	US-09-252-991A-8773	Sequence 8773, Ap
367	35.2	1.1	564	4	US-09-252-991A-15637	Sequence 15637, A
368	35.2	1.1	601	4	US-09-949-016-21142	Sequence 21142, A
369	35.2	1.1	601	4	US-09-949-016-21143	Sequence 21143, A
c 370	35.2	1.1	601	4	US-09-949-016-42622	Sequence 42622, A
c 371	35.2	1.1	601	4	US-09-949-016-42623	Sequence 42623, A
c 372	35.2	1.1	601	4	US-09-949-016-42654	Sequence 42654, A
c 373	35.2	1.1	601	4	US-09-949-016-42655	Sequence 42655, A
c 374	35.2	1.1	601	4	US-09-949-016-42686	Sequence 42686, A
c 375	35.2	1.1	601	4	US-09-949-016-42687	Sequence 42687, A
c 376	35.2	1.1	601	4	US-09-949-016-42718	Sequence 42718, A
c 377	35.2	1.1	601	4	US-09-949-016-42719	Sequence 42719, A
c 378	35.2	1.1	601	4	US-09-949-016-42750	Sequence 42750, A
c 379	35.2	1.1	601	4	US-09-949-016-42751	Sequence 42751, A
c 380	35.2	1.1	601	4	US-09-949-016-42782	Sequence 42782, A
c 381	35.2	1.1	601	4	US-09-949-016-42783	Sequence 42783, A
382	35.2	1.1	601	4	US-09-949-016-47510	Sequence 47510, A
383	35.2	1.1	601	4	US-09-949-016-47511	Sequence 47511, A
c 384	35.2	1.1	601	4	US-09-949-016-93576	Sequence 93576, A
c 385	35.2	1.1	601	4	US-09-949-016-93577	Sequence 93577, A
c 386	35.2	1.1	601	4	US-09-949-016-93608	Sequence 93608, A
c 387	35.2	1.1	601	4	US-09-949-016-93609	Sequence 93609, A
c 388	35.2	1.1	601	4	US-09-949-016-93640	Sequence 93640, A
c 389	35.2	1.1	601	4	US-09-949-016-93641	Sequence 93641, A
c 390	35.2	1.1	601	4	US-09-949-016-93672	Sequence 93672, A
c 391	35.2	1.1	601	4	US-09-949-016-93673	Sequence 93673, A
c 392	35.2	1.1	601	4	US-09-949-016-93704	Sequence 93704, A
c 393	35.2	1.1	601	4	US-09-949-016-93705	Sequence 93705, A
c 394	35.2	1.1	601	4	US-09-949-016-93736	Sequence 93736, A
c 395	35.2	1.1	601	4	US-09-949-016-93737	Sequence 93737, A
c 396	35.2	1.1	993	4	US-09-016-434-1069	Sequence 1069, Ap
c 397	35.2	1.1	993	4	US-09-023-655-884	Sequence 884, App
398	35.2	1.1	1140	3	US-09-105-537-15	Sequence 15, Appl
c 399	35.2	1.1	1206	4	US-09-949-016-5866	Sequence 5866, Ap
400	35.2	1.1	1615	4	US-09-270-767-30509	Sequence 30509, A
401	35.2	1.1	2022	4	US-09-252-991A-8890	Sequence 8890, Ap
402	35.2	1.1	2033	1	US-08-148-910-14	Sequence 14, Appl
403	35.2	1.1	2033	1	US-08-448-937A-14	Sequence 14, Appl
404	35.2	1.1	2286	4	US-09-270-767-14355	Sequence 14355, A
405	35.2	1.1	2325	1	US-08-314-309A-20	Sequence 20, Appl
406	35.2	1.1	3376	4	US-09-620-312D-116	Sequence 116, App
407	35.2	1.1	3442	4	US-09-620-312D-115	Sequence 115, App
c 408	35.2	1.1	6573	4	US-09-252-991A-9183	Sequence 9183, Ap
c 409	35.2	1.1	8831	4	US-09-949-016-17608	Sequence 17608, A
c 410	35.2	1.1	13613	3	US-09-105-537-3	Sequence 3, Appli

c 411	35.2	1.1	31467	4	US-09-949-016-13134	Sequence 13134, A
c 412	35.2	1.1	31868	4	US-09-949-016-11907	Sequence 11907, A
413	35.2	1.1	32068	4	US-09-949-016-12970	Sequence 12970, A
414	35.2	1.1	32068	4	US-09-949-016-12971	Sequence 12971, A
415	35.2	1.1	32068	4	US-09-949-016-12972	Sequence 12972, A
416	35.2	1.1	32068	4	US-09-949-016-12973	Sequence 12973, A
417	35.2	1.1	32068	4	US-09-949-016-12974	Sequence 12974, A
418	35.2	1.1	32068	4	US-09-949-016-12975	Sequence 12975, A
419	35.2	1.1	32068	4	US-09-949-016-14436	Sequence 14436, A
420	35.2	1.1	32068	4	US-09-949-016-14437	Sequence 14437, A
421	35.2	1.1	32068	4	US-09-949-016-14438	Sequence 14438, A
422	35.2	1.1	32068	4	US-09-949-016-14439	Sequence 14439, A
423	35.2	1.1	32068	4	US-09-949-016-14440	Sequence 14440, A
424	35.2	1.1	32068	4	US-09-949-016-14441	Sequence 14441, A
c 425	35.2	1.1	42693	4	US-09-949-016-17317	Sequence 17317, A
c 426	35.2	1.1	42693	4	US-09-949-016-17318	Sequence 17318, A
427	35.2	1.1	64377	4	US-09-949-016-15212	Sequence 15212, A
428	35.2	1.1	64377	4	US-09-949-016-15213	Sequence 15213, A
429	35.2	1.1	64377	4	US-09-949-016-15214	Sequence 15214, A
430	35.2	1.1	64377	4	US-09-949-016-15215	Sequence 15215, A
431	35.2	1.1	64377	4	US-09-949-016-15216	Sequence 15216, A
432	35.2	1.1	74804	4	US-09-949-016-15118	Sequence 15118, A
c 433	35	1.1	1034	4	US-09-673-395A-7	Sequence 7, Appli
434	35	1.1	1111	4	US-09-774-528-387	Sequence 387, App
435	35	1.1	1656	4	US-09-902-540-3251	Sequence 3251, Ap
436	35	1.1	1920	4	US-09-252-991A-7122	Sequence 7122, Ap
c 437	35	1.1	2004	1	US-08-471-033-18	Sequence 18, Appl
c 438	35	1.1	2004	2	US-08-471-044-18	Sequence 18, Appl
c 439	35	1.1	2004	2	US-08-463-483A-18	Sequence 18, Appl
c 440	35	1.1	2004	2	US-08-471-046A-18	Sequence 18, Appl
c 441	35	1.1	2004	2	US-08-470-566B-18	Sequence 18, Appl
c 442	35	1.1	2004	2	US-08-469-334-18	Sequence 18, Appl
c 443	35	1.1	2004	3	US-09-300-529-18	Sequence 18, Appl
444	35	1.1	2160	4	US-09-252-991A-7089	Sequence 7089, Ap
c 445	35	1.1	2576	1	US-08-471-033-35	Sequence 35, Appl
c 446	35	1.1	2576	2	US-08-471-044-35	Sequence 35, Appl
c 447	35	1.1	2576	2	US-08-463-483A-35	Sequence 35, Appl
c 448	35	1.1	2576	2	US-08-471-046A-35	Sequence 35, Appl
c 449	35	1.1	2576	2	US-08-470-566B-35	Sequence 35, Appl
c 450	35	1.1	2576	2	US-08-469-334-35	Sequence 35, Appl
c 451	35	1.1	2576	3	US-09-300-529-35	Sequence 35, Appl
c 452	35	1.1	2655	1	US-08-471-033-17	Sequence 17, Appl
c 453	35	1.1	2655	1	US-08-471-033-26	Sequence 26, Appl
c 454	35	1.1	2655	2	US-08-471-044-17	Sequence 17, Appl
c 455	35	1.1	2655	2	US-08-471-044-26	Sequence 26, Appl
c 456	35	1.1	2655	2	US-08-463-483A-17	Sequence 17, Appl
c 457	35	1.1	2655	2	US-08-463-483A-26	Sequence 26, Appl
c 458	35	1.1	2655	2	US-08-471-046A-17	Sequence 17, Appl
c 459	35	1.1	2655	2	US-08-471-046A-26	Sequence 26, Appl
c 460	35	1.1	2655	2	US-08-470-566B-17	Sequence 17, Appl
c 461	35	1.1	2655	2	US-08-470-566B-26	Sequence 26, Appl
c 462	35	1.1	2655	2	US-08-469-334-17	Sequence 17, Appl
c 463	35	1.1	2655	2	US-08-469-334-26	Sequence 26, Appl
c 464	35	1.1	2655	3	US-09-300-529-17	Sequence 17, Appl
c 465	35	1.1	2655	3	US-09-300-529-26	Sequence 26, Appl
c 466	35	1.1	4031	1	US-08-471-033-49	Sequence 49, Appl
c 467	35	1.1	4031	2	US-08-471-044-49	Sequence 49, Appl

c 468	35	1.1	4031	2	US-08-463-483A-49	Sequence 49, Appl
c 469	35	1.1	4031	2	US-08-471-046A-49	Sequence 49, Appl
c 470	35	1.1	4031	2	US-08-470-566B-49	Sequence 49, Appl
c 471	35	1.1	4031	2	US-08-469-334-49	Sequence 49, Appl
c 472	35	1.1	4031	3	US-09-300-529-49	Sequence 49, Appl
473	35	1.1	5523	4	US-09-902-540-3952	Sequence 3952, Ap
474	35	1.1	6226	1	US-08-542-363-1	Sequence 1, Appli
475	35	1.1	6226	3	US-09-100-089-1	Sequence 1, Appli
476	35	1.1	6226	3	US-09-670-827-1	Sequence 1, Appli
477	35	1.1	6226	4	US-09-827-949-1	Sequence 1, Appli
478	35	1.1	15849	4	US-09-054-272-50	Sequence 50, Appl
479	35	1.1	17628	4	US-09-949-016-16718	Sequence 16718, A
480	35	1.1	19954	4	US-09-902-540-1150	Sequence 1150, Ap
481	35	1.1	22156	4	US-09-902-540-1195	Sequence 1195, Ap
482	35	1.1	151256	4	US-09-949-016-12674	Sequence 12674, A
483	35	1.1	151261	4	US-09-949-016-13242	Sequence 13242, A
c 484	34.8	1.1	519	4	US-09-252-991A-3176	Sequence 3176, Ap
c 485	34.8	1.1	553	4	US-09-621-976-15491	Sequence 15491, A
c 486	34.8	1.1	601	4	US-09-949-016-122924	Sequence 122924,
c 487	34.8	1.1	601	4	US-09-949-016-123018	Sequence 123018,
c 488	34.8	1.1	601	4	US-09-949-016-123112	Sequence 123112,
c 489	34.8	1.1	601	4	US-09-949-016-123206	Sequence 123206,
c 490	34.8	1.1	601	4	US-09-949-016-123300	Sequence 123300,
491	34.8	1.1	1001	3	US-09-641-638-176	Sequence 176, App
492	34.8	1.1	1001	3	US-09-641-638-177	Sequence 177, App
493	34.8	1.1	1001	3	US-09-641-638-178	Sequence 178, App
494	34.8	1.1	1001	4	US-10-170-097-176	Sequence 176, App
495	34.8	1.1	1001	4	US-10-170-097-177	Sequence 177, App
496	34.8	1.1	1001	4	US-10-170-097-178	Sequence 178, App
c 497	34.8	1.1	1023	3	US-08-554-385-4	Sequence 4, Appli
c 498	34.8	1.1	1059	4	US-09-902-540-3651	Sequence 3651, Ap
499	34.8	1.1	1251	4	US-09-252-991A-11825	Sequence 11825, A
500	34.8	1.1	1414	4	US-09-270-767-15271	Sequence 15271, A
501	34.8	1.1	1629	4	US-09-252-991A-2699	Sequence 2699, Ap
c 502	34.8	1.1	1629	4	US-09-252-991A-2986	Sequence 2986, Ap
503	34.8	1.1	1725	4	US-09-252-991A-2884	Sequence 2884, Ap
c 504	34.8	1.1	1734	4	US-09-252-991A-11562	Sequence 11562, A
505	34.8	1.1	2187	4	US-09-252-991A-11888	Sequence 11888, A
c 506	34.8	1.1	4484	4	US-09-949-016-4498	Sequence 4498, Ap
507	34.8	1.1	6763	2	US-08-756-506-23	Sequence 23, Appl
508	34.8	1.1	10807	1	US-08-206-176-7	Sequence 7, Appli
509	34.8	1.1	10807	2	US-08-756-506-5	Sequence 5, Appli
510	34.8	1.1	15840	4	US-09-902-540-1134	Sequence 1134, Ap
c 511	34.8	1.1	16563	4	US-09-902-540-2000	Sequence 2000, Ap
512	34.8	1.1	16844	4	US-09-902-540-1176	Sequence 1176, Ap
c 513	34.8	1.1	33529	3	US-09-144-085-3	Sequence 3, Appli
514	34.8	1.1	87323	4	US-09-949-016-13828	Sequence 13828, A
c 515	34.8	1.1	151088	4	US-09-949-016-16240	Sequence 16240, A
c 516	34.6	1.1	427	4	US-09-513-597A-17	Sequence 17, Appl
c 517	34.6	1.1	601	4	US-09-949-016-33259	Sequence 33259, A
c 518	34.6	1.1	601	4	US-09-949-016-37029	Sequence 37029, A
c 519	34.6	1.1	601	4	US-09-949-016-59751	Sequence 59751, A
c 520	34.6	1.1	601	4	US-09-949-016-59768	Sequence 59768, A
521	34.6	1.1	623	4	US-09-902-540-9106	Sequence 9106, Ap
c 522	34.6	1.1	693	4	US-09-252-991A-11186	Sequence 11186, A
c 523	34.6	1.1	798	4	US-09-252-991A-2555	Sequence 2555, Ap
524	34.6	1.1	804	4	US-09-902-540-7794	Sequence 7794, Ap

525	34.6	1.1	831	4	US-09-902-540-7708	Sequence 7708, Ap
526	34.6	1.1	855	4	US-09-252-991A-11001	Sequence 11001, A
527	34.6	1.1	930	4	US-09-252-991A-11070	Sequence 11070, A
528	34.6	1.1	948	2	US-08-924-759-11	Sequence 11, Appl
529	34.6	1.1	948	3	US-09-248-335-11	Sequence 11, Appl
530	34.6	1.1	1482	4	US-09-252-991A-8923	Sequence 8923, Ap
c 531	34.6	1.1	1509	4	US-09-799-451-644	Sequence 644, App
c 532	34.6	1.1	1551	4	US-09-252-991A-2474	Sequence 2474, Ap
533	34.6	1.1	1560	4	US-09-252-991A-2199	Sequence 2199, Ap
c 534	34.6	1.1	1782	4	US-09-252-991A-9072	Sequence 9072, Ap
c 535	34.6	1.1	1825	4	US-09-907-794A-1	Sequence 1, Appli
c 536	34.6	1.1	1825	4	US-09-905-125A-1	Sequence 1, Appli
c 537	34.6	1.1	1825	4	US-09-902-775A-1	Sequence 1, Appli
c 538	34.6	1.1	1825	4	US-09-906-700-1	Sequence 1, Appli
c 539	34.6	1.1	1825	4	US-09-903-603A-1	Sequence 1, Appli
c 540	34.6	1.1	1825	4	US-09-904-920A-1	Sequence 1, Appli
c 541	34.6	1.1	1825	4	US-09-909-064-1	Sequence 1, Appli
c 542	34.6	1.1	1825	4	US-09-905-381A-1	Sequence 1, Appli
c 543	34.6	1.1	1825	4	US-09-906-618-1	Sequence 1, Appli
544	34.6	1.1	1889	4	US-09-774-528-247	Sequence 247, App
c 545	34.6	1.1	2121	4	US-09-252-991A-9159	Sequence 9159, Ap
c 546	34.6	1.1	2138	4	US-09-949-016-4729	Sequence 4729, Ap
547	34.6	1.1	3090	3	US-09-276-531-78	Sequence 78, Appl
c 548	34.6	1.1	3536	4	US-09-949-016-1083	Sequence 1083, Ap
c 549	34.6	1.1	5717	4	US-09-902-540-776	Sequence 776, App
c 550	34.6	1.1	6611	4	US-09-902-540-762	Sequence 762, App
551	34.6	1.1	9369	4	US-10-237-551-190	Sequence 190, App
552	34.6	1.1	9369	4	US-10-237-551-247	Sequence 247, App
553	34.6	1.1	10318	4	US-09-902-540-973	Sequence 973, App
c 554	34.6	1.1	11766	4	US-09-949-016-12531	Sequence 12531, A
c 555	34.6	1.1	11770	4	US-09-949-016-12720	Sequence 12720, A
c 556	34.6	1.1	11770	4	US-09-949-016-13487	Sequence 13487, A
c 557	34.6	1.1	11770	4	US-09-949-016-13488	Sequence 13488, A
558	34.6	1.1	87734	4	US-09-949-016-17521	Sequence 17521, A
559	34.6	1.1	114793	4	US-10-148-806-3	Sequence 3, Appli
560	34.4	1.1	504	4	US-09-902-540-3859	Sequence 3859, Ap
c 561	34.4	1.1	837	4	US-09-252-991A-15872	Sequence 15872, A
562	34.4	1.1	1158	4	US-09-252-991A-15820	Sequence 15820, A
563	34.4	1.1	1242	4	US-09-902-540-8726	Sequence 8726, Ap
564	34.4	1.1	1386	4	US-09-252-991A-6858	Sequence 6858, Ap
565	34.4	1.1	1446	3	US-09-491-772-6	Sequence 6, Appli
c 566	34.4	1.1	1980	4	US-09-252-991A-6896	Sequence 6896, Ap
567	34.4	1.1	2034	2	US-08-559-492-2	Sequence 2, Appli
c 568	34.4	1.1	2970	4	US-09-252-991A-15898	Sequence 15898, A
569	34.4	1.1	8207	4	US-09-902-540-925	Sequence 925, App
570	34.4	1.1	8580	3	US-09-491-772-1	Sequence 1, Appli
c 571	34.4	1.1	21964	4	US-09-902-540-1190	Sequence 1190, Ap
c 572	34.4	1.1	246240	2	US-08-724-394A-20	Sequence 20, Appl
c 573	34.4	1.1	246240	2	US-08-724-394A-21	Sequence 21, Appl
c 574	34.4	1.1	246240	2	US-08-724-394A-22	Sequence 22, Appl
c 575	34.2	1.1	285	4	US-09-252-991A-11646	Sequence 11646, A
576	34.2	1.1	299	4	US-09-313-294A-5947	Sequence 5947, Ap
c 577	34.2	1.1	430	4	US-09-621-976-16656	Sequence 16656, A
578	34.2	1.1	456	4	US-09-252-991A-14211	Sequence 14211, A
579	34.2	1.1	729	4	US-09-252-991A-11790	Sequence 11790, A
c 580	34.2	1.1	927	4	US-09-902-540-8306	Sequence 8306, Ap
581	34.2	1.1	975	4	US-09-902-540-3743	Sequence 3743, Ap

582	34.2	1.1	1096	4	US-09-270-767-14940	Sequence 14940, A
c 583	34.2	1.1	1200	4	US-09-252-991A-14709	Sequence 14709, A
584	34.2	1.1	1215	4	US-09-902-540-5031	Sequence 5031, Ap
585	34.2	1.1	1260	4	US-09-252-991A-11855	Sequence 11855, A
586	34.2	1.1	1278	4	US-09-252-991A-14164	Sequence 14164, A
587	34.2	1.1	1290	4	US-09-252-991A-15040	Sequence 15040, A
588	34.2	1.1	1449	4	US-09-252-991A-14921	Sequence 14921, A
c 589	34.2	1.1	1781	4	US-09-461-325-21	Sequence 21, Appl
c 590	34.2	1.1	1781	4	US-10-012-542-21	Sequence 21, Appl
c 591	34.2	1.1	1781	4	US-10-115-123-21	Sequence 21, Appl
c 592	34.2	1.1	1847	4	US-09-949-016-2255	Sequence 2255, Ap
c 593	34.2	1.1	1971	4	US-09-252-991A-14059	Sequence 14059, A
594	34.2	1.1	2046	4	US-09-252-991A-7996	Sequence 7996, Ap
595	34.2	1.1	2046	4	US-09-252-991A-8058	Sequence 8058, Ap
596	34.2	1.1	2194	3	US-09-310-463-19	Sequence 19, Appl
597	34.2	1.1	2194	3	US-08-842-248A-19	Sequence 19, Appl
598	34.2	1.1	2659	4	US-09-902-540-4695	Sequence 4695, Ap
c 599	34.2	1.1	3138	3	US-09-434-408-1	Sequence 1, Appli
600	34.2	1.1	3638	3	US-09-369-364A-8	Sequence 8, Appli
c 601	34.2	1.1	6339	4	US-09-902-540-866	Sequence 866, App
602	34.2	1.1	7826	4	US-09-902-540-860	Sequence 860, App
c 603	34.2	1.1	13644	4	US-09-949-016-13997	Sequence 13997, A
604	34.2	1.1	17897	4	US-09-902-540-1182	Sequence 1182, Ap
c 605	34.2	1.1	28054	4	US-09-902-540-1248	Sequence 1248, Ap
606	34.2	1.1	28558	4	US-09-902-540-1231	Sequence 1231, Ap
c 607	34.2	1.1	43267	4	US-09-949-016-17117	Sequence 17117, A
c 608	34.2	1.1	54576	4	US-09-949-016-15954	Sequence 15954, A
c 609	34.2	1.1	54576	4	US-09-949-016-15955	Sequence 15955, A
c 610	34.2	1.1	319608	4	US-09-539-333D-1	Sequence 1, Appli
c 611	34.2	1.1	319608	4	US-09-679-409-1	Sequence 1, Appli
c 612	34	1.1	399	4	US-09-621-976-8976	Sequence 8976, Ap
c 613	34	1.1	459	4	US-09-902-540-2412	Sequence 2412, Ap
614	34	1.1	522	3	US-08-928-917C-3	Sequence 3, Appli
615	34	1.1	522	3	US-09-374-678-3	Sequence 3, Appli
616	34	1.1	591	3	US-08-928-917C-5	Sequence 5, Appli
617	34	1.1	591	3	US-09-374-678-5	Sequence 5, Appli
618	34	1.1	594	4	US-09-252-991A-14647	Sequence 14647, A
c 619	34	1.1	601	4	US-09-949-016-47171	Sequence 47171, A
c 620	34	1.1	690	4	US-09-252-991A-15110	Sequence 15110, A
621	34	1.1	753	3	US-08-928-917C-7	Sequence 7, Appli
622	34	1.1	753	3	US-09-374-678-7	Sequence 7, Appli
623	34	1.1	894	4	US-09-902-540-5954	Sequence 5954, Ap
624	34	1.1	984	4	US-09-489-039A-4965	Sequence 4965, Ap
c 625	34	1.1	1074	4	US-09-949-016-3126	Sequence 3126, Ap
c 626	34	1.1	1107	4	US-09-252-991A-4153	Sequence 4153, Ap
627	34	1.1	1320	4	US-09-727-238-1	Sequence 1, Appli
c 628	34	1.1	1381	2	US-08-950-449A-13	Sequence 13, Appl
c 629	34	1.1	1423	1	US-08-469-421-13	Sequence 13, Appl
c 630	34	1.1	1423	1	US-08-250-975-13	Sequence 13, Appl
c 631	34	1.1	1423	2	US-08-605-002A-13	Sequence 13, Appl
c 632	34	1.1	1423	3	US-08-943-353-13	Sequence 13, Appl
c 633	34	1.1	1423	5	PCT-US94-10529-13	Sequence 13, Appl
634	34	1.1	1761	4	US-09-252-991A-7943	Sequence 7943, Ap
635	34	1.1	1857	4	US-09-949-016-1440	Sequence 1440, Ap
636	34	1.1	2463	4	US-09-902-540-9229	Sequence 9229, Ap
637	34	1.1	2464	1	US-07-863-169A-4	Sequence 4, Appli
638	34	1.1	2464	2	US-08-429-964-4	Sequence 4, Appli

639	34	1.1	2464	3	US-07-935-087-4	Sequence 4, Appli
640	34	1.1	2464	5	PCT-US93-08062-4	Sequence 4, Appli
c 641	34	1.1	2718	4	US-09-252-991A-7538	Sequence 7538, Ap
642	34	1.1	2940	4	US-09-963-137-132	Sequence 132, App
643	34	1.1	3351	4	US-09-252-991A-7803	Sequence 7803, Ap
c 644	34	1.1	3757	4	US-09-949-016-188	Sequence 188, App
c 645	34	1.1	3774	2	US-08-950-449A-11	Sequence 11, Appl
c 646	34	1.1	3813	1	US-08-469-421-11	Sequence 11, Appl
c 647	34	1.1	3813	1	US-08-250-975-11	Sequence 11, Appl
c 648	34	1.1	3813	2	US-08-605-002A-11	Sequence 11, Appl
c 649	34	1.1	3813	3	US-08-943-353-11	Sequence 11, Appl
c 650	34	1.1	3813	5	PCT-US94-10529-11	Sequence 11, Appl
651	34	1.1	3954	4	US-09-902-540-5203	Sequence 5203, Ap
c 652	34	1.1	4747	4	US-09-854-133-729	Sequence 729, App
c 653	34	1.1	5828	4	US-09-023-655-1386	Sequence 1386, Ap
c 654	34	1.1	5828	4	US-09-903-248-6	Sequence 6, Appli
c 655	34	1.1	5828	4	US-09-903-199-6	Sequence 6, Appli
c 656	34	1.1	5828	4	US-09-903-216-6	Sequence 6, Appli
c 657	34	1.1	5828	4	US-09-903-063-6	Sequence 6, Appli
c 658	34	1.1	5828	4	US-09-859-604-6	Sequence 6, Appli
c 659	34	1.1	5904	1	US-08-309-512-1	Sequence 1, Appli
c 660	34	1.1	5904	5	PCT-US92-08756A-1	Sequence 1, Appli
c 661	34	1.1	6306	1	US-08-466-390-3	Sequence 3, Appli
c 662	34	1.1	6306	1	US-08-470-950-3	Sequence 3, Appli
c 663	34	1.1	6306	1	US-08-467-781-3	Sequence 3, Appli
c 664	34	1.1	6306	1	US-08-195-487-3	Sequence 3, Appli
c 665	34	1.1	6306	2	US-08-483-924-3	Sequence 3, Appli
c 666	34	1.1	6306	5	PCT-US93-06160-3	Sequence 3, Appli
c 667	34	1.1	7218	4	US-09-949-016-1775	Sequence 1775, Ap
c 668	34	1.1	7218	4	US-09-949-016-1776	Sequence 1776, Ap
669	34	1.1	10505	4	US-09-902-540-1044	Sequence 1044, Ap
670	34	1.1	12779	4	US-09-949-016-13081	Sequence 13081, A
671	34	1.1	13466	4	US-09-902-540-1007	Sequence 1007, Ap
672	34	1.1	16782	4	US-09-902-540-1105	Sequence 1105, Ap
c 673	34	1.1	25202	4	US-09-949-016-13151	Sequence 13151, A
674	34	1.1	31826	4	US-09-902-540-1256	Sequence 1256, Ap
675	34	1.1	37875	4	US-09-949-016-13182	Sequence 13182, A
676	34	1.1	45716	3	US-08-965-048-5	Sequence 5, Appli
677	34	1.1	45989	3	US-08-965-048-6	Sequence 6, Appli
c 678	34	1.1	76985	4	US-09-949-016-12416	Sequence 12416, A
c 679	34	1.1	76986	4	US-09-949-016-13120	Sequence 13120, A
c 680	34	1.1	82125	4	US-09-949-016-13517	Sequence 13517, A
c 681	34	1.1	82125	4	US-09-949-016-13518	Sequence 13518, A
c 682	33.8	1.1	654	4	US-09-902-540-3006	Sequence 3006, Ap
683	33.8	1.1	675	4	US-09-902-540-7973	Sequence 7973, Ap
684	33.8	1.1	729	4	US-09-252-991A-8137	Sequence 8137, Ap
c 685	33.8	1.1	795	4	US-09-252-991A-8099	Sequence 8099, Ap
686	33.8	1.1	876	4	US-09-252-991A-1174	Sequence 1174, Ap
687	33.8	1.1	1002	4	US-09-902-540-3315	Sequence 3315, Ap
688	33.8	1.1	1011	4	US-09-902-540-4174	Sequence 4174, Ap
689	33.8	1.1	1044	4	US-09-252-991A-16192	Sequence 16192, A
c 690	33.8	1.1	1260	3	US-09-446-754-5	Sequence 5, Appli
c 691	33.8	1.1	1260	4	US-09-206-166-7	Sequence 7, Appli
692	33.8	1.1	1323	4	US-09-252-991A-7602	Sequence 7602, Ap
693	33.8	1.1	1339	4	US-09-501-115-1	Sequence 1, Appli
694	33.8	1.1	1377	4	US-09-902-540-3583	Sequence 3583, Ap
695	33.8	1.1	1401	4	US-09-489-039A-483	Sequence 483, App

696	33.8	1.1	1437	4	US-09-252-991A-15986	Sequence 15986, A
697	33.8	1.1	1518	1	US-08-095-726-7	Sequence 7, Appli
698	33.8	1.1	1518	1	US-08-096-043-7	Sequence 7, Appli
699	33.8	1.1	1518	1	US-08-096-623A-7	Sequence 7, Appli
700	33.8	1.1	1522	1	US-08-095-726-9	Sequence 9, Appli
701	33.8	1.1	1522	1	US-08-096-043-9	Sequence 9, Appli
702	33.8	1.1	1522	1	US-08-096-623A-9	Sequence 9, Appli
c 703	33.8	1.1	1598	3	US-08-888-429A-31	Sequence 31, Appl
c 704	33.8	1.1	1598	4	US-09-593-653-31	Sequence 31, Appl
c 705	33.8	1.1	1643	3	US-08-888-429A-27	Sequence 27, Appl
c 706	33.8	1.1	1643	4	US-09-593-653-27	Sequence 27, Appl
707	33.8	1.1	1689	4	US-09-902-540-2842	Sequence 2842, Ap
708	33.8	1.1	1794	4	US-09-252-991A-7681	Sequence 7681, Ap
c 709	33.8	1.1	1920	4	US-09-252-991A-2332	Sequence 2332, Ap
710	33.8	1.1	1980	4	US-09-252-991A-2583	Sequence 2583, Ap
c 711	33.8	1.1	1995	1	US-08-425-069-3	Sequence 3, Appli
c 712	33.8	1.1	1995	2	US-08-317-844B-3	Sequence 3, Appli
c 713	33.8	1.1	2046	4	US-09-252-991A-7996	Sequence 7996, Ap
c 714	33.8	1.1	2046	4	US-09-252-991A-8058	Sequence 8058, Ap
715	33.8	1.1	2270	4	US-09-229-151C-13	Sequence 13, Appl
716	33.8	1.1	2315	4	US-09-620-312D-621	Sequence 621, App
c 717	33.8	1.1	2484	4	US-09-252-991A-1388	Sequence 1388, Ap
718	33.8	1.1	2570	4	US-09-229-151C-14	Sequence 14, Appl
c 719	33.8	1.1	3092	4	US-09-902-540-636	Sequence 636, App
720	33.8	1.1	6063	4	US-09-902-540-807	Sequence 807, App
721	33.8	1.1	6858	4	US-09-252-991A-1219	Sequence 1219, Ap
c 722	33.8	1.1	15351	4	US-09-902-540-1154	Sequence 1154, Ap
c 723	33.8	1.1	16047	4	US-09-902-540-1136	Sequence 1136, Ap
c 724	33.8	1.1	19394	4	US-09-902-540-1172	Sequence 1172, Ap
725	33.8	1.1	22301	4	US-09-902-540-1208	Sequence 1208, Ap
726	33.8	1.1	35707	4	US-09-949-016-17120	Sequence 17120, A
c 727	33.8	1.1	41171	4	US-08-311-731A-122	Sequence 122, App
728	33.8	1.1	42053	4	US-09-949-016-15924	Sequence 15924, A
c 729	33.8	1.1	52874	4	US-09-949-016-14868	Sequence 14868, A
c 730	33.8	1.1	86947	4	US-09-949-016-11930	Sequence 11930, A
731	33.8	1.1	88036	4	US-09-949-016-15335	Sequence 15335, A
732	33.8	1.1	178883	4	US-09-949-016-12733	Sequence 12733, A
733	33.8	1.1	178884	4	US-09-949-016-13039	Sequence 13039, A
c 734	33.8	1.1	275110	4	US-09-949-016-12706	Sequence 12706, A
c 735	33.8	1.1	275110	4	US-09-949-016-16070	Sequence 16070, A
736	33.6	1.1	321	4	US-09-252-991A-3868	Sequence 3868, Ap
c 737	33.6	1.1	447	4	US-09-252-991A-6705	Sequence 6705, Ap
738	33.6	1.1	474	4	US-09-621-976-18033	Sequence 18033, A
739	33.6	1.1	481	4	US-09-644-907B-5	Sequence 5, Appli
740	33.6	1.1	522	3	US-08-149-101A-11	Sequence 11, Appl
741	33.6	1.1	522	5	PCT-US94-12873-11	Sequence 11, Appl
742	33.6	1.1	531	4	US-09-902-540-7651	Sequence 7651, Ap
743	33.6	1.1	588	4	US-09-252-991A-6313	Sequence 6313, Ap
744	33.6	1.1	601	4	US-09-949-016-46286	Sequence 46286, A
745	33.6	1.1	601	4	US-09-949-016-46287	Sequence 46287, A
746	33.6	1.1	601	4	US-09-949-016-46288	Sequence 46288, A
c 747	33.6	1.1	601	4	US-09-949-016-121715	Sequence 121715,
748	33.6	1.1	645	4	US-09-252-991A-6395	Sequence 6395, Ap
749	33.6	1.1	699	4	US-09-252-991A-3823	Sequence 3823, Ap
750	33.6	1.1	795	4	US-09-252-991A-1516	Sequence 1516, Ap
751	33.6	1.1	831	4	US-09-252-991A-1557	Sequence 1557, Ap
752	33.6	1.1	852	4	US-09-266-965-36	Sequence 36, Appl

c 753	33.6	1.1	1001	4	US-09-671-317-228	Sequence 228, App
c 754	33.6	1.1	1001	4	US-09-671-317-229	Sequence 229, App
755	33.6	1.1	1011	4	US-09-902-540-8881	Sequence 8881, Ap
756	33.6	1.1	1197	4	US-10-151-832-2	Sequence 2, Appli
757	33.6	1.1	1215	4	US-09-252-991A-9259	Sequence 9259, Ap
758	33.6	1.1	1308	4	US-10-151-832-1	Sequence 1, Appli
759	33.6	1.1	1410	4	US-09-252-991A-10147	Sequence 10147, A
c 760	33.6	1.1	1455	4	US-09-252-991A-6154	Sequence 6154, Ap
c 761	33.6	1.1	1488	4	US-09-252-991A-9307	Sequence 9307, Ap
c 762	33.6	1.1	1502	4	US-09-902-540-6160	Sequence 6160, Ap
c 763	33.6	1.1	1504	4	US-09-902-540-301	Sequence 301, App
c 764	33.6	1.1	1587	4	US-09-902-540-7908	Sequence 7908, Ap
765	33.6	1.1	1602	4	US-09-252-991A-9270	Sequence 9270, Ap
c 766	33.6	1.1	1623	4	US-09-252-991A-9839	Sequence 9839, Ap
767	33.6	1.1	1653	4	US-09-902-540-3348	Sequence 3348, Ap
768	33.6	1.1	1759	4	US-09-470-881-2	Sequence 2, Appli
769	33.6	1.1	1770	4	US-09-902-540-7504	Sequence 7504, Ap
770	33.6	1.1	1818	4	US-09-902-540-5126	Sequence 5126, Ap
c 771	33.6	1.1	1821	4	US-09-252-991A-1662	Sequence 1662, Ap
c 772	33.6	1.1	1926	3	US-09-249-585A-2	Sequence 2, Appli
c 773	33.6	1.1	1926	4	US-09-410-399-3	Sequence 3, Appli
774	33.6	1.1	2122	3	US-09-029-603-1	Sequence 1, Appli
775	33.6	1.1	2202	4	US-09-902-540-8501	Sequence 8501, Ap
776	33.6	1.1	2346	4	US-09-252-991A-1466	Sequence 1466, Ap
c 777	33.6	1.1	2352	4	US-09-902-540-4107	Sequence 4107, Ap
c 778	33.6	1.1	2580	3	US-09-050-863-2	Sequence 2, Appli
c 779	33.6	1.1	2580	3	US-09-359-081-2	Sequence 2, Appli
780	33.6	1.1	4026	4	US-09-252-991A-10214	Sequence 10214, A
781	33.6	1.1	5452	2	US-09-130-114-1	Sequence 1, Appli
c 782	33.6	1.1	5618	4	US-09-902-540-728	Sequence 728, App
783	33.6	1.1	6419	4	US-09-949-016-15768	Sequence 15768, A
c 784	33.6	1.1	6468	4	US-09-902-540-895	Sequence 895, App
c 785	33.6	1.1	6594	4	US-09-902-540-752	Sequence 752, App
786	33.6	1.1	7898	3	US-08-984-709A-49	Sequence 49, Appl
787	33.6	1.1	7994	4	US-09-902-540-797	Sequence 797, App
788	33.6	1.1	8705	4	US-09-647-344A-14	Sequence 14, Appl
c 789	33.6	1.1	9600	3	US-08-910-647-1	Sequence 1, Appli
c 790	33.6	1.1	9600	3	US-09-620-925-1	Sequence 1, Appli
791	33.6	1.1	9937	4	US-09-902-540-946	Sequence 946, App
c 792	33.6	1.1	10596	1	US-07-884-811-15	Sequence 15, Appl
c 793	33.6	1.1	10596	1	US-07-885-971-15	Sequence 15, Appl
c 794	33.6	1.1	10596	1	US-08-087-783A-15	Sequence 15, Appl
c 795	33.6	1.1	10596	1	US-08-194-088B-15	Sequence 15, Appl
c 796	33.6	1.1	10596	2	US-08-194-087-15	Sequence 15, Appl
c 797	33.6	1.1	10596	5	PCT-US93-04648-15	Sequence 15, Appl
798	33.6	1.1	10871	4	US-09-902-540-1025	Sequence 1025, Ap
c 799	33.6	1.1	11406	4	US-09-949-016-17355	Sequence 17355, A
c 800	33.6	1.1	11958	3	US-09-134-246-8	Sequence 8, Appli
c 801	33.6	1.1	11958	4	US-09-664-186-8	Sequence 8, Appli
802	33.6	1.1	16080	4	US-09-724-566A-48	Sequence 48, Appl
803	33.6	1.1	16080	4	US-09-471-669A-48	Sequence 48, Appl
804	33.6	1.1	18537	4	US-09-902-540-1157	Sequence 1157, Ap
805	33.6	1.1	24020	4	US-09-949-016-17353	Sequence 17353, A
c 806	33.6	1.1	28058	4	US-09-902-540-1252	Sequence 1252, Ap
807	33.6	1.1	28257	4	US-09-949-016-13076	Sequence 13076, A
808	33.6	1.1	43414	4	US-09-949-016-12839	Sequence 12839, A
809	33.6	1.1	43415	4	US-09-949-016-16491	Sequence 16491, A

c 810	33.6	1.1	48316	4	US-09-949-016-12853	Sequence 12853, A
c 811	33.6	1.1	48316	4	US-09-949-016-13405	Sequence 13405, A
c 812	33.6	1.1	53500	4	US-09-266-965-76	Sequence 76, Appl
813	33.6	1.1	91279	4	US-09-949-016-15146	Sequence 15146, A
c 814	33.6	1.1	140844	4	US-09-949-016-14199	Sequence 14199, A
815	33.6	1.1	536165	4	US-09-214-808-1	Sequence 1, Appli
816	33.4	1.1	464	4	US-09-621-976-1342	Sequence 1342, Ap
c 817	33.4	1.1	531	4	US-09-702-705-53	Sequence 53, Appl
c 818	33.4	1.1	531	4	US-09-736-457-53	Sequence 53, Appl
c 819	33.4	1.1	531	4	US-09-614-124B-53	Sequence 53, Appl
c 820	33.4	1.1	531	4	US-09-671-325-53	Sequence 53, Appl
c 821	33.4	1.1	531	4	US-09-589-184-53	Sequence 53, Appl
c 822	33.4	1.1	531	4	US-09-658-824-53	Sequence 53, Appl
823	33.4	1.1	601	4	US-09-949-016-38520	Sequence 38520, A
824	33.4	1.1	601	4	US-09-949-016-109161	Sequence 109161,
825	33.4	1.1	601	4	US-09-949-016-152044	Sequence 152044,
826	33.4	1.1	601	4	US-09-949-016-152117	Sequence 152117,
827	33.4	1.1	601	4	US-09-949-016-152190	Sequence 152190,
828	33.4	1.1	601	4	US-09-949-016-152263	Sequence 152263,
829	33.4	1.1	601	4	US-09-949-016-159349	Sequence 159349,
830	33.4	1.1	601	4	US-09-949-016-159422	Sequence 159422,
831	33.4	1.1	601	4	US-09-949-016-159495	Sequence 159495,
832	33.4	1.1	601	4	US-09-949-016-159568	Sequence 159568,
c 833	33.4	1.1	956	4	US-09-949-016-1403	Sequence 1403, Ap
834	33.4	1.1	970	3	US-09-248-335-47	Sequence 47, Appl
c 835	33.4	1.1	1080	1	US-08-225-757B-1	Sequence 1, Appli
c 836	33.4	1.1	1080	2	US-08-722-050-1	Sequence 1, Appli
c 837	33.4	1.1	1080	4	US-09-883-985-1	Sequence 1, Appli
838	33.4	1.1	1098	4	US-09-252-991A-14407	Sequence 14407, A
839	33.4	1.1	1134	4	US-09-902-540-6707	Sequence 6707, Ap
c 840	33.4	1.1	1164	4	US-09-252-991A-1310	Sequence 1310, Ap
841	33.4	1.1	1266	4	US-09-902-540-7594	Sequence 7594, Ap
c 842	33.4	1.1	1311	4	US-09-252-991A-1355	Sequence 1355, Ap
843	33.4	1.1	1326	4	US-09-252-991A-1156	Sequence 1156, Ap
844	33.4	1.1	1419	4	US-09-252-991A-1246	Sequence 1246, Ap
845	33.4	1.1	1434	4	US-09-902-540-5463	Sequence 5463, Ap
846	33.4	1.1	1512	4	US-09-252-991A-1481	Sequence 1481, Ap
c 847	33.4	1.1	1566	4	US-09-252-991A-14264	Sequence 14264, A
c 848	33.4	1.1	1719	4	US-09-902-540-2792	Sequence 2792, Ap
849	33.4	1.1	1908	4	US-09-252-991A-14353	Sequence 14353, A
850	33.4	1.1	1977	4	US-09-902-540-7785	Sequence 7785, Ap
851	33.4	1.1	2034	4	US-09-252-991A-1531	Sequence 1531, Ap
c 852	33.4	1.1	2363	3	US-09-721-383-1	Sequence 1, Appli
c 853	33.4	1.1	2363	3	US-09-721-137-1	Sequence 1, Appli
c 854	33.4	1.1	2363	4	US-09-721-251-1	Sequence 1, Appli
c 855	33.4	1.1	2363	4	US-10-114-764-1	Sequence 1, Appli
c 856	33.4	1.1	2537	4	US-09-902-540-415	Sequence 415, App
857	33.4	1.1	2948	4	US-09-774-528-145	Sequence 145, App
c 858	33.4	1.1	2976	4	US-09-949-016-2013	Sequence 2013, Ap
c 859	33.4	1.1	3595	4	US-09-949-016-492	Sequence 492, App
860	33.4	1.1	4079	4	US-09-016-434-1449	Sequence 1449, Ap
c 861	33.4	1.1	4408	4	US-09-902-540-744	Sequence 744, App
c 862	33.4	1.1	5175	4	US-09-902-540-774	Sequence 774, App
863	33.4	1.1	15271	4	US-09-902-540-1051	Sequence 1051, Ap
c 864	33.4	1.1	15644	4	US-09-902-540-1133	Sequence 1133, Ap
c 865	33.4	1.1	24166	4	US-09-949-016-13755	Sequence 13755, A
c 866	33.4	1.1	24735	4	US-09-949-016-12850	Sequence 12850, A

c 867	33.4	1.1	28172	4	US-09-902-540-1221	Sequence 1221, Ap
c 868	33.4	1.1	41310	4	US-09-902-540-1264	Sequence 1264, Ap
869	33.4	1.1	42741	4	US-09-949-016-11857	Sequence 11857, A
870	33.4	1.1	51807	4	US-09-949-016-15333	Sequence 15333, A
c 871	33.4	1.1	78846	4	US-09-949-016-12396	Sequence 12396, A
c 872	33.4	1.1	78846	4	US-09-949-016-12791	Sequence 12791, A
c 873	33.4	1.1	78846	4	US-09-949-016-12792	Sequence 12792, A
c 874	33.4	1.1	78846	4	US-09-949-016-12793	Sequence 12793, A
c 875	33.4	1.1	78850	4	US-09-949-016-16013	Sequence 16013, A
c 876	33.4	1.1	78850	4	US-09-949-016-16014	Sequence 16014, A
c 877	33.4	1.1	78850	4	US-09-949-016-16015	Sequence 16015, A
c 878	33.4	1.1	78850	4	US-09-949-016-16016	Sequence 16016, A
c 879	33.4	1.1	78850	4	US-09-949-016-16201	Sequence 16201, A
c 880	33.4	1.1	78850	4	US-09-949-016-16202	Sequence 16202, A
c 881	33.4	1.1	78850	4	US-09-949-016-16203	Sequence 16203, A
c 882	33.4	1.1	78850	4	US-09-949-016-16204	Sequence 16204, A
c 883	33.4	1.1	91665	4	US-09-949-016-12234	Sequence 12234, A
c 884	33.4	1.1	152655	4	US-09-949-016-16246	Sequence 16246, A
c 885	33.4	1.1	192700	4	US-09-949-016-11820	Sequence 11820, A
c 886	33.4	1.1	192704	4	US-09-949-016-17182	Sequence 17182, A
c 887	33.2	1.1	459	4	US-09-707-919A-13	Sequence 13, Appl
888	33.2	1.1	468	4	US-09-252-991A-16533	Sequence 16533, A
889	33.2	1.1	516	4	US-09-252-991A-1809	Sequence 1809, Ap
c 890	33.2	1.1	516	4	US-09-083-268-1	Sequence 1, Appli
c 891	33.2	1.1	543	4	US-09-252-991A-1126	Sequence 1126, Ap
892	33.2	1.1	571	1	US-08-322-742-14	Sequence 14, Appl
c 893	33.2	1.1	595	3	US-09-328-111-330	Sequence 330, App
c 894	33.2	1.1	601	4	US-09-949-016-105795	Sequence 105795,
c 895	33.2	1.1	601	4	US-09-949-001-758	Sequence 758, App
c 896	33.2	1.1	684	4	US-09-252-991A-1812	Sequence 1812, Ap
897	33.2	1.1	717	4	US-09-252-991A-2148	Sequence 2148, Ap
898	33.2	1.1	738	4	US-09-252-991A-10479	Sequence 10479, A
899	33.2	1.1	828	4	US-09-252-991A-2078	Sequence 2078, Ap
900	33.2	1.1	837	4	US-09-252-991A-5035	Sequence 5035, Ap
c 901	33.2	1.1	837	4	US-09-252-991A-5100	Sequence 5100, Ap
902	33.2	1.1	885	4	US-09-252-991A-10382	Sequence 10382, A
903	33.2	1.1	909	4	US-09-252-991A-5120	Sequence 5120, Ap
c 904	33.2	1.1	1047	4	US-09-252-991A-5002	Sequence 5002, Ap
905	33.2	1.1	1062	4	US-09-016-434-1286	Sequence 1286, Ap
906	33.2	1.1	1062	4	US-08-134-231C-33	Sequence 33, Appl
907	33.2	1.1	1062	4	US-09-023-655-1327	Sequence 1327, Ap
908	33.2	1.1	1062	4	US-08-728-160-33	Sequence 33, Appl
c 909	33.2	1.1	1365	4	US-09-252-991A-1996	Sequence 1996, Ap
910	33.2	1.1	1389	4	US-09-252-991A-1733	Sequence 1733, Ap
911	33.2	1.1	1458	4	US-09-489-039A-2996	Sequence 2996, Ap
912	33.2	1.1	1782	4	US-09-252-991A-5094	Sequence 5094, Ap
913	33.2	1.1	1804	4	US-09-949-016-4941	Sequence 4941, Ap
c 914	33.2	1.1	1827	2	US-08-824-878-2	Sequence 2, Appli
c 915	33.2	1.1	1827	3	US-09-353-688-2	Sequence 2, Appli
916	33.2	1.1	1855	3	US-09-150-133-6	Sequence 6, Appli
917	33.2	1.1	1855	3	US-09-150-141-6	Sequence 6, Appli
918	33.2	1.1	1855	3	US-09-374-493-6	Sequence 6, Appli
919	33.2	1.1	1855	3	US-09-374-824-6	Sequence 6, Appli
920	33.2	1.1	1855	3	US-09-374-492-6	Sequence 6, Appli
921	33.2	1.1	1855	4	US-09-785-343-6	Sequence 6, Appli
922	33.2	1.1	1855	4	US-10-411-976-6	Sequence 6, Appli
923	33.2	1.1	1855	4	US-09-949-016-519	Sequence 519, App

c 924	33.2	1.1	1974	4	US-09-252-991A-1089	Sequence 1089, Ap
925	33.2	1.1	2031	4	US-09-252-991A-5180	Sequence 5180, Ap
926	33.2	1.1	2169	4	US-09-252-991A-10268	Sequence 10268, A
927	33.2	1.1	2331	4	US-09-252-991A-999	Sequence 999, App
c 928	33.2	1.1	2525	4	US-09-620-312D-1044	Sequence 1044, Ap
929	33.2	1.1	3650	4	US-09-949-016-3694	Sequence 3694, Ap
c 930	33.2	1.1	4481	3	US-09-041-886-18	Sequence 18, Appl
c 931	33.2	1.1	4481	4	US-09-648-281-1	Sequence 1, Appli
c 932	33.2	1.1	4481	4	US-09-707-919A-20	Sequence 20, Appl
c 933	33.2	1.1	4481	4	US-09-083-268-2	Sequence 2, Appli
c 934	33.2	1.1	5587	4	US-09-949-016-5651	Sequence 5651, Ap
c 935	33.2	1.1	5601	4	US-09-949-016-1039	Sequence 1039, Ap
c 936	33.2	1.1	10280	4	US-09-902-540-980	Sequence 980, App
c 937	33.2	1.1	13178	4	US-09-949-016-17116	Sequence 17116, A
938	33.2	1.1	13875	2	US-08-734-344-1	Sequence 1, Appli
939	33.2	1.1	14449	4	US-09-949-016-12108	Sequence 12108, A
c 940	33.2	1.1	22156	4	US-09-902-540-1195	Sequence 1195, Ap
941	33.2	1.1	22911	4	US-09-949-016-16683	Sequence 16683, A
942	33.2	1.1	23673	3	US-09-773-816-1	Sequence 1, Appli
943	33.2	1.1	30656	4	US-09-949-016-14613	Sequence 14613, A
944	33.2	1.1	39754	4	US-09-949-016-14689	Sequence 14689, A
c 945	33.2	1.1	43414	4	US-09-949-016-12839	Sequence 12839, A
c 946	33.2	1.1	43415	4	US-09-949-016-16491	Sequence 16491, A
947	33.2	1.1	68283	4	US-09-949-016-12261	Sequence 12261, A
948	33.2	1.1	134987	4	US-09-949-016-15348	Sequence 15348, A
949	33.2	1.1	134987	4	US-09-949-016-15349	Sequence 15349, A
950	33.2	1.1	134987	4	US-09-949-016-15350	Sequence 15350, A
951	33.2	1.1	134987	4	US-09-949-016-15507	Sequence 15507, A
952	33.2	1.1	134987	4	US-09-949-016-15508	Sequence 15508, A
953	33.2	1.1	134987	4	US-09-949-016-15509	Sequence 15509, A
c 954	33.2	1.1	152132	4	US-09-949-016-13845	Sequence 13845, A
c 955	33.2	1.1	152145	4	US-09-949-016-12371	Sequence 12371, A
c 956	33.2	1.1	198632	4	US-09-949-016-12781	Sequence 12781, A
c 957	33.2	1.1	198637	4	US-09-949-016-17393	Sequence 17393, A
958	33.2	1.1	346112	4	US-09-949-016-13165	Sequence 13165, A
959	33.2	1.1	767677	4	US-09-949-016-12147	Sequence 12147, A
960	33.2	1.1	767677	4	US-09-949-016-17361	Sequence 17361, A
c 961	33	1.0	378	4	US-09-902-540-4782	Sequence 4782, Ap
962	33	1.0	396	4	US-09-513-597A-16	Sequence 16, Appl
963	33	1.0	412	4	US-09-513-597A-15	Sequence 15, Appl
c 964	33	1.0	601	4	US-09-949-016-23036	Sequence 23036, A
c 965	33	1.0	601	4	US-09-949-016-23037	Sequence 23037, A
c 966	33	1.0	601	4	US-09-949-016-23038	Sequence 23038, A
c 967	33	1.0	601	4	US-09-949-016-26784	Sequence 26784, A
c 968	33	1.0	601	4	US-09-949-016-56277	Sequence 56277, A
c 969	33	1.0	601	4	US-09-949-016-175321	Sequence 175321,
c 970	33	1.0	601	4	US-09-949-016-183033	Sequence 183033,
c 971	33	1.0	601	4	US-09-949-016-200508	Sequence 200508,
c 972	33	1.0	601	4	US-09-949-016-200509	Sequence 200509,
c 973	33	1.0	601	4	US-09-949-016-200510	Sequence 200510,
974	33	1.0	666	4	US-09-252-991A-2587	Sequence 2587, Ap
975	33	1.0	708	4	US-09-902-540-8487	Sequence 8487, Ap
976	33	1.0	713	4	US-09-919-039-310	Sequence 310, App
c 977	33	1.0	732	4	US-09-252-991A-8860	Sequence 8860, Ap
978	33	1.0	834	4	US-09-252-991A-12686	Sequence 12686, A
979	33	1.0	1074	4	US-09-252-991A-350	Sequence 350, App
c 980	33	1.0	1083	4	US-09-252-991A-13113	Sequence 13113, A

981	33	1.0	1092	4	US-09-902-540-8845	Sequence 8845, Ap
c 982	33	1.0	1198	4	US-09-513-597A-3	Sequence 3, Appli
c 983	33	1.0	1207	4	US-09-513-597A-14	Sequence 14, Appl
c 984	33	1.0	1218	4	US-09-252-991A-316	Sequence 316, App
c 985	33	1.0	1233	4	US-09-252-991A-2330	Sequence 2330, Ap
986	33	1.0	1263	4	US-09-252-991A-341	Sequence 341, App
987	33	1.0	1269	4	US-09-252-991A-3750	Sequence 3750, Ap
c 988	33	1.0	1285	4	US-09-949-016-1480	Sequence 1480, Ap
c 989	33	1.0	1287	4	US-09-252-991A-3628	Sequence 3628, Ap
990	33	1.0	1299	4	US-09-976-594-814	Sequence 814, App
991	33	1.0	1374	4	US-09-252-991A-8560	Sequence 8560, Ap
992	33	1.0	1377	4	US-09-902-540-2474	Sequence 2474, Ap
993	33	1.0	1419	4	US-09-489-039A-5224	Sequence 5224, Ap
c 994	33	1.0	1488	4	US-09-252-991A-9538	Sequence 9538, Ap
995	33	1.0	1904	4	US-09-949-016-1334	Sequence 1334, Ap
996	33	1.0	1977	4	US-09-252-991A-9748	Sequence 9748, Ap
997	33	1.0	2017	3	US-09-291-922-21	Sequence 21, Appl
998	33	1.0	2034	4	US-09-252-991A-3835	Sequence 3835, Ap
999	33	1.0	2078	2	US-08-785-310A-1	Sequence 1, Appli
1000	33	1.0	2124	4	US-09-252-991A-12830	Sequence 12830, A
1001	33	1.0	2128	4	US-09-620-312D-197	Sequence 197, App
1002	33	1.0	2147	4	US-09-949-016-5245	Sequence 5245, Ap
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c1005	33	1.0	2462	4	US-09-254-590-48	Sequence 48, Appl
c1006	33	1.0	2462	4	US-10-115-415-48	Sequence 48, Appl
c1007	33	1.0	2462	4	US-10-116-260-48	Sequence 48, Appl
c1008	33	1.0	2462	4	US-10-115-671-48	Sequence 48, Appl
1009	33	1.0	2463	4	US-09-252-991A-8582	Sequence 8582, Ap
c1010	33	1.0	2748	4	US-09-252-991A-8662	Sequence 8662, Ap
1011	33	1.0	3000	3	US-08-460-269C-3	Sequence 3, Appli
1012	33	1.0	3000	3	US-08-460-269C-5	Sequence 5, Appli
c1013	33	1.0	3210	4	US-09-902-540-4272	Sequence 4272, Ap
1014	33	1.0	3237	4	US-10-101-464A-858	Sequence 858, App
c1015	33	1.0	3293	2	US-08-442-809A-75	Sequence 75, Appl
c1016	33	1.0	5228	3	US-09-428-711A-15	Sequence 15, Appl
c1017	33	1.0	6250	4	US-09-949-016-13222	Sequence 13222, A
1018	33	1.0	6268	4	US-09-566-921-57	Sequence 57, Appl
1019	33	1.0	6385	4	US-09-902-540-941	Sequence 941, App
1020	33	1.0	7529	4	US-09-902-540-893	Sequence 893, App
c1021	33	1.0	9080	4	US-09-902-540-1963	Sequence 1963, Ap
c1022	33	1.0	14124	4	US-09-949-016-16087	Sequence 16087, A
1023	33	1.0	15209	4	US-09-902-540-1110	Sequence 1110, Ap
1024	33	1.0	19818	4	US-09-949-016-12198	Sequence 12198, A
1025	33	1.0	19819	4	US-09-949-016-16987	Sequence 16987, A
c1026	33	1.0	26012	4	US-09-902-540-1212	Sequence 1212, Ap
1027	33	1.0	27490	4	US-09-902-540-1227	Sequence 1227, Ap
1028	33	1.0	27903	4	US-09-902-540-1235	Sequence 1235, Ap
c1029	33	1.0	37711	4	US-09-949-016-12832	Sequence 12832, A
c1030	33	1.0	37712	4	US-09-949-016-16704	Sequence 16704, A
1031	33	1.0	49272	1	US-08-614-770A-1	Sequence 1, Appli
c1032	33	1.0	52199	4	US-09-949-016-12763	Sequence 12763, A
c1033	33	1.0	52203	4	US-09-949-016-16330	Sequence 16330, A
c1034	33	1.0	52821	4	US-09-949-016-15857	Sequence 15857, A
c1035	33	1.0	52824	4	US-09-949-016-12116	Sequence 12116, A
c1036	33	1.0	74177	4	US-09-949-016-11988	Sequence 11988, A
c1037	33	1.0	74177	4	US-09-949-016-17388	Sequence 17388, A

1038	33	1.0	173992	4	US-09-949-016-13379	Sequence 13379, A
c1039	33	1.0	193169	4	US-09-949-016-15091	Sequence 15091, A
1040	32.8	1.0	601	4	US-09-949-016-52692	Sequence 52692, A
1041	32.8	1.0	601	4	US-09-949-016-59909	Sequence 59909, A
c1042	32.8	1.0	601	4	US-09-949-016-132008	Sequence 132008,
c1043	32.8	1.0	601	4	US-09-949-016-132077	Sequence 132077,
1044	32.8	1.0	624	4	US-09-902-540-3091	Sequence 3091, Ap
1045	32.8	1.0	767	4	US-09-501-115-35	Sequence 35, Appl
1046	32.8	1.0	777	4	US-09-252-991A-9681	Sequence 9681, Ap
c1047	32.8	1.0	860	4	US-09-919-172-101	Sequence 101, App
c1048	32.8	1.0	860	4	US-09-976-594-466	Sequence 466, App
1049	32.8	1.0	927	4	US-09-252-991A-9722	Sequence 9722, Ap
1050	32.8	1.0	981	4	US-09-252-991A-13867	Sequence 13867, A
1051	32.8	1.0	1086	4	US-09-252-991A-15474	Sequence 15474, A
c1052	32.8	1.0	1155	4	US-09-902-540-3570	Sequence 3570, Ap
c1053	32.8	1.0	1197	4	US-09-902-540-6772	Sequence 6772, Ap
c1054	32.8	1.0	1278	4	US-09-252-991A-13473	Sequence 13473, A
1055	32.8	1.0	1284	4	US-09-902-540-8073	Sequence 8073, Ap
1056	32.8	1.0	1342	3	US-09-500-569-9	Sequence 9, Appli
1057	32.8	1.0	1342	4	US-09-971-823B-9	Sequence 9, Appli
c1058	32.8	1.0	1402	4	US-09-205-258-22	Sequence 22, Appl
1059	32.8	1.0	1530	4	US-09-252-991A-13672	Sequence 13672, A
1060	32.8	1.0	1533	4	US-09-657-013-21	Sequence 21, Appl
1061	32.8	1.0	1652	4	US-09-657-013-26	Sequence 26, Appl
1062	32.8	1.0	1669	4	US-09-657-013-20	Sequence 20, Appl
c1063	32.8	1.0	1785	4	US-09-949-016-5043	Sequence 5043, Ap
c1064	32.8	1.0	1785	4	US-09-949-016-5044	Sequence 5044, Ap
c1065	32.8	1.0	1824	4	US-09-252-991A-9566	Sequence 9566, Ap
1066	32.8	1.0	2106	4	US-09-949-016-708	Sequence 708, App
c1067	32.8	1.0	2163	4	US-09-252-991A-5310	Sequence 5310, Ap
1068	32.8	1.0	2249	3	US-08-814-052-19	Sequence 19, Appl
1069	32.8	1.0	2279	3	US-08-814-052-17	Sequence 17, Appl
1070	32.8	1.0	2300	3	US-08-814-052-18	Sequence 18, Appl
1071	32.8	1.0	2351	4	US-09-657-013-23	Sequence 23, Appl
c1072	32.8	1.0	2371	2	US-08-343-443B-1	Sequence 1, Appli
c1073	32.8	1.0	2592	3	US-09-591-025-8	Sequence 8, Appli
c1074	32.8	1.0	2592	4	US-09-894-927B-8	Sequence 8, Appli
1075	32.8	1.0	3183	2	US-08-939-218A-1	Sequence 1, Appli
1076	32.8	1.0	3192	1	US-08-940-661A-1	Sequence 1, Appli
1077	32.8	1.0	3192	2	US-09-083-485-1	Sequence 1, Appli
1078	32.8	1.0	3282	4	US-09-252-991A-5256	Sequence 5256, Ap
c1079	32.8	1.0	4158	4	US-09-252-991A-5348	Sequence 5348, Ap
1080	32.8	1.0	4755	4	US-09-799-451-377	Sequence 377, App
c1081	32.8	1.0	4835	1	US-08-386-495-9	Sequence 9, Appli
c1082	32.8	1.0	4835	5	PCT-US96-02331-9	Sequence 9, Appli
1083	32.8	1.0	4836	4	US-09-799-451-376	Sequence 376, App
c1084	32.8	1.0	4898	4	US-09-919-497-35	Sequence 35, Appl
1085	32.8	1.0	4953	4	US-09-252-991A-5227	Sequence 5227, Ap
c1086	32.8	1.0	8658	4	US-09-902-540-943	Sequence 943, App
1087	32.8	1.0	10091	4	US-09-657-013-24	Sequence 24, Appl
1088	32.8	1.0	10182	4	US-09-657-013-25	Sequence 25, Appl
1089	32.8	1.0	10182	4	US-09-657-013-27	Sequence 27, Appl
1090	32.8	1.0	10182	4	US-09-657-013-28	Sequence 28, Appl
1091	32.8	1.0	10182	4	US-09-949-016-4338	Sequence 4338, Ap
1092	32.8	1.0	11502	4	US-09-902-540-1064	Sequence 1064, Ap
1093	32.8	1.0	15236	4	US-09-949-016-16778	Sequence 16778, A
1094	32.8	1.0	15789	4	US-09-902-540-1139	Sequence 1139, Ap

c1095	32.8	1.0	27525	4	US-09-949-016-16835	Sequence 16835, A
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c1097	32.8	1.0	34534	4	US-09-949-016-15141	Sequence 15141, A
c1098	32.8	1.0	43657	4	US-09-949-016-13777	Sequence 13777, A
1099	32.8	1.0	44870	4	US-09-949-016-12554	Sequence 12554, A
1100	32.8	1.0	44881	4	US-09-949-016-16349	Sequence 16349, A
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c1102	32.8	1.0	52655	4	US-09-949-016-13495	Sequence 13495, A
1103	32.8	1.0	60304	4	US-09-949-016-11995	Sequence 11995, A
1104	32.8	1.0	60304	4	US-09-949-016-17264	Sequence 17264, A
c1105	32.8	1.0	62636	4	US-09-949-016-15464	Sequence 15464, A
c1106	32.8	1.0	62636	4	US-09-949-016-15465	Sequence 15465, A
1107	32.8	1.0	79858	4	US-09-949-016-16080	Sequence 16080, A
c1108	32.8	1.0	84875	4	US-09-949-016-17334	Sequence 17334, A
c1109	32.8	1.0	84875	4	US-09-949-016-17335	Sequence 17335, A
c1110	32.8	1.0	84875	4	US-09-949-016-17336	Sequence 17336, A
c1111	32.8	1.0	84875	4	US-09-949-016-17337	Sequence 17337, A
c1112	32.8	1.0	85152	4	US-09-949-016-12665	Sequence 12665, A
c1113	32.8	1.0	85152	4	US-09-949-016-12666	Sequence 12666, A
c1114	32.8	1.0	85152	4	US-09-949-016-12667	Sequence 12667, A
c1115	32.8	1.0	85152	4	US-09-949-016-12668	Sequence 12668, A
1116	32.8	1.0	94855	4	US-09-949-016-12264	Sequence 12264, A
c1117	32.8	1.0	102409	4	US-09-949-016-15148	Sequence 15148, A
c1118	32.8	1.0	132456	4	US-09-949-016-13750	Sequence 13750, A
c1119	32.8	1.0	160759	4	US-09-949-016-16514	Sequence 16514, A
1120	32.8	1.0	678533	4	US-09-949-016-14577	Sequence 14577, A
1121	32.8	1.0	678533	4	US-09-949-016-14578	Sequence 14578, A
1122	32.6	1.0	286	4	US-09-313-294A-987	Sequence 987, App
1123	32.6	1.0	399	4	US-09-902-540-6041	Sequence 6041, Ap
c1124	32.6	1.0	516	4	US-09-252-991A-10359	Sequence 10359, A
c1125	32.6	1.0	601	4	US-09-949-016-34266	Sequence 34266, A
c1126	32.6	1.0	601	4	US-09-949-016-39281	Sequence 39281, A
c1127	32.6	1.0	601	4	US-09-949-016-45927	Sequence 45927, A
c1128	32.6	1.0	601	4	US-09-949-016-45928	Sequence 45928, A
c1129	32.6	1.0	601	4	US-09-949-016-58545	Sequence 58545, A
1130	32.6	1.0	601	4	US-09-949-016-124157	Sequence 124157,
1131	32.6	1.0	601	4	US-09-949-016-124158	Sequence 124158,
c1132	32.6	1.0	601	4	US-09-949-016-146419	Sequence 146419,
c1133	32.6	1.0	601	4	US-09-949-016-146420	Sequence 146420,
c1134	32.6	1.0	601	4	US-09-949-016-175116	Sequence 175116,
c1135	32.6	1.0	606	4	US-09-252-991A-15290	Sequence 15290, A
c1136	32.6	1.0	672	4	US-09-252-991A-10291	Sequence 10291, A
1137	32.6	1.0	687	4	US-09-252-991A-10793	Sequence 10793, A
1138	32.6	1.0	723	4	US-09-311-784A-33	Sequence 33, Appl
1139	32.6	1.0	734	4	US-09-692-081-9	Sequence 9, Appli
1140	32.6	1.0	804	4	US-09-252-991A-6840	Sequence 6840, Ap
c1141	32.6	1.0	816	4	US-09-252-991A-6879	Sequence 6879, Ap
1142	32.6	1.0	846	4	US-09-902-540-5052	Sequence 5052, Ap
1143	32.6	1.0	864	4	US-09-252-991A-6057	Sequence 6057, Ap
1144	32.6	1.0	888	4	US-09-902-540-3105	Sequence 3105, Ap
1145	32.6	1.0	942	4	US-09-252-991A-15446	Sequence 15446, A
1146	32.6	1.0	960	4	US-09-252-991A-6745	Sequence 6745, Ap
1147	32.6	1.0	990	4	US-09-252-991A-1499	Sequence 1499, Ap
1148	32.6	1.0	1075	4	US-09-660-107-12	Sequence 12, Appl
1149	32.6	1.0	1110	4	US-09-252-991A-15552	Sequence 15552, A
1150	32.6	1.0	1119	4	US-09-902-540-4364	Sequence 4364, Ap
c1151	32.6	1.0	1131	4	US-09-252-991A-1675	Sequence 1675, Ap

1152	32.6	1.0	1152	4	US-09-252-991A-7217	Sequence 7217, Ap
c1153	32.6	1.0	1167	4	US-09-252-991A-6408	Sequence 6408, Ap
1154	32.6	1.0	1224	4	US-09-266-965-22	Sequence 22, Appl
1155	32.6	1.0	1230	4	US-10-105-319-1	Sequence 1, Appli
c1156	32.6	1.0	1266	4	US-09-252-991A-4132	Sequence 4132, Ap
1157	32.6	1.0	1270	4	US-09-949-016-5072	Sequence 5072, Ap
1158	32.6	1.0	1270	4	US-09-949-016-5073	Sequence 5073, Ap
1159	32.6	1.0	1278	4	US-09-270-767-7544	Sequence 7544, Ap
1160	32.6	1.0	1278	4	US-09-270-767-22826	Sequence 22826, A
1161	32.6	1.0	1362	4	US-09-252-991A-4074	Sequence 4074, Ap
1162	32.6	1.0	1389	4	US-09-252-991A-7279	Sequence 7279, Ap
c1163	32.6	1.0	1389	4	US-09-252-991A-15246	Sequence 15246, A
1164	32.6	1.0	1395	4	US-09-902-540-3192	Sequence 3192, Ap
1165	32.6	1.0	1404	4	US-09-902-540-242	Sequence 242, App
c1166	32.6	1.0	1428	4	US-09-252-991A-7419	Sequence 7419, Ap
1167	32.6	1.0	1689	4	US-09-902-540-3347	Sequence 3347, Ap
1168	32.6	1.0	1734	4	US-09-489-039A-4357	Sequence 4357, Ap
1169	32.6	1.0	2085	2	US-08-668-128B-7	Sequence 7, Appli
1170	32.6	1.0	2085	2	US-08-905-445-7	Sequence 7, Appli
1171	32.6	1.0	2100	4	US-09-270-767-12398	Sequence 12398, A
c1172	32.6	1.0	2308	3	US-09-382-256-9	Sequence 9, Appli
c1173	32.6	1.0	2308	3	US-09-395-115-9	Sequence 9, Appli
c1174	32.6	1.0	2308	3	US-08-436-265-9	Sequence 9, Appli
c1175	32.6	1.0	2308	3	US-09-679-187-9	Sequence 9, Appli
c1176	32.6	1.0	2308	4	US-09-267-963D-9	Sequence 9, Appli
c1177	32.6	1.0	2308	4	US-09-949-016-657	Sequence 657, App
c1178	32.6	1.0	2404	4	US-09-902-540-3817	Sequence 3817, Ap
1179	32.6	1.0	2535	4	US-09-252-991A-10613	Sequence 10613, A
c1180	32.6	1.0	2685	4	US-09-252-991A-4555	Sequence 4555, Ap
1181	32.6	1.0	2826	4	US-09-390-134B-30	Sequence 30, Appl
1182	32.6	1.0	2887	3	US-09-183-253-1	Sequence 1, Appli
1183	32.6	1.0	3741	4	US-09-949-016-3795	Sequence 3795, Ap
1184	32.6	1.0	3889	4	US-09-568-559-1	Sequence 1, Appli
1185	32.6	1.0	3924	4	US-09-252-991A-4296	Sequence 4296, Ap
1186	32.6	1.0	4530	4	US-09-566-921-134	Sequence 134, App
1187	32.6	1.0	4530	4	US-09-919-039-358	Sequence 358, App
c1188	32.6	1.0	4665	4	US-09-252-991A-10243	Sequence 10243, A
1189	32.6	1.0	4676	3	US-09-130-491-1	Sequence 1, Appli
1190	32.6	1.0	4858	3	US-09-392-184-1	Sequence 1, Appli
1191	32.6	1.0	5857	4	US-09-220-132-79	Sequence 79, Appl
c1192	32.6	1.0	9408	4	US-09-949-016-13867	Sequence 13867, A
1193	32.6	1.0	12249	4	US-09-266-965-74	Sequence 74, Appl
1194	32.6	1.0	15499	4	US-09-902-540-1140	Sequence 1140, Ap
c1195	32.6	1.0	17262	4	US-09-902-540-1146	Sequence 1146, Ap
1196	32.6	1.0	18331	4	US-09-266-965-96	Sequence 96, Appl
c1197	32.6	1.0	21010	4	US-09-902-540-1188	Sequence 1188, Ap
c1198	32.6	1.0	21784	4	US-09-820-002-3	Sequence 3, Appli
c1199	32.6	1.0	22906	4	US-09-949-016-16471	Sequence 16471, A
c1200	32.6	1.0	23694	4	US-09-902-540-1216	Sequence 1216, Ap
1201	32.6	1.0	27250	4	US-09-949-016-15537	Sequence 15537, A
c1202	32.6	1.0	28809	4	US-09-949-016-12825	Sequence 12825, A
1203	32.6	1.0	29569	4	US-09-949-016-15875	Sequence 15875, A
c1204	32.6	1.0	30135	4	US-09-902-540-1249	Sequence 1249, Ap
1205	32.6	1.0	30291	4	US-09-949-016-12875	Sequence 12875, A
c1206	32.6	1.0	30337	4	US-09-949-016-13053	Sequence 13053, A
1207	32.6	1.0	31571	1	US-08-323-443B-1	Sequence 1, Appli
1208	32.6	1.0	38653	4	US-09-949-016-15987	Sequence 15987, A

1209	32.6	1.0	47981	4	US-09-679-279-1	Sequence 1, Appli
c1210	32.6	1.0	47981	4	US-09-679-279-1	Sequence 1, Appli
1211	32.6	1.0	53526	3	US-08-658-136-2	Sequence 2, Appli
1212	32.6	1.0	53577	3	US-08-658-136-1	Sequence 1, Appli
c1213	32.6	1.0	55195	4	US-09-949-016-15854	Sequence 15854, A
1214	32.6	1.0	65561	4	US-09-949-016-15365	Sequence 15365, A
c1215	32.6	1.0	86936	4	US-09-949-016-17314	Sequence 17314, A
c1216	32.6	1.0	107800	4	US-09-949-016-13118	Sequence 13118, A
c1217	32.6	1.0	116425	4	US-09-949-016-11809	Sequence 11809, A
c1218	32.6	1.0	137226	4	US-09-949-016-13763	Sequence 13763, A
1219	32.4	1.0	216	4	US-09-252-991A-7160	Sequence 7160, Ap
1220	32.4	1.0	329	4	US-08-956-171E-4360	Sequence 4360, Ap
1221	32.4	1.0	329	4	US-08-781-986A-4360	Sequence 4360, Ap
c1222	32.4	1.0	435	4	US-09-252-991A-10001	Sequence 10001, A
1223	32.4	1.0	581	2	US-08-557-309B-22	Sequence 22, Appl
1224	32.4	1.0	581	3	US-08-834-306-22	Sequence 22, Appl
1225	32.4	1.0	581	3	US-08-993-674A-22	Sequence 22, Appl
1226	32.4	1.0	581	3	US-09-256-976-22	Sequence 22, Appl
1227	32.4	1.0	601	4	US-09-949-016-40459	Sequence 40459, A
1228	32.4	1.0	601	4	US-09-949-016-40460	Sequence 40460, A
c1229	32.4	1.0	601	4	US-09-949-016-55209	Sequence 55209, A
c1230	32.4	1.0	601	4	US-09-949-016-131726	Sequence 131726,
1231	32.4	1.0	601	4	US-09-949-016-168358	Sequence 168358,
1232	32.4	1.0	750	4	US-09-252-991A-12401	Sequence 12401, A
1233	32.4	1.0	834	4	US-09-621-976-2574	Sequence 2574, Ap
1234	32.4	1.0	886	4	US-08-134-231C-31	Sequence 31, Appl
1235	32.4	1.0	886	4	US-08-728-160-31	Sequence 31, Appl
1236	32.4	1.0	999	4	US-09-902-540-2460	Sequence 2460, Ap
1237	32.4	1.0	1119	4	US-09-902-540-2952	Sequence 2952, Ap
1238	32.4	1.0	1304	4	US-09-902-540-2596	Sequence 2596, Ap
1239	32.4	1.0	1320	4	US-09-902-540-7483	Sequence 7483, Ap
1240	32.4	1.0	1488	4	US-09-902-540-4238	Sequence 4238, Ap
c1241	32.4	1.0	1581	4	US-09-252-991A-12190	Sequence 12190, A
c1242	32.4	1.0	1620	4	US-09-252-991A-12255	Sequence 12255, A
1243	32.4	1.0	1626	4	US-09-252-991A-3266	Sequence 3266, Ap
1244	32.4	1.0	1701	4	US-09-252-991A-8109	Sequence 8109, Ap
1245	32.4	1.0	1776	4	US-09-902-540-6344	Sequence 6344, Ap
c1246	32.4	1.0	1802	4	US-09-949-016-1604	Sequence 1604, Ap
1247	32.4	1.0	1872	4	US-09-252-991A-3296	Sequence 3296, Ap
c1248	32.4	1.0	1920	4	US-09-252-991A-9817	Sequence 9817, Ap
c1249	32.4	1.0	1923	4	US-09-252-991A-3380	Sequence 3380, Ap
1250	32.4	1.0	2034	4	US-09-902-540-5490	Sequence 5490, Ap
c1251	32.4	1.0	2131	4	US-09-976-594-441	Sequence 441, App
c1252	32.4	1.0	2151	4	US-09-902-540-9468	Sequence 9468, Ap
1253	32.4	1.0	2299	4	US-09-475-515-81	Sequence 81, Appl
1254	32.4	1.0	2300	4	US-09-475-515-83	Sequence 83, Appl
c1255	32.4	1.0	2301	1	US-08-306-691B-23	Sequence 23, Appl
c1256	32.4	1.0	2301	4	US-09-167-206-3	Sequence 3, Appli
c1257	32.4	1.0	2301	5	PCT-US93-06251-78	Sequence 78, Appl
1258	32.4	1.0	2305	4	US-09-475-515-80	Sequence 80, Appl
1259	32.4	1.0	2306	4	US-09-475-515-82	Sequence 82, Appl
1260	32.4	1.0	2312	4	US-09-475-515-84	Sequence 84, Appl
c1261	32.4	1.0	2370	4	US-09-902-540-401	Sequence 401, App
c1262	32.4	1.0	2472	4	US-09-252-991A-8197	Sequence 8197, Ap
c1263	32.4	1.0	2483	1	US-08-464-340A-3	Sequence 3, Appli
c1264	32.4	1.0	2483	5	PCT-US94-08449A-3	Sequence 3, Appli
c1265	32.4	1.0	3433	4	US-09-902-540-6810	Sequence 6810, Ap

c1266	32.4	1.0	3434	4	US-09-902-540-564	Sequence 564, App
1267	32.4	1.0	4168	4	US-09-266-225D-17	Sequence 17, Appl
1268	32.4	1.0	4279	3	US-09-041-886-22	Sequence 22, Appl
1269	32.4	1.0	4319	4	US-09-475-515-6	Sequence 6, Appli
1270	32.4	1.0	4515	4	US-09-252-991A-10037	Sequence 10037, A
c1271	32.4	1.0	4758	4	US-09-774-528-129	Sequence 129, App
1272	32.4	1.0	5590	3	US-09-050-159-129	Sequence 129, App
c1273	32.4	1.0	5802	4	US-09-949-016-13346	Sequence 13346, A
1274	32.4	1.0	6333	4	US-09-949-016-15447	Sequence 15447, A
1275	32.4	1.0	11254	4	US-09-902-540-1040	Sequence 1040, Ap
1276	32.4	1.0	14077	4	US-09-902-540-1109	Sequence 1109, Ap
c1277	32.4	1.0	14467	4	US-09-902-540-1058	Sequence 1058, Ap
1278	32.4	1.0	15756	4	US-09-949-016-13607	Sequence 13607, A
1279	32.4	1.0	16442	3	US-08-781-891-208	Sequence 208, App
1280	32.4	1.0	16442	4	US-09-618-166-208	Sequence 208, App
1281	32.4	1.0	16584	4	US-09-902-540-1119	Sequence 1119, Ap
c1282	32.4	1.0	18836	4	US-09-949-016-12654	Sequence 12654, A
c1283	32.4	1.0	18838	4	US-09-949-016-15633	Sequence 15633, A
c1284	32.4	1.0	23856	4	US-09-949-016-15732	Sequence 15732, A
1285	32.4	1.0	24791	4	US-09-902-540-1211	Sequence 1211, Ap
c1286	32.4	1.0	25603	4	US-09-819-607-3	Sequence 3, Appli
1287	32.4	1.0	25686	4	US-09-902-540-1246	Sequence 1246, Ap
1288	32.4	1.0	27555	4	US-09-949-016-17466	Sequence 17466, A
1289	32.4	1.0	29165	4	US-09-949-016-12340	Sequence 12340, A
c1290	32.4	1.0	32487	4	US-09-949-016-12950	Sequence 12950, A
1291	32.4	1.0	33109	4	US-09-949-016-14301	Sequence 14301, A
1292	32.4	1.0	33870	4	US-09-949-016-16306	Sequence 16306, A
c1293	32.4	1.0	36311	4	US-09-949-016-13627	Sequence 13627, A
1294	32.4	1.0	44166	4	US-09-949-016-15829	Sequence 15829, A
1295	32.4	1.0	54180	4	US-09-949-016-14894	Sequence 14894, A
1296	32.4	1.0	100550	4	US-09-949-016-11835	Sequence 11835, A
1297	32.4	1.0	100551	4	US-09-949-016-16207	Sequence 16207, A
1298	32.4	1.0	119032	4	US-09-949-016-12160	Sequence 12160, A
c1299	32.4	1.0	119032	4	US-09-949-016-12160	Sequence 12160, A
1300	32.4	1.0	119032	4	US-09-949-016-17268	Sequence 17268, A
c1301	32.4	1.0	119032	4	US-09-949-016-17268	Sequence 17268, A
1302	32.4	1.0	211049	4	US-09-949-016-15770	Sequence 15770, A
1303	32.4	1.0	225127	4	US-09-949-016-16480	Sequence 16480, A
c1304	32.4	1.0	767677	4	US-09-949-016-12147	Sequence 12147, A
c1305	32.4	1.0	767677	4	US-09-949-016-17361	Sequence 17361, A
1306	32.2	1.0	601	4	US-09-949-016-22545	Sequence 22545, A
1307	32.2	1.0	601	4	US-09-949-016-41496	Sequence 41496, A
c1308	32.2	1.0	601	4	US-09-949-016-43068	Sequence 43068, A
c1309	32.2	1.0	601	4	US-09-949-016-43069	Sequence 43069, A
1310	32.2	1.0	601	4	US-09-949-016-67075	Sequence 67075, A
c1311	32.2	1.0	601	4	US-09-949-016-76722	Sequence 76722, A
1312	32.2	1.0	601	4	US-09-949-016-109158	Sequence 109158,
1313	32.2	1.0	601	4	US-09-949-016-109159	Sequence 109159,
1314	32.2	1.0	601	4	US-09-949-016-109160	Sequence 109160,
1315	32.2	1.0	601	4	US-09-949-016-152781	Sequence 152781,
1316	32.2	1.0	601	4	US-09-949-016-152782	Sequence 152782,
c1317	32.2	1.0	601	4	US-09-949-016-166471	Sequence 166471,
c1318	32.2	1.0	601	4	US-09-949-016-166472	Sequence 166472,
1319	32.2	1.0	618	4	US-09-902-540-4224	Sequence 4224, Ap
c1320	32.2	1.0	621	4	US-09-252-991A-4174	Sequence 4174, Ap
1321	32.2	1.0	702	4	US-09-252-991A-6791	Sequence 6791, Ap
c1322	32.2	1.0	732	1	US-08-145-006C-21	Sequence 21, Appl

c1323	32.2	1.0	732	5	PCT-US94-00545-22	Sequence 22, Appl
c1324	32.2	1.0	738	4	US-09-252-991A-14234	Sequence 14234, A
c1325	32.2	1.0	765	4	US-09-252-991A-6948	Sequence 6948, Ap
c1326	32.2	1.0	774	4	US-09-902-540-2962	Sequence 2962, Ap
1327	32.2	1.0	1038	4	US-09-252-991A-419	Sequence 419, App
1328	32.2	1.0	1059	4	US-09-489-039A-6329	Sequence 6329, Ap
c1329	32.2	1.0	1065	1	US-08-145-006C-11	Sequence 11, Appl
c1330	32.2	1.0	1107	4	US-09-252-991A-14146	Sequence 14146, A
1331	32.2	1.0	1113	4	US-09-902-540-6584	Sequence 6584, Ap
1332	32.2	1.0	1233	4	US-09-252-991A-4433	Sequence 4433, Ap
1333	32.2	1.0	1446	4	US-09-252-991A-6746	Sequence 6746, Ap
c1334	32.2	1.0	1474	5	PCT-US94-00545-19	Sequence 19, Appl
c1335	32.2	1.0	1498	4	US-09-919-172-100	Sequence 100, App
c1336	32.2	1.0	1498	4	US-09-976-594-468	Sequence 468, App
1337	32.2	1.0	1521	4	US-09-252-991A-13990	Sequence 13990, A
c1338	32.2	1.0	1557	4	US-09-252-991A-422	Sequence 422, App
1339	32.2	1.0	1584	4	US-09-252-991A-383	Sequence 383, App
1340	32.2	1.0	1680	4	US-09-902-540-9561	Sequence 9561, Ap
1341	32.2	1.0	1740	4	US-09-252-991A-6553	Sequence 6553, Ap
c1342	32.2	1.0	1761	4	US-09-252-991A-4120	Sequence 4120, Ap
1343	32.2	1.0	1800	4	US-09-252-991A-4085	Sequence 4085, Ap
1344	32.2	1.0	1863	4	US-09-252-991A-4539	Sequence 4539, Ap
c1345	32.2	1.0	1931	4	US-09-949-016-4419	Sequence 4419, Ap
1346	32.2	1.0	2172	4	US-09-252-991A-1708	Sequence 1708, Ap
1347	32.2	1.0	2229	4	US-09-902-540-4193	Sequence 4193, Ap
c1348	32.2	1.0	2241	4	US-09-252-991A-2016	Sequence 2016, Ap
1349	32.2	1.0	2247	4	US-09-252-991A-1856	Sequence 1856, Ap
c1350	32.2	1.0	2469	4	US-09-252-991A-6519	Sequence 6519, Ap
1351	32.2	1.0	2561	4	US-09-616-289-48	Sequence 48, Appl
1352	32.2	1.0	2824	3	US-07-757-022B-13	Sequence 13, Appl
c1353	32.2	1.0	2839	5	PCT-US94-07297-38	Sequence 38, Appl
c1354	32.2	1.0	2847	4	US-09-902-540-7588	Sequence 7588, Ap
c1355	32.2	1.0	2865	4	US-09-252-991A-4317	Sequence 4317, Ap
c1356	32.2	1.0	2986	4	US-09-023-655-930	Sequence 930, App
1357	32.2	1.0	3066	3	US-07-757-022B-83	Sequence 83, Appl
1358	32.2	1.0	3117	3	US-07-757-022B-73	Sequence 73, Appl
1359	32.2	1.0	3147	2	US-08-781-802-7	Sequence 7, Appli
1360	32.2	1.0	3147	3	US-08-694-078-7	Sequence 7, Appli
1361	32.2	1.0	3147	3	US-09-058-260-7	Sequence 7, Appli
1362	32.2	1.0	3148	3	US-07-757-022B-57	Sequence 57, Appl
1363	32.2	1.0	3420	3	US-07-757-022B-103	Sequence 103, App
c1364	32.2	1.0	3478	1	US-08-396-479B-1	Sequence 1, Appli
c1365	32.2	1.0	3478	1	US-08-818-823-1	Sequence 1, Appli
c1366	32.2	1.0	3489	2	US-08-728-323A-1	Sequence 1, Appli
c1367	32.2	1.0	3489	3	US-09-298-568-1	Sequence 1, Appli
c1368	32.2	1.0	3489	4	US-09-410-399-1	Sequence 1, Appli
c1369	32.2	1.0	3489	4	US-09-894-273-1	Sequence 1, Appli
c1370	32.2	1.0	3516	4	US-09-417-197-130	Sequence 130, App
c1371	32.2	1.0	3546	4	US-09-417-197-132	Sequence 132, App
1372	32.2	1.0	3813	3	US-07-757-022B-43	Sequence 43, Appl
c1373	32.2	1.0	3860	4	US-09-902-540-494	Sequence 494, App
1374	32.2	1.0	3936	3	US-07-757-022B-41	Sequence 41, Appl
1375	32.2	1.0	3942	3	US-07-757-022B-141	Sequence 141, App
1376	32.2	1.0	3945	3	US-07-757-022B-49	Sequence 49, Appl
1377	32.2	1.0	3963	3	US-07-757-022B-45	Sequence 45, Appl
1378	32.2	1.0	3963	3	US-07-757-022B-59	Sequence 59, Appl
1379	32.2	1.0	4065	3	US-07-757-022B-47	Sequence 47, Appl

1380	32.2	1.0	4086	3	US-07-757-022B-39	Sequence 39, Appl
1381	32.2	1.0	4092	3	US-07-757-022B-51	Sequence 51, Appl
1382	32.2	1.0	4190	3	US-08-938-291A-2	Sequence 2, Appli
1383	32.2	1.0	4190	4	US-09-589-619-2	Sequence 2, Appli
1384	32.2	1.0	4215	3	US-07-757-022B-61	Sequence 61, Appl
c1385	32.2	1.0	4237	1	US-07-844-298B-1	Sequence 1, Appli
1386	32.2	1.0	4847	4	US-10-164-595-57	Sequence 57, Appl
1387	32.2	1.0	5008	3	US-07-757-022B-1	Sequence 1, Appli
1388	32.2	1.0	5017	4	US-09-949-016-4956	Sequence 4956, Ap
1389	32.2	1.0	5041	4	US-09-023-655-981	Sequence 981, App
1390	32.2	1.0	5041	4	US-09-298-970A-2	Sequence 2, Appli
c1391	32.2	1.0	7218	1	US-08-232-463-14	Sequence 14, Appl
c1392	32.2	1.0	7266	4	US-09-949-016-16428	Sequence 16428, A
c1393	32.2	1.0	7704	4	US-09-902-540-743	Sequence 743, App
c1394	32.2	1.0	7970	4	US-09-193-707-6	Sequence 6, Appli
1395	32.2	1.0	9208	4	US-09-068-506-1	Sequence 1, Appli
c1396	32.2	1.0	9521	3	US-08-972-218-2	Sequence 2, Appli
c1397	32.2	1.0	9521	4	US-09-193-707-2	Sequence 2, Appli
c1398	32.2	1.0	11703	1	US-08-801-263A-8	Sequence 8, Appli
c1399	32.2	1.0	11703	3	US-09-102-248-8	Sequence 8, Appli
c1400	32.2	1.0	11703	4	US-09-367-764-8	Sequence 8, Appli
c1401	32.2	1.0	11740	3	US-09-415-784-103	Sequence 103, App
c1402	32.2	1.0	11740	3	US-09-415-785A-103	Sequence 103, App
c1403	32.2	1.0	11740	3	US-08-944-465-103	Sequence 103, App
c1404	32.2	1.0	11740	3	US-09-415-868-103	Sequence 103, App
c1405	32.2	1.0	11740	3	US-09-415-900-103	Sequence 103, App
c1406	32.2	1.0	11740	4	US-09-507-362-103	Sequence 103, App
1407	32.2	1.0	13863	4	US-09-814-915A-83	Sequence 83, Appl
c1408	32.2	1.0	13905	3	US-08-972-218-1	Sequence 1, Appli
c1409	32.2	1.0	13905	4	US-09-193-707-1	Sequence 1, Appli
c1410	32.2	1.0	14862	4	US-09-949-016-14789	Sequence 14789, A
1411	32.2	1.0	14967	4	US-09-949-016-15448	Sequence 15448, A
c1412	32.2	1.0	15172	4	US-09-902-540-1086	Sequence 1086, Ap
c1413	32.2	1.0	15500	3	US-09-080-983-1	Sequence 1, Appli
1414	32.2	1.0	16344	4	US-09-949-016-16034	Sequence 16034, A
c1415	32.2	1.0	16387	4	US-09-902-540-1156	Sequence 1156, Ap
c1416	32.2	1.0	16656	1	US-08-741-881-1	Sequence 1, Appli
c1417	32.2	1.0	16656	1	US-08-739-158-1	Sequence 1, Appli
c1418	32.2	1.0	16656	2	US-08-739-167-1	Sequence 1, Appli
c1419	32.2	1.0	16656	3	US-08-404-796-1	Sequence 1, Appli
c1420	32.2	1.0	16656	3	US-08-931-869-1	Sequence 1, Appli
c1421	32.2	1.0	16656	3	US-09-350-399-1	Sequence 1, Appli
c1422	32.2	1.0	16656	3	US-09-236-140A-1	Sequence 1, Appli
c1423	32.2	1.0	16924	4	US-09-949-016-13720	Sequence 13720, A
1424	32.2	1.0	19979	4	US-09-949-016-12309	Sequence 12309, A
1425	32.2	1.0	19980	4	US-09-949-016-13533	Sequence 13533, A
c1426	32.2	1.0	21330	4	US-09-902-540-1209	Sequence 1209, Ap
1427	32.2	1.0	21707	4	US-09-949-016-16698	Sequence 16698, A
1428	32.2	1.0	23704	4	US-09-949-016-12104	Sequence 12104, A
1429	32.2	1.0	23704	4	US-09-949-016-15312	Sequence 15312, A
1430	32.2	1.0	25973	4	US-09-949-016-14140	Sequence 14140, A
c1431	32.2	1.0	28509	4	US-09-902-540-1240	Sequence 1240, Ap
1432	32.2	1.0	30755	4	US-09-949-016-16497	Sequence 16497, A
1433	32.2	1.0	32207	2	US-08-770-379-20	Sequence 20, Appl
1434	32.2	1.0	32207	3	US-08-757-669A-20	Sequence 20, Appl
1435	32.2	1.0	32207	3	US-09-230-371A-20	Sequence 20, Appl
c1436	32.2	1.0	69834	4	US-09-949-016-11959	Sequence 11959, A

c1437	32.2	1.0	69834	4	US-09-949-016-12925	Sequence 12925, A
c1438	32.2	1.0	72742	4	US-09-949-016-16161	Sequence 16161, A
c1439	32.2	1.0	101558	4	US-09-949-016-12243	Sequence 12243, A
1440	32.2	1.0	119801	4	US-09-949-016-13453	Sequence 13453, A
c1441	32.2	1.0	152481	4	US-09-949-016-12521	Sequence 12521, A
c1442	32.2	1.0	152798	4	US-09-949-016-12775	Sequence 12775, A
c1443	32.2	1.0	152822	4	US-09-949-016-17518	Sequence 17518, A
c1444	32.2	1.0	152822	4	US-09-949-016-17519	Sequence 17519, A
c1445	32.2	1.0	154600	4	US-09-949-016-14757	Sequence 14757, A
1446	32.2	1.0	187916	4	US-09-949-016-12980	Sequence 12980, A
c1447	32.2	1.0	323820	4	US-09-949-016-14139	Sequence 14139, A
1448	32	1.0	420	4	US-09-252-991A-7090	Sequence 7090, Ap
1449	32	1.0	484	4	US-09-270-767-1056	Sequence 1056, Ap
1450	32	1.0	484	4	US-09-270-767-16338	Sequence 16338, A
1451	32	1.0	489	4	US-09-252-991A-15440	Sequence 15440, A
1452	32	1.0	552	4	US-09-902-540-4927	Sequence 4927, Ap
1453	32	1.0	600	4	US-09-252-991A-9052	Sequence 9052, Ap
c1454	32	1.0	601	4	US-09-949-016-28496	Sequence 28496, A
1455	32	1.0	601	4	US-09-949-016-28715	Sequence 28715, A
1456	32	1.0	601	4	US-09-949-016-28716	Sequence 28716, A
c1457	32	1.0	601	4	US-09-949-016-48721	Sequence 48721, A
c1458	32	1.0	601	4	US-09-949-016-58398	Sequence 58398, A
c1459	32	1.0	601	4	US-09-949-016-58399	Sequence 58399, A
1460	32	1.0	601	4	US-09-949-016-70380	Sequence 70380, A
1461	32	1.0	601	4	US-09-949-016-77709	Sequence 77709, A
1462	32	1.0	601	4	US-09-949-016-77710	Sequence 77710, A
c1463	32	1.0	601	4	US-09-949-016-85113	Sequence 85113, A
c1464	32	1.0	601	4	US-09-949-016-85264	Sequence 85264, A
c1465	32	1.0	601	4	US-09-949-016-125334	Sequence 125334, A
c1466	32	1.0	601	4	US-09-949-016-139410	Sequence 139410, A
1467	32	1.0	601	4	US-09-949-016-168357	Sequence 168357, A
c1468	32	1.0	601	4	US-09-949-001-759	Sequence 759, App
1469	32	1.0	630	4	US-09-252-991A-953	Sequence 953, App
1470	32	1.0	687	4	US-09-902-540-6577	Sequence 6577, Ap
c1471	32	1.0	777	4	US-09-252-991A-1127	Sequence 1127, Ap
c1472	32	1.0	834	4	US-09-252-991A-15248	Sequence 15248, A
1473	32	1.0	876	3	US-09-149-476-315	Sequence 315, App
1474	32	1.0	915	4	US-09-252-991A-9133	Sequence 9133, Ap
1475	32	1.0	948	4	US-09-252-991A-9121	Sequence 9121, Ap
1476	32	1.0	951	4	US-09-902-540-7965	Sequence 7965, Ap
1477	32	1.0	958	4	US-09-949-016-2799	Sequence 2799, Ap
1478	32	1.0	958	4	US-09-949-016-2800	Sequence 2800, Ap
c1479	32	1.0	993	4	US-09-252-991A-8950	Sequence 8950, Ap
1480	32	1.0	1017	4	US-09-489-039A-4439	Sequence 4439, Ap
c1481	32	1.0	1035	4	US-09-902-540-8589	Sequence 8589, Ap
c1482	32	1.0	1047	4	US-09-270-767-10455	Sequence 10455, A
1483	32	1.0	1059	4	US-09-949-016-5611	Sequence 5611, Ap
1484	32	1.0	1092	4	US-09-902-540-3977	Sequence 3977, Ap
1485	32	1.0	1119	4	US-09-252-991A-15496	Sequence 15496, A
1486	32	1.0	1122	4	US-09-902-540-8842	Sequence 8842, Ap
c1487	32	1.0	1131	4	US-09-252-991A-1055	Sequence 1055, Ap
c1488	32	1.0	1176	4	US-09-252-991A-11771	Sequence 11771, A
1489	32	1.0	1203	4	US-09-252-991A-10851	Sequence 10851, A
c1490	32	1.0	1332	4	US-09-252-991A-15340	Sequence 15340, A
c1491	32	1.0	1332	4	US-09-902-540-9662	Sequence 9662, Ap
1492	32	1.0	1335	4	US-09-252-991A-4449	Sequence 4449, Ap
c1493	32	1.0	1341	4	US-09-252-991A-10828	Sequence 10828, A

c1494	32	1.0	1347	4	US-09-252-991A-4158	Sequence 4158, Ap
c1495	32	1.0	1416	4	US-09-955-732A-20	Sequence 20, Appl
c1496	32	1.0	1434	4	US-09-252-991A-8967	Sequence 8967, Ap
1497	32	1.0	1452	4	US-09-252-991A-3387	Sequence 3387, Ap
1498	32	1.0	1521	4	US-09-902-540-7920	Sequence 7920, Ap
1499	32	1.0	1545	4	US-09-252-991A-11637	Sequence 11637, A
c1500	32	1.0	1557	4	US-09-252-991A-7033	Sequence 7033, Ap

ALIGNMENTS

RESULT 1

US-09-578-063-17

; Sequence 17, Application US/09578063

; Patent No. 6764677

; GENERAL INFORMATION:

; APPLICANT: McCarthy, Sean A

; APPLICANT: Barnes, Thomas M

; APPLICANT: Fraser, Christopher C

; APPLICANT: Sharp, John D

; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING DIAGNOSTIC,

; TITLE OF INVENTION: PREVENTIVE, THERAPEUTIC, AND OTHER USES

; FILE REFERENCE: 210147.0023/6U1

; CURRENT APPLICATION NUMBER: US/09/578,063

; CURRENT FILING DATE: 2000-05-24

; PRIOR APPLICATION NUMBER: US 09/333,159

; PRIOR FILING DATE: 1999-06-14

; NUMBER OF SEQ ID NOS: 79

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; SOFTWARE: PatentIn Ver. 2.1
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; SEQ ID NO 17

; LENGTH: 3104

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-578-063-17

Query Match 96.7%; Score 3040.8; DB 4; Length 3104;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 3053; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

Qy 89 CAGTCTGTGGCTGAGCATGGCCCTCCCAGCCCTGGGCCTGGACCCCTGGAGCCTCCTGGG 148

Db 16 CGGTCTGTGGCTGAGCATGGCCCTCCCAGCCCTGGGCTGGACCCCTGGAGCCTCCTGGG 75

Qy 149 CCTTTTCCTCTTCCAAGTCTTCAGCTGCTGCTGCCGACGACACCGCGGGGGGAGGCGG 208

Db 76 CCTTTTCCTCTTCCAAGTCTTCAGCTGCTGCTGCCGACGACGACCGCGGGGGGAGGCGG 135

Qy 209 GCAGGGGCCCATGCCAGGGTCAGATACTATGCAGGGGATGAACGTAGGGCACTTAGCTT 268

Db 136 GCAGGGGCCCATGCCCAGGGTCAGATACTATGCAGGGGATGAACGTAGGGCACTTAGCTT 195

Qy 269 CTTCCACCAGAAGGGCCTCCAGGATTTTGACACTCTGCTCCTGAGTGGTGATGGAAATAC 328

Db 196 CTTCCACCAGAAGGGCCTCCAGGATTTTGACACTCTGCTCCTGAGTGGTGATGGAAATAC 255

Qy 329 TCTCTACGTGGGGGCTCGAGAAGCCATTCTGGCCTTGGATATCCAGGATCCAGGGGTCCC 388

Db	256	 TCTCTACGTGGGGGCTCGAGAAGCCATTCTGGCCTTGGATATCCAGGATCCAGGGGTCCC	315
Qy	389	CAGGCTAAAGAACATGATACCGTGGCCAGCCAGTGACAGAAAAAAGAGTGAATGTGCCTT	448
Db	316	 CAGGCTAAAGAACATGATACCGTGGCCAGCCAGTGACAGAAAAAAGAGTGAATGTGCCTT	375
Qy	449	TAAGAAGAAGAGCAATGAGACACAGTGTTCACCTTCATCCGTGTCTGGTTTCTTACAA	508
Db	376	 TAAGAAGAAGAGCAATGAGACACAGTGTTCACCTTCATCCGTGTCTGGTTTCTTACAA	435
Qy	509	TGTCACCCATCTCTACACCTGCGGCACCTTCGCCTTCAGCCCTGCTTGTACCTTCATTGA	568
Db	436	 TGTCACCCATCTCTACACCTGCGGCACCTTCGCCTTCAGCCCTGCTTGTACCTTCATTGA	495
Qy	569	ACTTCAAGATTCCTACCTGTTGCCCATCTCGGAGGACAAGGTCATGGAGGAAAAGGCCA	628
Db	496	 ACTTCAAGATTCCTACCTGTTGCCCATCTCGGAGGACAAGGTCATGGAGGAAAAGGCCA	555
Qy	629	AAGCCCCCTTTGACCCCGCTCACAAGCATACGGCTGTCTTGGTGGATGGGATGCTCTATTC	688
Db	556	 AAGCCCCCTTTGACCCCGCTCACAAGCATACGGCTGTCTTGGTGGATGGGATGCTCTATTC	615
Qy	689	TGGTACTATGAACAACTTCCTGGGCAGTGAGCCCATCCTGATGCGCACACTGGGATCCCA	748
Db	616	 TGGTACTATGAACAACTTCCTGGGCAGTGAGCCCATCCTGATGCGCACACTGGGATCCCA	675
Qy	749	GCCTGTCTCTCAAGACCGACAACCTTCCTCCGCTGGCTGCATCATGACGCCCTCCTTTGTGGC	808
Db	676	 GCCTGTCTCTCAAGACCGACAACCTTCCTCCGCTGGCTGCATCATGACGCCCTCCTTTGTGGC	735
Qy	809	AGCCATCCCTTCGACCCAGGTCGTCTACTTCTTCTTCGAGGAGACAGCCAGCGAGTTTGA	868
Db	736	 AGCCATCCCTTCGACCCAGGTCGTCTACTTCTTCTTCGAGGAGACAGCCAGCGAGTTTGA	795
Qy	869	CTTCTTTGAGAGGCTCCACACATCGCGGGTGGCTAGAGTCTGCAAGAATGACGTGGGCGG	928
Db	796	 CTTCTTTGAGAGGCTCCACACATCGCGGGTGGCTAGAGTCTGCAAGAATGACGTGGGCGG	855
Qy	929	CGAAAAGCTGCTGCAGAAGAAGTGGACCACCTTCCTGAAGGCCAGCTGCTCTGCACCCA	988
Db	856	 CGAAAAGCTGCTGCAGAAGAAGTGGACCACCTTCCTGAAGGCCAGCTGCTCTGCACCCA	915
Qy	989	GCCGGGGCAGCTGCCCTTCAACGTCATCCGCCACGCGGTCTGCTCCCCGCCGATTCTCC	1048
Db	916	 GCCGGGGCAGCTGCCCTTCAACGTCATCCGCCACGCGGTCTGCTCCCCGCCGATTCTCC	975
Qy	1049	CACAGCTCCCCACATCTACGCAGTCTTCACCTCCCAGTGGCAGGTTGGCGGGACCAGGAG	1108
Db	976	 CACAGCTCCCCACATCTACGCAGTCTTCACCTCCCAGTGGCAGGTTGGCGGGACCAGGAG	1035
Qy	1109	CTCTGCGGTTTGTGCCTTCTCTCTCTTGGACATTGAACGTGTCTTTAAGGGGAAATACAA	1168
Db	1036	 CTCTGCGGTTTGTGCCTTCTCTCTCTTGGACATTGAACGTGTCTTTAAGGGGAAATACAA	1095
Qy	1169	AGAGTTGAACAAAGAACTTCACGCTGGACTACTTATAGGGGCCCTGAGACCAACCCCCG	1228

Db	1096	AGAGTTGAACAAAGAAACTTCACGCTGGACTACTTATAGGGGCCCTGAGACCAACCCCCG	1155
Qy	1229	GCCAGGCAGTTGCTCAGTGGGCCCCCTCCTCTGATAAGGCCCTGACCTTCATGAAGGACCA	1288
Db	1156	GCCAGGCAGTTGCTCAGTGGGCCCCCTCCTCTGATAAGGCCCTGACCTTCATGAAGGACCA	1215
Qy	1289	TTTCCTGATGGATGAGCAAGTGGTGGGGACGCCCCTGCTGGTGAAATCTGGCGTGGAGTA	1348
Db	1216	TTTCCTGATGGATGAGCAAGTGGTGGGGACGCCCCTGCTGGTGAAATCTGGCGTGGAGTA	1275
Qy	1349	TACACGGCTTGCAGTGGAGACAGCCAGGGCCTTGATGGGCACAGCCATCTTGTTCATGTA	1408
Db	1276	TACACGGCTTGCAGTGGAGACAGCCAGGGCCTTGATGGGCACAGCCATCTTGTTCATGTA	1335
Qy	1409	CCTGGGAACCACCACAGGGTCGCTCCACAAGGCTGTGGTAAGTGGGGACAGCAGTGTCTCA	1468
Db	1336	CCTGGGAACCACCACAGGGTCGCTCCACAAGGCTGTGGTAAGTGGGGACAGCAGTGTCTCA	1395
Qy	1469	TCTGGTGGAAGAGATTTCAGCTGTTCCCTGACCCTGAACCTGTTTCGCAACCTGCAGCTGGC	1528
Db	1396	TCTGGTGGAAGAGATTTCAGCTGTTCCCTGACCCTGAACCTGTTTCGCAACCTGCAGCTGGC	1455
Qy	1529	CCCCACCCAGGGTGCAGTGTTCGTAGGCTTCTCAGGAGGTGTCTGGAGGGTGCCCCGAGC	1588
Db	1456	CCCCACCCAGGGTGCAGTGTTCGTAGGCTTCTCAGGAGGTGTCTGGAGGGTGCCCCGAGC	1515
Qy	1589	CAACTGTAGTGTCTATGAGAGCTGTGTGGACTGTGTCTTGCCCGGGACCCCCACTGTGC	1648
Db	1516	CAACTGTAGTGTCTATGAGAGCTGTGTGGACTGTGTCTTGCCCGGGACCCCCACTGTGC	1575
Qy	1649	CTGGGACCCCTGAGTCCCGAACCTGTTGCCTCCTGTCTGCCCCAACCTGAACCTCCTGGAA	1708
Db	1576	CTGGGACCCCTGAGTCCCGAACCTGTTGCCTCCTGTCTGCCCCAACCTGAACCTCCTGGAA	1635
Qy	1709	GCAGGACATGGAGCGGGGGAACCCAGAGTGGGCATGTGCCAGTGGCCCCATGAGCAGGAG	1768
Db	1636	GCAGGACATGGAGCGGGGGAACCCAGAGTGGGCATGTGCCAGTGGCCCCATGAGCAGGAG	1695
Qy	1769	CCTTCGGCCTCAGAGCCGCCCGCAAATCATTAAGAAGTCCTGGCTGTCCCCAACTCCAT	1828
Db	1696	CCTTCGGCCTCAGAGCCGCCCGCAAATCATTAAGAAGTCCTGGCTGTCCCCAACTCCAT	1755
Qy	1829	CCTGGAGCTCCCCTGCCCCACCTGTCAGCCTTGGCCTCTTATTATTGGAGTCATGGCCC	1888
Db	1756	CCTGGAGCTCCCCTGCCCCACCTGTCAGCCTTGGCCTCTTATTATTGGAGTCATGGCCC	1815
Qy	1889	AGCAGCAGTCCCAGAAGCCTCTTCCACTGTCTACAATGGCTCCCTCTTGCTGATAGTGCA	1948
Db	1816	AGCAGCAGTCCCAGAAGCCTCTTCCACTGTCTACAATGGCTCCCTCTTGCTGATAGTGCA	1875
Qy	1949	GGATGGAGTTGGGGGTCTCTACCACTGCTGGGCAACTGAGAATGGCTTTTCATACCCTGT	2008
Db	1876	GGATGGAGTTGGGGGTCTCTACCACTGCTGGGCAACTGAGAATGGCTTTTCATACCCTGT	1935
Qy	2009	GATCTCCTACTGGGTGGACAGCCAGGACCAGACCCTGGCCCTGGATCCTGAACTGGCAGG	2068
Db	1936	GATCTCCTACTGGGTGGACAGCCAGGACCAGACCCTGGCCCTGGATCCTGAACTGGCAGG	1995

Qy	2069	CATCCCCCGGGAGCATGTGAAGGTCCCCTTGACCAGGGTCAGTGGTGGGGCCGCCCTGGC	2128
Db	1996	CATCCCCCGGGAGCATGTGAAGGTCCCCTTGACCAGGGTCAGTGGTGGGGCCGCCCTGGC	2055
Qy	2129	TGCCCAGCAGTCCTACTGGCCCCACTTTGTCACTGTCACTGTCCTCTTTGCCTTAGTGCT	2188
Db	2056	TGCCCAGCAGTCCTACTGGCCCCACTTTGTCACTGTCACTGTCCTCTTTGCCTTAGTGCT	2115
Qy	2189	TTCAGGAGCCCTCATCATCCTCGTGGCCTCCCCATTGAGAGCACTCCGGGCTCGGGGCAA	2248
Db	2116	TTCAGGAGCCCTCATCATCCTCGTGGCCTCCCCATTGAGAGCACTCCGGGCTCGGGGCAA	2175
Qy	2249	GGTTCAGGGCTGTGAGACCCCTGCGCCCTGGGGAGAAGGCCCGTTAAGCAGAGAGCAACA	2308
Db	2176	GGTTCAGGGCTGTGAGACCCCTGCGCCCTGGGGAGAAGGCCCGTTAAGCAGAGAGCAACA	2235
Qy	2309	CCTCCAGTCTCCCAAGGAATGCAGGACCTCTGCCAGTGATGTGGACGCTGACAACAACCTG	2368
Db	2236	CCTCCAGTCTCCCAAGGAATGCAGGACCTCTGCCAGTGATGTGGACGCTGACAACAACCTG	2295
Qy	2369	CCTAGGCACTGAGGTAGCTTAAACTCTAGGCACAGGCCGGGGCTGCGGTGCAGGCACCTG	2428
Db	2296	CCTAGGCACTGAGGTAGCTTAAACTCTAGGCACAGGCCGGGGCTGCGGTGCAGGCACCTG	2355
Qy	2429	GCCATGCTGGCTGGGCGGCCCAAGCACAGCCCTGACTAGGATGACAGCAGCACAAAAGAC	2488
Db	2356	GCCATGCTGGCTGGGCGGCCCAAGCACAGCCCTGACTAGGATGACAGCAGCACAAAAGAC	2415
Qy	2489	CACCTTTCTCCCCTGAGAGGAGCTTCTGCTACTCTGCATCACTGATGACACTCAGCAGGG	2548
Db	2416	CACCTTTCTCCCCTGAGAGGAGCTTCTGCTACTCTGCATCACTGATGACACTCAGCAGGG	2475
Qy	2549	TGATGCACAGCAGTCTGCCTCCCCTATGGGACTCCCTTCTACCAAGCACATGAGCTCTCT	2608
Db	2476	TGATGCACAGCAGTCTGCCTCCCCTATGGGACTCCCTTCTACCAAGCACATGAGCTCTCT	2535
Qy	2609	AACAGGGTGGGGGCTACCCCCAGACCTGCTCCTACACTGATATTGAAGAACCTGGAGAGG	2668
Db	2536	AACAGGGTGGGGGCTACCCCCAGACCTGCTCCTACACTGATATTGAAGAACCTGGAGAGG	2595
Qy	2669	ATCCTTCAGTTCTGGCCATTCCAGGGACCTCCAGAAACACAGTGTTCAGAGACCCT-	2727
Db	2596	ATCCTTCAGTTCTGGCCATTCCAGGGACCTCCAGAAACACAGTGTTCAGAGATCCTA	2655
Qy	2728	AAAAAACCTGCCTGTCCCAGGACCTTATGGTAATGAACACCAAACATCTAAACAATCATA	2787
Db	2656	AAAAAACCTGCCTGTCCCAGGACCTTATGGTAATGAACACCAAACATCTAAACAATCATA	2715
Qy	2788	TGCTAACATGCCACTCCTGGAAACTCCACTCTGAAGCTGCCGCTTTGGACACCAACACTC	2847
Db	2716	TGCTAACATGCCACTCCTGGAAACTCCACTCTGAAGCTGCCGCTTTGGACACCAACACTC	2775
Qy	2848	CCTTCTCCCAGGGTCATGCAGGGATCTGCTCCCTCCTGCTTCCCTTACCAGTCGTGCACC	2907
Db	2776	CCTTCTCCCAGGGTCATGCAGGGATCTGCTCCCTCCTGCTTCCCTTACCAGTCGTGCACC	2835

Qy 2908 GCTGACTCCCAGGAAGTCTTTCCTGAAGTCTGACCACCTTCTTCTTGCTTCAGTTGGGG 2967
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 Qy 2968 CAGACTCTGATCCCTTCTGCCCTGGCAGAAATGGCAGGGGTAATCTGAGCCTTCTTCACTC 3027
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 Qy 3028 CTTTACCCTAGCTGACCCCTTCACCTCTCCCCCTCCCTTTTCCTTTGTTTTGGGATTCAG 3087
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RESULT 2

US-09-578-063-18

; Sequence 18, Application US/09578063

; Patent No. 6764677

; GENERAL INFORMATION:

; APPLICANT: McCarthy, Sean A

; APPLICANT: Barnes, Thomas M

; APPLICANT: Fraser, Christopher C

; APPLICANT: Sharp, John D

; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING DIAGNOSTIC,

; TITLE OF INVENTION: PREVENTIVE, THERAPEUTIC, AND OTHER USES

; FILE REFERENCE: 210147.0023/6U1

; CURRENT APPLICATION NUMBER: US/09/578,063

; CURRENT FILING DATE: 2000-05-24

; PRIOR APPLICATION NUMBER: US 09/333,159

; PRIOR FILING DATE: 1999-06-14

; NUMBER OF SEQ ID NOS: 79

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 18

; LENGTH: 2283

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-578-063-18

Query Match 72.6%; Score 2283; DB 4; Length 2283;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2283; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 105 ATGGCCCTCCCAGCCCTGGGCCTGGACCCCTGGAGCCTCCTGGGCCTTTTCCTCTTCCAA 164
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 Qy 165 CTGCTTCAGCTGCTGCTGCCGACGACGACCGCGGGGGAGGCGGGCAGGGGCCCATGCCC 224
 |||
 Db 61 CTGCTTCAGCTGCTGCTGCCGACGACGACCGCGGGGGAGGCGGGCAGGGGCCCATGCCC 120
 |||
 Qy 225 AGGGTCAGATACTATGCAGGGGATGAACGTAGGGCACTTAGCTTCTTCCACCAGAAGGGC 284
 |||
 Db 121 AGGGTCAGATACTATGCAGGGGATGAACGTAGGGCACTTAGCTTCTTCCACCAGAAGGGC 180
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Qy	285	CTCCAGGATTTTGACACTCTGCTCCTGAGTGGTGATGGAAATACTCTCTACGTGGGGGCT	344
Db	181	CTCCAGGATTTTGACACTCTGCTCCTGAGTGGTGATGGAAATACTCTCTACGTGGGGGCT	240
Qy	345	CGAGAAGCCATTCTGGCCTTGGATATCCAGGATCCAGGGGTCCCAGGCTAAAGAACATG	404
Db	241	CGAGAAGCCATTCTGGCCTTGGATATCCAGGATCCAGGGGTCCCAGGCTAAAGAACATG	300
Qy	405	ATACCGTGGCCAGCCAGTGACAGAAAAAAGAGTGAATGTGCCTTTAAGAAGAAGAGCAAT	464
Db	301	ATACCGTGGCCAGCCAGTGACAGAAAAAAGAGTGAATGTGCCTTTAAGAAGAAGAGCAAT	360
Qy	465	GAGACACAGTGTTTCAACTTCATCCGTGTCCTGGTTTCTTACAATGTCACCCATCTCTAC	524
Db	361	GAGACACAGTGTTTCAACTTCATCCGTGTCCTGGTTTCTTACAATGTCACCCATCTCTAC	420
Qy	525	ACCTGCGGCACCTTCGCCCTCAGCCCTGCTTGTACCTTCATTGAACTTCAAGATTCCTAC	584
Db	421	ACCTGCGGCACCTTCGCCCTCAGCCCTGCTTGTACCTTCATTGAACTTCAAGATTCCTAC	480
Qy	585	CTGTTGCCCATCTCGGAGGACAAGGTGATGGAGGGAAAAGGCCAAAGCCCCCTTTGACCCC	644
Db	481	CTGTTGCCCATCTCGGAGGACAAGGTGATGGAGGGAAAAGGCCAAAGCCCCCTTTGACCCC	540
Qy	645	GCTCACAAGCATACGGCTGTCTTGGTGGATGGGATGCTCTATTCTGGTACTATGAACAAC	704
Db	541	GCTCACAAGCATACGGCTGTCTTGGTGGATGGGATGCTCTATTCTGGTACTATGAACAAC	600
Qy	705	TTCTTGGGCAGTGAGCCCATCCTGATGCGCACACTGGGATCCCAGCCTGTCTCAAGACC	764
Db	601	TTCTTGGGCAGTGAGCCCATCCTGATGCGCACACTGGGATCCCAGCCTGTCTCAAGACC	660
Qy	765	GACAAC'TCCTCCGCTGGCTGCATCATGACGCCCTCCTTTGTGGCAGCCATCCCTTCGACC	824
Db	661	GACAAC'TCCTCCGCTGGCTGCATCATGACGCCCTCCTTTGTGGCAGCCATCCCTTCGACC	720
Qy	825	CAGGTCGTCTACTTCTTCTTCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAGAGGCTC	884
Db	721	CAGGTCGTCTACTTCTTCTTCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAGAGGCTC	780
Qy	885	CACACATCGCGGGTGGCTAGAGTCTGCAAGAATGACGTGGGCGGCGAAAAGCTGCTGCAG	944
Db	781	CACACATCGCGGGTGGCTAGAGTCTGCAAGAATGACGTGGGCGGCGAAAAGCTGCTGCAG	840
Qy	945	AAGAAGTGGACCACCTTCCTGAAGGCCAGCTGCTCTGCACCCAGCCGGGGCAGCTGCCC	1004
Db	841	AAGAAGTGGACCACCTTCCTGAAGGCCAGCTGCTCTGCACCCAGCCGGGGCAGCTGCCC	900
Qy	1005	TTCAACGTCATCCGCCACGCGGTCTGCTCCCCGCCGATTCTCCACAGCTCCCCACATC	1064
Db	901	TTCAACGTCATCCGCCACGCGGTCTGCTCCCCGCCGATTCTCCACAGCTCCCCACATC	960
Qy	1065	TACGCAGTCTTCACCTCCCAGTGGCAGGTTGGCGGGACCAGGAGCTCTGCGGTTTGTGCC	1124
Db	961	TACGCAGTCTTCACCTCCCAGTGGCAGGTTGGCGGGACCAGGAGCTCTGCGGTTTGTGCC	1020
Qy	1125	TTCTCTCTCTTGGACATTGAACGTGTCTTTAAGGGGAAATACAAAGAGTTGAACAAAGAA	1184

Db	1021	 TTCTCTCTCTGGACATTGAACGTGTCTTTAAGGGGAAATACAAAGAGTTGAACAAAGAA	1080
Qy	1185	ACTTCACGCTGGACTACTTATAGGGGCCCTGAGACCAACCCCCGGCCAGGCAGTTGCTCA	1244
Db	1081	 ACTTCACGCTGGACTACTTATAGGGGCCCTGAGACCAACCCCCGGCCAGGCAGTTGCTCA	1140
Qy	1245	GTGGGGCCCTCCTCTGATAAGGCCCTGACCTTCATGAAGGACCATTTCCTGATGGATGAG	1304
Db	1141	 GTGGGGCCCTCCTCTGATAAGGCCCTGACCTTCATGAAGGACCATTTCCTGATGGATGAG	1200
Qy	1305	CAAGTGGTGGGGACGCCCCCTGCTGGTGAAATCTGGCGTGGAGTATACACGGCTTGCACTG	1364
Db	1201	 CAAGTGGTGGGGACGCCCCCTGCTGGTGAAATCTGGCGTGGAGTATACACGGCTTGCACTG	1260
Qy	1365	GAGACAGCCCAGGGCCTTGATGGGCACAGCCATCTTGTCATGTACCTGGGAACCACCACA	1424
Db	1261	 GAGACAGCCCAGGGCCTTGATGGGCACAGCCATCTTGTCATGTACCTGGGAACCACCACA	1320
Qy	1425	GGGTCGCTCCACAAGGCTGTGGTAAGTGGGGACAGCAGTGCTCATCTGGTGGAAGAGATT	1484
Db	1321	 GGGTCGCTCCACAAGGCTGTGGTAAGTGGGGACAGCAGTGCTCATCTGGTGGAAGAGATT	1380
Qy	1485	CAGCTGTTCCCTGACCCTGAACCTGTTTCGCAACCTGCAGCTGGCCCCACCCAGGGTGCA	1544
Db	1381	 CAGCTGTTCCCTGACCCTGAACCTGTTTCGCAACCTGCAGCTGGCCCCACCCAGGGTGCA	1440
Qy	1545	GTGTTTGTAGGCTTCTCAGGAGGTGTCTGGAGGGTGCCCCGAGCCAACCTGTAGTGTCTAT	1604
Db	1441	 GTGTTTGTAGGCTTCTCAGGAGGTGTCTGGAGGGTGCCCCGAGCCAACCTGTAGTGTCTAT	1500
Qy	1605	GAGAGCTGTGTGGACTGTGTCCCTTGCCCGGGACCCCCACTGTGCCTGGGACCCTGAGTCC	1664
Db	1501	 GAGAGCTGTGTGGACTGTGTCCCTTGCCCGGGACCCCCACTGTGCCTGGGACCCTGAGTCC	1560
Qy	1665	CGAACCTGTTGCCTCCTGTCTGCCCCAACCTGAACTCCTGGAAGCAGGACATGGAGCGG	1724
Db	1561	 CGAACCTGTTGCCTCCTGTCTGCCCCAACCTGAACTCCTGGAAGCAGGACATGGAGCGG	1620
Qy	1725	GGGAACCCAGAGTGGGCATGTGCCAGTGGCCCCATGAGCAGGAGCCTTCGGCCTCAGAGC	1784
Db	1621	 GGGAACCCAGAGTGGGCATGTGCCAGTGGCCCCATGAGCAGGAGCCTTCGGCCTCAGAGC	1680
Qy	1785	CGCCCGCAAATCATTAAGAAGTCCTGGCTGTCCCCAACTCCATCCTGGAGCTCCCCTGC	1844
Db	1681	 CGCCCGCAAATCATTAAGAAGTCCTGGCTGTCCCCAACTCCATCCTGGAGCTCCCCTGC	1740
Qy	1845	CCCCACCTGTCAGCCTTGCCCTCTTATTATTGGAGTCATGGCCCAGCAGCAGTCCCAGAA	1904
Db	1741	 CCCCACCTGTCAGCCTTGCCCTCTTATTATTGGAGTCATGGCCCAGCAGCAGTCCCAGAA	1800
Qy	1905	GCCTCTTCCACTGTCTACAATGGCTCCCTCTTGCTGATAGTGCAGGATGGAGTTGGGGGT	1964
Db	1801	 GCCTCTTCCACTGTCTACAATGGCTCCCTCTTGCTGATAGTGCAGGATGGAGTTGGGGGT	1860
Qy	1965	CTCTACCAGTGCTGGGCAACTGAGAATGGCTTTTTCATACCCTGTGATCTCCTACTGGGTG	2024

Db 1861 CTCTACCAGTGCTGGGCAACTGAGAATGGCTTTTCATACCCCTGTGATCTCCTACTGGGTG 1920
 Qy 2025 GACAGCCAGGACCAGACCCTGGCCCTGGATCCTGAACTGGCAGGCATCCCCGGGAGCAT 2084
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1921 GACAGCCAGGACCAGACCCTGGCCCTGGATCCTGAACTGGCAGGCATCCCCGGGAGCAT 1980
 Qy 2085 GTGAAGGTCCCGTTGACCAGGGTCAGTGGTGGGGCCGCCCTGGCTGCCCAGCAGTCCTAC 2144
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1981 GTGAAGGTCCCGTTGACCAGGGTCAGTGGTGGGGCCGCCCTGGCTGCCCAGCAGTCCTAC 2040
 Qy 2145 TGGCCCCACTTTGTCACTGTCACTGTCTCTTTGCCTTAGTGCTTTCAGGAGCCCTCATC 2204
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 2041 TGGCCCCACTTTGTCACTGTCACTGTCTCTTTGCCTTAGTGCTTTCAGGAGCCCTCATC 2100
 Qy 2205 ATCCTCGTGGCCTCCCCATTGAGAGCACTCCGGGCTCGGGGCAAGGTTTCAGGGCTGTGAG 2264
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 2101 ATCCTCGTGGCCTCCCCATTGAGAGCACTCCGGGCTCGGGGCAAGGTTTCAGGGCTGTGAG 2160
 Qy 2265 ACCCTGCGCCCTGGGGAGAAGGCCCCGTTAAGCAGAGAGCAACACCTCCAGTCTCCCAAG 2324
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 2161 ACCCTGCGCCCTGGGGAGAAGGCCCCGTTAAGCAGAGAGCAACACCTCCAGTCTCCCAAG 2220
 Qy 2325 GAATGCAGGACCTCTGCCAGTGATGTGGACGCTGACAACAACCTGCCTAGGCACTGAGGTA 2384
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 2221 GAATGCAGGACCTCTGCCAGTGATGTGGACGCTGACAACAACCTGCCTAGGCACTGAGGTA 2280
 Qy 2385 GCT 2387
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 Db 2281 GCT 2283

RESULT 3

US-09-578-063-71

; Sequence 71, Application US/09578063

; Patent No. 6764677

; GENERAL INFORMATION:

; APPLICANT: McCarthy, Sean A

; APPLICANT: Barnes, Thomas M

; APPLICANT: Fraser, Christopher C

; APPLICANT: Sharp, John D

; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING DIAGNOSTIC,

; TITLE OF INVENTION: PREVENTIVE, THERAPEUTIC, AND OTHER USES

; FILE REFERENCE: 210147.0023/6U1

; CURRENT APPLICATION NUMBER: US/09/578,063

; CURRENT FILING DATE: 2000-05-24

; PRIOR APPLICATION NUMBER: US 09/333,159

; PRIOR FILING DATE: 1999-06-14

; NUMBER OF SEQ ID NOS: 79

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 71

; LENGTH: 3046

; TYPE: DNA

; ORGANISM: Mus sp.

US-09-578-063-71

Query Match 55.0%; Score 1727.6; DB 4; Length 3046;

Best Local Similarity 76.0%; Pred. No. 0;

Matches 2338; Conservative 0; Mismatches 644; Indels 94; Gaps 13;

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Qy      69 GCTCCAGAGCTCCCTGGTGACAGTCTGTGGCTGAGCATGGCCCTCCCAGCCCTGGGCCTG 128
      |||  || |  ||||| |||  ||||| ||||| |||  ||||| |||
Db      30 GCTGGGGAACCATCTGGTGACCATCTCAGGCTGACCATGGCCCTACCATCCCTGGGCCAG 89

Qy     129 GACCCCTGGAGCCTCCTGGGCCTTTTCCTCTTCCAACCTGCTTCAGCTGCTGCTGCCGACG 188
      ||| | ||||| ||||| |  |||  ||||| ||||| | | |||||  | | |
Db      90 GACTCATGGAGTCTCCTGCGTGTTTTTTCTTCCAACCTCTTCCTGCTGCCATCACTGCCA 149

Qy     189 ACGACCGCGGGGGAGGCGGGCAGGGGCCCATGCCCAGGGTCAGATACTATGCAGGGGAT 248
      | | | | |  ||  || ||||| ||||| ||||| ||||| ||||| || | |
Db     150 CCTGCTTCTGGGACTGGTGGTCAGGGGCCCATGCCCAGAGTCAAATACCATGCTGGAGAC 209

Qy     249 GAACGTAGGGCACTTAGCTTCTTCCACCAGAAGGGCCTCCAGGATTTTGACACTCTGCTC 308
      | |  ||||| || ||||| ||||| || || |||||  || ||||| |||||
Db     210 GGGCACAGGGCCCTCAGCTTCTTCCAACAAAAGGCCTCCGAGACTTTGACACGCTGCTC 269

Qy     309 CTGAGTGGTGATGGAATACTCTCTACGTGGGGGCTCGAGAAGCCATTCTGGCCTTGGAT 368
      ||||| ||||| || ||||| ||||| ||||| || || ||||| || ||
Db     270 CTGAGTGACGATGGCAACACTCTCTATGTGGGGGCTCGAGAGACCGTCCTGGCCTTGAAT 329

Qy     369 ATCCAGGATCCAGGGGTCCCCAGGCTAAAGAACATGATACCGTGGCCAGCCAGTGACAGA 428
      ||||| | |||||  |||  ||||| ||||| ||||| ||||| ||||| |||
Db     330 ATCCAGAACCCAGGAATCCCAAGGCTAAAGAACATGATACCCTGGCCAGCCAGTGAGAGA 389

Qy     429 AAAAAGAGTGAATGTGCCTTTAAGAAGAAGAGCAATGAGACACAGTGTTTCAACTTCATC 488
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db     390 AAAAAGACCGAATGTGCCTTTAAGAAGAAGAGCAATGAGACACAGTGTTTCAACTTCATT 449

Qy     489 CGTGTCTTGGTTTCTTACAATGTCAACCATCTCTACACCTGCGGCACCTTCGCCTTCAGC 548
      || ||||| ||||| ||||| || || |||||  ||| || ||||| |||||
Db     450 CGAGTCTTGGTCTCTTACAATGCTACTCACCTCTATGCCTGTGGGACCTTTGCCTTCAGC 509

Qy     549 CCTGCTTGTAACCTTCATTGAACTTCAAGATTCCCTACCTGTTGCCCATCTCGGAGGACAAG 608
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db     510 CCTGCCTGTACCTTCATTGAACTCCAAGATTCCCTCCTGTTGCCCATCTTGATAGACAAG 569

Qy     609 GTCATGGAGGGAAAAGGCCAAAGCCCCCTTTGACCCCGCTCACAAGCATAC-GGCTGTCTT 667
      ||||| || || ||||| ||||| ||||| ||||| || ||||| |||||
Db     570 GTCATGGACGGGAAGGGCCAAAG-CCCTTTGACCCTGTTTACAAGCACACAAGCTGTCTT 628

Qy     668 GGTGGATGGGATGCTCTATTCTGGTACTATGAACAACCTCCTGGGCAGTGAGCCCATCCT 727
      ||| ||||| ||||| || || ||||| ||||| ||||| ||||| |||||
Db     629 GGTGATGGGATGCTTTATTCCGGCACCATGAACAACCTCCTGGGCAGCGAGCCCATCCT 688

Qy     728 GATGCGCACACTGGGATCCCAGCCTGTCTCAAGACCGACAACCTCCTCCGCTGGCTGCA 787
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db     689 GATGCGGACACTGGGATCCCATCCTGTTCTCAAGACTGACATCTTCTTACGCTGGCTGCA 748

Qy     788 TCATGACGCCTCCTTTGTGGCAGCCATCCCTTCGACCCAGGTCGTCTACTTCTTCTTCGA 847
      || ||||| ||||| ||||| || || ||||| ||||| ||||| |||||
Db     749 CGCGGATGCCCTCCTTCGTGGCAGCCATTCCATCCACCCAGGTCGTCTATTTCTTCTTTGA 808

Qy     848 GGAGACAGCCAGCGAGTTTGACTTCTTTGAGAGGCTCCACACATCGCGGGTGGCTAGAGT 907
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db     809 GGAGACAGCCAGCGAGTTTGACTTCTTTGAAGAGCTGTATATATCCAGGGTGGCTCAAGT 868
```

Qy	908	CTGCAAGAATGACGTGGGCGGCGAAAAGCTGCTGCAGAAGAAGTGGACCACCTTCCTGAA	967
Db	869	CTGCAAGAACGACGTGGGCGGTGAAAAGCTGCTGCAGAAGAAGTGGACCACCTTCCTCAA	928
Qy	968	GGCCCAGCTGCTCTGCACCCAGCCGGGGCAGCTGCCCTTCAACGTCATCCGCCACGCGGT	1027
Db	929	AGCCCAGTTGCTCTGCGCTCAGCCAGGGCAGCTGCCATTCAACATCATCCGCCACGCGGT	988
Qy	1028	CCTGCTCCCCGCCGATTCTCCACAGCTCCCCACATCTACGCAGTCTTCACCTCCAGTG	1087
Db	989	CCTGCTGCCCGCCGATTCTCCCTCTGTTTCCCGCATCTACGCAGTCTTTACCTCCAGTG	1048
Qy	1088	GCAGGTTGGCGGGACCAGGAGCTCTGCGGTTTGTGCCTTCTCTCTCTGGACATTGAACG	1147
Db	1049	GCAGGTTGGCGGGACCAGGAGCTCAGCAGTCTGTGCCTTCTCTCTCACGGACATTGAGCG	1108
Qy	1148	TGTCTTTAAGGGGAAATACAAAGAGTTGAACAAAGAACTTCACGCTGGACTACTTATAG	1207
Db	1109	AGTCTTTAAAGGGAAGTACAAGGAGCTGAACAAGGAGACCTCCCGCTGGACCACTTACCG	1168
Qy	1208	GGGCCCTGAGACCAACCCCGGCCAGGCAGTTGCTCAGTGGGCCCTCCTCTGATAAGGC	1267
Db	1169	GGGCTCAGAGGTCAGCCCGAGGCCAGGCAGTTGCTCCATGGGCCCTCCTCTGACAAAGC	1228
Qy	1268	CCTGACCTTCATGAAGGACCATTTCCTGATGGATGAGCAAGTGGTGGGGACGCCCCTGCT	1327
Db	1229	CTTGACCTTCATGAAGGACCATTTCCTGATGGATGAGCACGTGGTAGGAACACCCCTGCT	1288
Qy	1328	GGTGAAATCTGGCGTGGAGTATACACGGCTTGCACTGGAGACAGCCCAGGGCCTTGATGG	1387
Db	1289	GGTGAAGTCTGGTGTGGAGTACACACGGCTTGCTGTGGAGTCAGCTCGGGGCCTTGATGG	1348
Qy	1388	GCACAGCCATCTTGTCTGTACCTGGGAACCACCACAGGGTCGCTCCACAAGGCTGTGGT	1447
Db	1349	GAGCAGCCATGTGGTCATGTATCTGGGTACCTCCACGGGTCCCCTGCACAAGGCTGTGGT	1408
Qy	1448	AAGTGGGGACAGCAGTGCTCATCTGGTGGAGAGATTCAGCTGTTCCCTGACCCTGAACC	1507
Db	1409	GCCTCAGGACAGCAGTGCTTATCTCGTGGAGGAGATTCAGCTGAGCCCTGACTCTGAGCC	1468
Qy	1508	TGTTTCGCAACCTGCAGCTGGCCCCACCCAGGGTGCAGTGTTTGTAGGCTTCTCAGGAGG	1567
Db	1469	TGTTTCGAAACCTGCAGCTGGCCCCCGCCAGGGTGCAGTGTTTGCAGGCTTCTCTGGAGG	1528
Qy	1568	TGTCTGGAGGGTGCCCCGAGCCAACGTAGTGTCTATGAGAGCTGTGTGGACTGTGTCTT	1627
Db	1529	CATCTGGAGAGTTCCCAGGGCCAATTCAGTGTCTACGAGAGCTGTGTGGACTGTGTGCT	1588
Qy	1628	TGCCCCGGGACCCCCACTGTGCCTGGGACCTGAGTCCCGAACCTGTTGCCTCCTGTCTGC	1687
Db	1589	TGCCAGGGACCTCAGTGTGCCTGGGACCTGAATCAAGACTCTGCAGCCTTCTGTCTGG	1648
Qy	1688	CCCCAACCTGAACTCCTGGAAGCAGGACATGGAGCGGGGGAACCCAGAGTGGGCATGTGC	1747
Db	1649	CTCTACC---AAGCCTTGGAAGCAGGACATGGAACGCGGCAACCCGGAGTGGGTATGCAC	1705

Qy	1748	CAGTGGCCCCATGAGCAGGAGCCTTCGGCCTCAGAGCCGCCCCGAAATCATTTAAAGAAGT	1807
Db	1706	CCGTGGCCCCATGGCCAGGAGCCCCCGGCGTCAGAGCCCCCTCAACTAATTAAAGAAGT	1765
Qy	1808	CCTGGCTGTCCCCAACTCCATCCTGGAGCTCCCCTGCCCCACCTGTCAGCCTTGGCCTC	1867
Db	1766	CCTGACAGTCCCCAACTCCATCCTGGAGCTGCGCTGCCCCACCTGTCAGCACTGGCCTC	1825
Qy	1868	TTATTATTGGAGTCATGGCCAGCAGCAGTCCCAGAAGCCTCTTCCACTGTCTACAATGG	1927
Db	1826	TTACCACTGGAGTCATGGCCGAGCCAAAATCTCAGAAGCCTCTGCTACCGTCTACAATGG	1885
Qy	1928	CTCCCTCTTGCTGATAGTGCAGGATGGAGTTGGGGGTCTCTACCAGTGCTGGGCAACTGA	1987
Db	1886	CTCCCTCTTGCTGCTGCCGAGGATGGTGTGCGGGGGCTCTACCAGTGCTGGGCGACTGA	1945
Qy	1988	GAATGGCTTTTCATACCCTGTGATCTCCTACTGGGTGGACAGCCAGGACCAGACCCTGGC	2047
Db	1946	GAACGGCTACTCATACCCTGTGGTCTCCTATTGGGTAGACAGCCAGGACCAGCCCCTGGC	2005
Qy	2048	CCTGGATCCTGAACTGGCAGGCATCCCCGGGAGCATGTGAAGGTCCCCTTGACCAGGGT	2107
Db	2006	GCTGGACCCTGAGCTGGCGGGCGTTCCCCGTGAGCGTGTGCAGGTCCCCTGACCAGGGT	2065
Qy	2108	CAGTGGTGGGGCCGCCCTGGCTGCCAGCAGTCCCTACTGGCCCCACTTTGTCACTGTCAC	2167
Db	2066	CGGAGGCGGAGCTTCCATGGCTGCCAGCGGTCCCTACTGGCCCCATTTTCTCATCGTTAC	2125
Qy	2168	TGTCCTCTTTGCCCTTAGTGCTTTTCAGGAGCCCTCATCATCCTCGTGGCCTCCCCATTGAG	2227
Db	2126	CGTCCTCCTGGCCATCGTGCTCCTGGGAGTGCTCACTCTCCTCCTCGCTTCCCCACTGGG	2185
Qy	2228	AGCACTCCGGGCTCGGGGCAAGGTTTCAGGGCTGTGAGACCCTGCGCCCTGGGGAGAAGGC	2287
Db	2186	GGCGCTGCGGGCTCGGGGTAAGGTTTCAGGGCTGTGGGATGCTGCCCCCAGGGAAAAGGC	2245
Qy	2288	CCCGTTAAGCAGAGAGCAACACCTCCAGTCTCCCAAGGAATGCAGGACCTCTGCCAGTGA	2347
Db	2246	TCCACTGAGCAGGGACCAGCACCTCCAGCCCTCCAAGGACCACAGGACCTCTGCCAGTGA	2305
Qy	2348	TGTGGACGCTGACAACAACCTGCCTAGGCACTGAGGTAGCTTAAACTCTAGGCACAGGCCG	2407
Db	2306	CGTAGATGCCGACAACAACCATCTGGGCGCCGAAGTGGCTTAAACAGGGACACAGATCCG	2365
Qy	2408	GGGCT--GCGGTGCAGGCACCTGGCCATGCTGGCTGGGCGGCCCAAGCACAGCCCTGACT	2465
Db	2366	CAGCTGAGCAGAGCAAGCCACTGGCCTTGTTGGCTATGC-----	2404
Qy	2466	AGGATGACAGCAGCACAAAAGACCACCTTTCTCCCCTGAGAGGAGCTTCTGCTACTCTGC	2525
Db	2405	-----CAGGCACAGTGCCACTCTGACCAGGGTAGGAGGCTCTCCTGCTAACGTGT	2454
Qy	2526	ATCACTGATGACACTCAGCAGGGTGATGCACAGCAGTCTGCCTCCCCTATGGGACTCCCT	2585
Db	2455	GTCACCTACAGCACCCAGTAGG-----TCCTCCCCTGTGGGACTCTCT	2497
Qy	2586	TCTACCAAGCACATGAGCTCTCTAACAGGGTGGGGGCTACCCCCAGACCTGCTCCTACAC	2645

; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 77
; LENGTH: 3046
; TYPE: DNA
; ORGANISM: Mus sp.
US-09-578-063-77

Query Match 55.0%; Score 1727.6; DB 4; Length 3046;
Best Local Similarity 76.0%; Pred. No. 0;
Matches 2338; Conservative 0; Mismatches 644; Indels 94; Gaps 13;

Qy	69	GCTCCAGAGCTCCCTGGTGACAGTCTGTGGCTGAGCATGGCCCTCCCAGCCCTGGGCCTG	128
Db	30	GCTGGGGAACCATCTGGTGACCATCTCAGGCTGACCATGGCCCTACCATCCCTGGGCCAG	89
Qy	129	GACCCCTGGAGCCTCCTGGGCCTTTTCTCTTCCAACCTGCTTTCAGCTGCTGCTGCCGACG	188
Db	90	GACTCATGGAGTCTCCTGCGTGTTTTCTTCCAACCTCTCCTGCTGCCATCACTGCCA	149
Qy	189	ACGACCGCGGGGGAGGCGGGCAGGGGCCCATGCCAGGGTCAGATACTATGCAGGGGAT	248
Db	150	CCTGCTTCTGGGACTGGTGGTCAGGGGCCCATGCCAGAGTCAAATACCATGCTGGAGAC	209
Qy	249	GAACGTAGGGCACTTAGCTTCTTCCACCAGAAGGGCCTCCAGGATTTTGACACTCTGCTC	308
Db	210	GGGCACAGGGCCCTCAGCTTCTTCCAACAAAAGGCCTCCGAGACTTTGACACGCTGCTC	269
Qy	309	CTGAGTGGTGATGGAAATACTCTCTACGTGGGGGCTCGAGAAGCCATTCTGGCCTTGGAT	368
Db	270	CTGAGTGACGATGGCAACACTCTCTATGTGGGGGCTCGAGAGACCGTCCTGGCCTTGAAT	329
Qy	369	ATCCAGGATCCAGGGGTCCCCAGGCTAAAGAACATGATACCGTGGCCAGCCAGTGACAGA	428
Db	330	ATCCAGAACCCAGGAATCCCAAGGCTAAAGAACATGATACCCTGGCCAGCCAGTGAGAGA	389
Qy	429	AAAAAGAGTGAATGTGCCTTTAAGAAGAAGAGCAATGAGACACAGTGTTCAACTTCATC	488
Db	390	AAAAAGACCGAATGTGCCTTTAAGAAGAAGAGCAATGAGACACAGTGTTCAACTTCATT	449
Qy	489	CGTGTCTCTGGTTTCTTACAATGTCACCCATCTCTACACCTGCGGCACCTTCGCCTTCAGC	548
Db	450	CGAGTCTTGGTCTCTTACAATGCTACTCACCTCTATGCCTGTGGGACCTTTGCCTTCAGC	509
Qy	549	CCTGCTTGTTACCTTCATTGAAC'TTCAAGATTCCCTACCTGTTGCCCATCTCGGAGGACAAG	608
Db	510	CCTGCCTGTACCTTCATTGAAC'TCCAAGATTCCCTCCTGTTGCCCATCTTGATAGACAAG	569
Qy	609	GTCATGGAGGGAAGGGCCAAAGCCCCCTTTGACCCCGCTCACAAGCATAC-GGCTGTCTT	667
Db	570	GTCATGGACGGGAAGGGCCAAAG-CCCTTTGACCCTGTTTACAAGCACACAAGCTGTCTT	628
Qy	668	GGTGGATGGGATGCTCTATTCTGGTACTATGAACAAC'TTCCCTGGGCAGTGAGCCCATCCT	727
Db	629	GGTCGATGGGATGCTTTATTCCGGCACCATGAACAAC'TTCCCTGGGCAGCGAGCCCATCCT	688
Qy	728	GATGCGCACACTGGGATCCCAGCCTGTCTCAAGACCGACAAC'TTCCCTCCGCTGGCTGCA	787

Db	689	GATGCGGACACTGGGATCCCCATCCTGTCTCAAGACTGACATCTTCTTACGCTGGCTGCA	748
Qy	788	TCATGACGCCTCCTTTGTGGCAGCCATCCCTTCGACCCAGGTCGTCTACTTCTTCTTCGA	847
Db	749	CGCGGATGCCTCCTTCGTGGCAGCCATTCCATCCACCCAGGTCGTCTATTCTTCTTTGA	808
Qy	848	GGAGACAGCCAGCGAGTTTGACTTCTTTGAGAGGCTCCACACATCGCGGGTGGCTAGAGT	907
Db	809	GGAGACAGCCAGCGAGTTTGACTTCTTTGAAGAGCTGTATATATCCAGGGTGGCTCAAGT	868
Qy	908	CTGCAAGAATGACGTGGGCGGCGAAAAGCTGCTGCAGAAGAAGTGGACCACCTTCCTGAA	967
Db	869	CTGCAAGAACGACGTGGGCGGCTGAAAAGCTGCTGCAGAAGAAGTGGACCACCTTCCTCAA	928
Qy	968	GGCCCAGCTGCTCTGCACCCAGCCGGGGCAGCTGCCCTTCAACGTCATCCGCCACGCGGT	1027
Db	929	AGCCCAGTTGCTCTGCGCTCAGCCAGGGCAGCTGCCATTCAACATCATCCGCCACGCGGT	988
Qy	1028	CCTGCTCCCCGCCGATTCTCCACAGCTCCCCACATCTACGCAGTCTTCACCTCCCAGTG	1087
Db	989	CCTGCTGCCCGCCGATTCTCCCTCTGTTTCCCGCATCTACGCAGTCTTTACCTCCCAGTG	1048
Qy	1088	GCAGGTTGGCGGGACCAGGAGCTCTGCGGTTTGTGCCTTCTCTCTTGGACATTGAACG	1147
Db	1049	GCAGGTTGGCGGGACCAGGAGCTCAGCAGTCTGTGCCTTCTCTCTCACGGACATTGAGCG	1108
Qy	1148	TGCTTTTAAGGGGAAATACAAAGAGTTGAACAAAGAAACTTCACGCTGGACTACTTATAG	1207
Db	1109	AGTCTTTAAAGGGAAGTACAAGGAGCTGAACAAGGAGACCTCCCGCTGGACCACTTACCG	1168
Qy	1208	GGGCCCTGAGACCAACCCCCGGCCAGGCAGTTGCTCAGTGGGCCCTCCTCTGATAAGGC	1267
Db	1169	GGGCTCAGAGGTCAGCCGAGGCCAGGCAGTTGCTCCATGGGCCCTCCTCTGACAAAGC	1228
Qy	1268	CCTGACCTTCATGAAGGACCATTTCTGATGGATGAGCAAGTGGTGGGGACGCCCCCTGCT	1327
Db	1229	CTTGACCTTCATGAAGGACCATTTCTGATGGATGAGCACGTGGTAGGAACACCCCTGCT	1288
Qy	1328	GGTGAAATCTGGCGTGGAGTATACACGGCTTGCAGTGGAGACAGCCAGGGCCTTGATGG	1387
Db	1289	GGTGAAGTCTGGTGTGGAGTACACACGGCTTGCTGTGGAGTCAGCTCGGGGCCTTGATGG	1348
Qy	1388	GCACAGCCATCTTGTCTGTACCTGGGAACCAACACAGGGTCGCTCCACAAGGCTGTGGT	1447
Db	1349	GAGCAGCCATGTGGTCTGTATCTGGGTACCTCCACGGGTCCCTTGACAAGGCTGTGGT	1408
Qy	1448	AAGTGGGGACAGCAGTGTCTCATCTGGTGAAGAGATTGAGCTGTTCCCTGACCCTGAACC	1507
Db	1409	GCCTCAGGACAGCAGTGCTTATCTCGTGGAGGAGATTGAGCTGAGCCCTGACTCTGAGCC	1468
Qy	1508	TGTTTCGAAACCTGCAGCTGGCCCCCACCAGGGTGCAGTGTTTGTAGGCTTCTCAGGAGG	1567
Db	1469	TGTTTCGAAACCTGCAGCTGGCCCCCACCAGGGTGCAGTGTTTGCAGGCTTCTCTGGAGG	1528
Qy	1568	TGTCTGGAGGGTGCCCCGAGCCAAGTGTAGTGTCTATGAGAGCTGTGTGGACTGTGTCCT	1627
Db	1529	CATCTGGAGAGTTCCAGGGCCAATTGCAGTGTCTACGAGAGCTGTGTGGACTGTGTGCT	1588

Qy	1628	TGCCCCGGGACCCCCACTGTGCCTGGGACCCTGAGTCCCGAACCTGTTGCCTCCTGTCTGC	1687
Db	1589	TGCCAGGGACCCCTCACTGTGCCTGGGACCCTGAATCAAGACTCTGCAGCCTTCTGTCTGG	1648
Qy	1688	CCCCAACCTGAACTCCTGGAAGCAGGACATGGAGCGGGGGAACCCAGAGTGGGCATGTGC	1747
Db	1649	CTCTACC---AAGCCTTGGAAGCAGGACATGGAACGCGGCAACCCGGAGTGGGTATGCAC	1705
Qy	1748	CAGTGGCCCCATGAGCAGGAGCCTTCGGCCTCAGAGCCGCCCGCAAATCATTAAGAAGT	1807
Db	1706	CCGTGGCCCCATGGCCAGGAGCCCCCGGCGTCAGAGCCCCCTCAACTAATTAAAGAAGT	1765
Qy	1808	CCTGGCTGTCCCCAACTCCATCCTGGAGCTCCCCGCCCCACCTGTCAGCCTTGGCCTC	1867
Db	1766	CCTGACAGTCCCCAACTCCATCCTGGAGCTGCGCTGCCCCACCTGTCAGCACTGGCCTC	1825
Qy	1868	TTATTATTGGAGTCATGGCCCAGCAGCAGTCCCAGAAGCCTCTTCCACTGTCTACAATGG	1927
Db	1826	TTACCACTGGAGTCATGGCCGAGCCAAAATCTCAGAAGCCTCTGCTACCGTCTACAATGG	1885
Qy	1928	CTCCCTCTTGCTGATAGTGCAGGATGGAGTTGGGGGTCTCTACCAGTGCTGGGCAACTGA	1987
Db	1886	CTCCCTCTTGCTGCTGCCGAGGATGGTGTGCGGGGCCCTCTACCAGTGCTGGCGACTGA	1945
Qy	1988	GAATGGCTTTTCATACCCTGTGATCTCCTACTGGGTGGACAGCCAGGACCAGACCCTGGC	2047
Db	1946	GAACGGCTACTCATACCCTGTGGTCTCCTATTGGGTAGACAGCCAGGACCAGCCCCCTGGC	2005
Qy	2048	CCTGGATCCTGAACTGGCAGGCATCCCCGGGAGCATGTGAAGGTCCCGTTGACCAGGGT	2107
Db	2006	GCTGGACCCTGAGCTGGCGGGCGTTCCCCGTGAGCGTGTGCAGGTCCCGCTGACCAGGGT	2065
Qy	2108	CAGTGGTGGGGCCGCCCTGGCTGCCCAGCAGTCCCTACTGGCCCCACTTTGTCACTGTCAC	2167
Db	2066	CGGAGGCGGAGCTTCCATGGCTGCCCAGCGGTCTACTGGCCCCATTTTCTCATCGTTAC	2125
Qy	2168	TGTCCTCTTTGCCTTAGTGCTTTCAGGAGCCCTCATCATCCTCGTGGCCTCCCCATTGAG	2227
Db	2126	CGTCCTCCTGGCCATCGTGCTCCTGGGAGTGCTCACTCTCCTCCTCGCTTCCCCACTGGG	2185
Qy	2228	AGCACTCCGGGCTCGGGGCAAGGTTCAAGGCTGTGAGACCCTGCGCCCTGGGGAGAAGGC	2287
Db	2186	GGCGCTGCGGGCTCGGGGTAAGGTTCAAGGCTGTGGGATGCTGCCCCCAGGGAAAAGGC	2245
Qy	2288	CCCGTTAAGCAGAGAGCAACACCTCCAGTCTCCCAAGGAATGCAGGACCTCTGCCAGTGA	2347
Db	2246	TCCACTGAGCAGGGACCAGCACCTCCAGCCCTCCAAGGACCACAGGACCTCTGCCAGTGA	2305
Qy	2348	TGTGGACGCTGACAACAACCTGCCCTAGGCAGTGGAGTAGCTTAAACTCTAGGCACAGGCCG	2407
Db	2306	CGTAGATGCCGACAACAACCATCTGGGCGCCGAAGTGGCTTAAACAGGGACACAGATCCG	2365
Qy	2408	GGGCT--GCGGTGCAGGCACCTGGCCATGCTGGCTGGGCGGCCCAAGCACAGCCCTGACT	2465
Db	2366	CAGCTGAGCAGAGCAAGCCACTGGCCTTGTGGCTATGC-----	2404

Qy	2466	AGGATGACAGCAGCACAAAAGACCACCTTTCTCCCCTGAGAGGAGCTTCTGCTACTCTGC	2525
Db	2405	-----CAGGCACAGTGCCACTCTGACCAGGGTAGGAGGCTCTCCTGCTAACGTGT	2454
Qy	2526	ATCACTGATGACACTCAGCAGGGTGATGCACAGCAGTCTGCCTCCCCTATGGGACTCCCT	2585
Db	2455	GTCACCTACAGCACCCAGTAGG-----TCCTCCCCTGTGGGACTCTCT	2497
Qy	2586	TCTACCAAGCACATGAGCTCTCTAACAGGGTGGGGGTACCCCCAGACCTGCTCCTACAC	2645
Db	2498	TCTGCAAGCACATTGGGCTGTCT-----CCATACCTGTACTTGTGC	2538
Qy	2646	TGATATTGAAGAACCTGGAGAGGATCCTTCAGTTCTGGCCATTCCAGGGACCTCCAGAA	2705
Db	2539	TGTGACAGGAAGAGCCAGACAGGTTTCTTTGATTTTGATTGACCCAAGAGCCCTGCCTGT	2598
Qy	2706	ACACAGTGTTTCAAGAGACCCTAAAAAACCTGCCTGTCCCAGGACCTATGGTAATGAAC	2765
Db	2599	AACAAACGTGCTCCAGGAGACCATGAAAGGTGTGGCTGTCTGGGATTCTGTGGTGACAAA	2658
Qy	2766	ACCAAACATCTAAACAATCATATGCTA-----ACATGCCACTCCTGGAACTCCACTC	2818
Db	2659	CCTAAGCATCCGAGCAAGCTGGGGCTATTCCCTGCAAACCTCATCCTGAACGCTGTCACTC	2718
Qy	2819	T----GAAGCTGCCGCTTTGGACACCAACACTCCCTTC-TCCCAGGGTCATGCAGGGATC	2873
Db	2719	TAGAAGCAGCTGCTGCTTTGAACACCAGCCACCCTCCTTCCCAAGAGTCTCTATGGAGT	2778
Qy	2874	TGCTCCCTCCTGCTTCCCTTACCAGTCGTGCACCGCTGACTCCCAGGAAGTCTTTCCTGA	2933
Db	2779	TGGCCCCCTTGTTGTTTCCCTTACCAGTCGGGCCATACTGTTT---GGGAAGTCATCTCTGA	2835
Qy	2934	AGTCTGACCACCTTTCTTCTTGCTTCAGTTGGGGCAGACTCTGATCCCT---TCTGCCCT	2990
Db	2836	AGTCTAACCACCTTCCTTCTTGTTTCAGTTTGGACAGATTGTTATTATTGTCTCTGCCCT	2895
Qy	2991	GGCAGAATGGCAGGGGTAATCTGAGCCTTCTTCACTCCTTTACCCTAGCTGACCCCTTCA	3050
Db	2896	GGCTAGAATGGGGGCATAATCTGAGCCTTGTTCCCTTGTCAGTGTGGCTGACCCCTTGAC	2955
Qy	3051	CCTCTCCCCCTCCCTTTTCCCTTGTGTTTGGGATTCAGAAAACCTGCTTGTGACAGACTGTT	3110
Db	2956	CTCTT--CCTTCCTCCTCCCTTTGTTTGGGATTCAGAAAACCTGCTTGTGACAGACAATT	3013
Qy	3111	TATTTTTTTATTAAAAA	3126
Db	3014	TATTTTTTTATTAAAAA	3029

RESULT 5

US-09-300-958A-24

; Sequence 24, Application US/09300958A

; Patent No. 6495319

; GENERAL INFORMATION:

; APPLICANT: McClelland, Michael

; APPLICANT: Welsh, John

; APPLICANT: Trenkle, Thomas

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; TITLE OF INVENTION: Reduced Complexity Nucleic Acid Targets and Methods of
; TITLE OF INVENTION: Using Same
; FILE REFERENCE: P-PH 3457
; CURRENT APPLICATION NUMBER: US/09/300,958A
; CURRENT FILING DATE: 1999-04-27
; PRIOR APPLICATION NUMBER: 60/083,331
; PRIOR FILING DATE: 1998-04-27
; PRIOR APPLICATION NUMBER: 60/098,070
; PRIOR FILING DATE: 1998-08-27
; PRIOR APPLICATION NUMBER: 60/118,624
; PRIOR FILING DATE: 1999-02-04
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 24
; LENGTH: 2433
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-300-958A-24
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Query Match          7.3%; Score 230; DB 4; Length 2433;
Best Local Similarity 50.2%; Pred. No. 6.8e-53;
Matches 906; Conservative 0; Mismatches 805; Indels 93; Gaps 10;
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Qy      301 CTCTGCTCCTGAGTGGTGATGGAAATACTCTCTACGTGGGGGCTCGAGAAGCCATTCTGG 360
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Db      53 CCCTTCTGCTGAGCCAGGATGGAAAGACGCTGTATGTGGGGGCCCGAGAGGCCCTCTTTG 112

Qy      361 CCTTGGATATCCAGGATCCAGGGGTCCC---CAGGCTAAAGAACATGATACCGTGGCCAG 417
        | | | | | | | | | | | | | | | | | | | | | | | |
Db      113 CACTTAACAGCAACCTCAGCTTCTTGCCAGGCGGGGAGTACCAAGAGCTACTGTGGAGTG 172

Qy      418 CCAGTGACAGAAAAAAGAGTGAATGTGCCTTTAAGAAGAAGAGCAATGAGACACAGTGTT 477
        | | | | | | | | | | | | | | | | | | | | | | | |
Db      173 CAGATGCTGACAGGAAGCAGCAGTGCAGCTTCAAGGCAAGGACCCAAAGCGTGACTGTC 232

Qy      478 TCAACTTCATCCGTGTCCTGGTTTCTTACAATGTCACCCATCTCTACACCTGCGGCACCT 537
        | | | | | | | | | | | | | | | | | | | | | | | |
Db      233 AAAACTACATCAAGATCCTCCTGCCACTCAACAGCAGCCACCTGCTCACCTGTGGCACGG 292

Qy      538 TCGCCTTCAGCCCTGCTTGTACCTTCATTGAACTTCAAGATTCCCTACCTGTTGCCCATCT 597
        | | | | | | | | | | | | | | | | | | | | | | | |
Db      293 CCGCCTTCAGCCCCCTGTGTGCTTACATTACATAGCGAGCTTTACTTTAGCCCAAGATG 352

Qy      598 CGGAGGACAAGGTCAT-----GGAGGGAAAAGGCCAAAGCCCCCTTTGACCCCGCTCACA 651
        | | | | | | | | | | | | | | | | | | | | | | | |
Db      353 AGGCCGGTAATGTCATTCTGGAGGATGGCAAGGGTCATTGTCCCTTTGACCCCAACTTCA 412

Qy      652 AGCATACGGCTGTCTTGGTGATGGGATGCTCTATTCTGGTACTATGAACAACTTCCCTGG 711
        | | | | | | | | | | | | | | | | | | | | | | | |
Db      413 AGTCCACGGCTCTGGTGGTTGATGGTGAGCTGTACACTGGAACAGTCAGTAGCTTCCAGG 472

Qy      712 GCAGTGAGCCCATCCTGATGCGCACACTGGGATCCCAGCCTGTCTCAAGACCGACAAC 771
        | | | | | | | | | | | | | | | | | | | | | | | |
Db      473 GAAACGACCCAGCCATTTCCCGGAGCCAGAGTTCCTCCGCC---CACCAAGACTGAGAGCT 529

Qy      772 TCCTCCGCTGGCTGCATCATGACGCCTCCTTTGTGGCAGCCATCCCTTCGACCCAGGTCG 831
        | | | | | | | | | | | | | | | | | | | | | | | |
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Db 530 CCCTCAACTGGCTACAAGACCCCTGCCTTTGTGGCCTCGGCTACGTCCCCGAGAGCCTGG 589
 Qy 832 -----TCTACTTCTTCTTCGAGGAGACAGCCAGCGAGT 864
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 Db 590 GCAGCCCCATAGGTGATGATGATAAGATCTACTTCTTCTTCAGCGAGACGGGCCAGGAGT 649
 Qy 865 TTGACTTCTTTGAGAGGCTCCACACATCGCGGGTGGCTAGAGTCTGCAAGAATGACGTGG 924
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 Db 650 TTGAGTTCTTTGAGAACACCATCGTGTCCCGAGTTGCCCGAGTCTGTAAGGGCGATGAGG 709
 Qy 925 GCGGCGAAAAGCTGCTGCAGAAGAAGTGGACCACCTTCC'TGAAGGCCAGCTGC'TCTGCA 984
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 710 GTGGAGAGCGGGTGT'TGCAGCAACGCTGGACCTCCTTTCTCAAGGCTCAGCTCCTGTGCT 769
 Qy 985 CCCAGCCGGGGCA---GCTGCCCTTCAACGTATCCGCCACGCGGTCTGCTCCCCGCCG 1041
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 770 CCCGGCCTGATGATGGCTTTCCCTTTAACGTGCTACAAGATGTCTTACCCTGAACCCCA 829
 Qy 1042 ATTCTCCACAGCTCCCCACATCTA-----CGCAGTCTTACCTCCCAGTGGCAGGTTG 1095
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 830 ACCCTCAGGATTGGCGCAAGACCCCTTCTATCGGGGTCTTTACCTCCCAGTGGCACAGAG 889
 Qy 1096 GCGGGACCAGGAGCTCTGCGGTTTGTGCCTTCTCTCTCTTGGACATTGAACGTGTCTTTA 1155
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 890 GGACCACAGAAGGCTCTGCCATCTGCGTCTTACCATGAATGATGTGCAGAAGGCCCTTG 949
 Qy 1156 AGGGGAAATACAAAGAGTTGAACAAAGAAACTTACGCTGGACTACTTATAGGGGGCCCTG 1215
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 950 ACGGCCTGTACAAGAAAGTAAACAGAGAGACACAGCAGTGGTATACCGAGACCCACCAGG 1009
 Qy 1216 AGACCAACCCCCGGCCAGGCAGTTG-----CT 1242
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 Db 1010 TGCCACACACCGCGGCCGGGAGCGTGCATTACCAACAGTGCCCGGGAACGGAAGATCAACT 1069
 Qy 1243 CAGTGGGCCCCCTCCTCTGATAAGGCCCTGACCTTCATGAAGGACCATTTCCTGATGGATG 1302
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 Db 1070 CGTCCCTGCAGCTCCCAGACCGAGTGTGAAC'TCCTCAAGGATCACTTCTTGATGGATG 1129
 Qy 1303 AGCAAGTGGTGGGGACGCCCTGCTGGTGAAATCTGGCGTGGAGTATACACGGCTTGCAG 1362
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 Db 1130 GGCAGTCCGCAGTCGCCCTGCTGCTGCTGCAGCCAGAGCCCGCTACCAGCGTGTGGCTG 1189
 Qy 1363 TGGAGACAGCCAGGGCC'TTGATGGGCACAGCCATCTTGTATGTACCTGGGAACCACCA 1422
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 Db 1190 TGCACCGTGTGCCTGGCCTGCACAG---CACTTATGATGTCTATTTCTGGGCACTGGTG 1246
 Qy 1423 CAGGGTCGCTCCACAAGGCTGTGGTAAGTGGGGACAGCAGTGTCTATCTGGTGGAAGAGA 1482
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 Db 1247 ATGGCCGCCCTGCACAAAGCAGTG---ACCCTGAGCTCCAGAGTCCACATCATTTAGAGAGC 1303
 Qy 1483 TTCAGCTGTTCCCTGACCTGAACCTGTTCGCAACCTGCAGCTGGCCCCCACCAGGGTG 1542
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 1304 TGCAGATCTTCCCTCAAGGACAGCCTGTGCAGAACCTGCTCTTGGACAGCCATGGGGGAC 1363
 Qy 1543 CAGTGT'TTGTAGGCTTCTCAGGAGGTGTCTGGAGGGTGCCCCGAGCCAAC'TGTAGTGTCT 1602
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 Db 1364 TGT'TGTATGCCTCCTCCCATTCGGGGTGGTGCAAGTGCCCGTAGCCAAC'TGCAGCCTGT 1423

Qy 1603 ATGAGAGCTGTGTGGACTGTGTCCTTGCCCGGGACCCCACTGTGCCTGGGACCCTGAGT 1662
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 Db 1424 ACCCAACCTGTGGAGACTGCCTCCTGGCTCGAGACCCCTACTGCGCCTGGACTGGCTCTG 1483

Qy 1663 CCCGAACCTGTTGCCTCCTGTCTGCCCCAACCTGAACTCCTGGAAGCAGGACATGGAGC 1722
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 Db 1484 CCTGCAGGCTCGCTAGCCTCTACCAGCCTGATCTGGCCTCCAGGCCATGGACCCAGGACA 1543

Qy 1723 GGGGGAACCCAGAGTGGGCATGTGCCAGTGGCCCCATGAGCAGGAGCCTTCGGCCTCAGA 1782
 | | | | | | | | | | | | | | | | | | | | | |
 Db 1544 TTGAGGGTGCCAGTGTCAAGGAACCTCTGCAAGAATTCTCATACAAGGCCCGGTTTCTTG 1603

Qy 1783 GCCGCCCGCAAATCATTAAGAAGTCCTGGCTGTCCCCAACTCCATCCTGGAGCTCCCCT 1842
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 Db 1604 TGCCAGGTAAGCCATGTAAACAAGTCCAGATCCAACCAAACACAGTGAACACCCTGGCCT 1663

Qy 1843 GCCCCACCTGTCAGCCTTGGCCTCTTATTATTGGAGTCATGGCCAGCAGCAGTCCCAG 1902
 | | | | | | | | | | | | | | | | | | | | | |
 Db 1664 GCCCACTCCTCTCAAACCTGGCCACTCGGCTCTGGGTGCACAATGGAGCCCCAGTCAATG 1723

Qy 1903 AAGCCTCTTCCACTGTCTA-----CAATGGCTCCCTCTTGCTGATAGTGCAGGATGGAG 1956
 | | | | | | | | | | | | | | | | | | | | | |
 Db 1724 CCTCTGCCTCCTGCCGCGTGTACCCACCGGGGACCTGCTGCTGGTGGGCAGCCAGCAGG 1783

Qy 1957 TTGGGGGTCTCTACCAGTGCTGGGCAACTGAGAATGGCTTTTCATACCCTGTGATCTCCT 2016
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 Db 1784 GTTTGGGGGTGTCCAGTGTGGTGCATAGAAGAAGGATTCCAGCAGCTTGTGGCCAGCT 1843

Qy 2017 ACTG 2020
 | | | |
 Db 1844 ACTG 1847

RESULT 6

US-08-556-422A-1

; Sequence 1, Application US/08556422A
 ; Patent No. 6576754
 ; GENERAL INFORMATION:
 ; APPLICANT: HALL, Kathryn T.
 ; APPLICANT: FREEMAN, Gordon J.
 ; APPLICANT: SCHULTZE, Joachim L.
 ; APPLICANT: BOUSSIOTIS, Vassiliki
 ; APPLICANT: NADLER, Lee M.
 ; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING CD100 MOLECULES
 ; FILE REFERENCE: DFN-005CPA2
 ; CURRENT APPLICATION NUMBER: US/08/556,422A
 ; CURRENT FILING DATE: 1995-11-09
 ; NUMBER OF SEQ ID NOS: 7
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 1
 ; LENGTH: 4157
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (88)...(2673)

Query Match 4.9%; Score 153.4; DB 4; Length 4157;
 Best Local Similarity 50.0%; Pred. No. 1.5e-31;
 Matches 743; Conservative 0; Mismatches 636; Indels 108; Gaps 10;

Qy	270	TTCCACCAGAAGGGCCTCCAGGATTTTGACACTCTGCTCCTGAGTGGTGATGGAAATACT	329
Db	211	TTTCATGAGCCAGACATCTACAATACTCAGCCTTGCTGCTGAGCGAGGACAAGGACACC	270
Qy	330	CTCTACGTGGGGGCTCGAGAAGCCATTCTGGCCTTGATATCCAGGATCCAGGGGTCCCC	389
Db	271	TTGTACATAGGTGCCCCGGGAGGC-----GGTCTTCGCTGTGAACGCACTCAACATCTCC	324
Qy	390	AGGCTAAAGAACATGATACCGTGGCCAGCCAGTGACAGAAAAAAGAGTGAATGTGCCCTTT	449
Db	325	GAGAAGCAGCATGAGGTGTATTGGAAGGTCTCAGAAGACAAAAAGCAAAATGTGCAGAA	384
Qy	450	AAGAAGAAGAGCAATGAGACACAGTGTTCACACTTCATCCGTGTCCTGGTTTCTTACAAT	509
Db	385	AAGGGGAAATCAAAACAGACAGAGTGCCTCAACTACATCCGGGTGCTGCAGCCACTCAGC	444
Qy	510	GTCACCCATCTCTACACCTGCGGCACCTTCGCCTTCAGCCCTGCTTGTACCTTCATTGAA	569
Db	445	GCCACTTCCTTTACGTGTGTGGGACCAACGCATTCAGCCGGCCTGTGACCACCTGAAC	504
Qy	570	CTTCAAGATTCCTACCTGTTGCCCATCTCGGAGGACAAGGTCATGGAGGGAAAAGGCCAA	629
Db	505	TTAACATCCTTTAAGTTTCTGGGGAAAAATGAAGAT-----GGCAAAGGAAGA	552
Qy	630	AGCCCCCTTTGACCCCGCTCACAAGCATAACGGCTGTCTTGGTGGATGGGATGCTCTATTCT	689
Db	553	TGTCCCTTTGACCCAGCACACAGCTACACATCCGTGATGGTTGATGGAGAACTTTATTTCG	612
Qy	690	GGTACTATGAACAACCTTCTGGGCAGTGAGCCCATCCTGATGCGCACACTGGGATCCCAG	749
Db	613	GGGACGTCGTATAATTTTGGGAAGTGAACCCATCATCTCCCGAAATTCTTCCCACAGT	672
Qy	750	CCTGTCTCAAGACCGACAACCTTCCTCCGCTGGCTGCATCATGACGCCTCCTTTGTGGCA	809
Db	673	CCTCTGAGGACAGAATATGCAATCCCTTGGCTGAACGAGCCTAGTTTCGTGTTTGTCTGAC	732
Qy	810	GCCATCCCTTCGACCCAGGTC-----GTCTACTTCTTCTTC	845
Db	733	GTGATCCGAAAAAGCCAGACAGCCCCGACGGCGAGGATGACAGGGTCTACTTCTTCTTC	792
Qy	846	GAGGAGACAGCCAGCGAGTTTGACTTCTTTGAGAGGCTCCACACATCGCGGGTGGCTAGA	905
Db	793	ACGGAGGTGTCTGTGGAGTATGAGTTTGTGTTTCAGGGTGTGATCCCACGGATAGCAAGA	852
Qy	906	GTCTGCAAGAATGACGTGGGCGGCGAAAAGCTGCTGCAGAAGAAGTGACACCTTCCTG	965
Db	853	GTGTGCAAGGGGGACAGGGCGGCCCTGAGGACCTTGCAGAAGAAATGGACCTCCTTCCTG	912
Qy	966	AAGGCCAGCTGCTCTGCACCCAGCCGG---GGCAGCTGCCCTTCAACGTATCCGCCAC	1022
Db	913	AAAGCCCAGCTCATCTGCTCCCGGCCAGACAGCGGCTTGGTCTTCAATGTGCTGCGGGAT	972


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; FILE REFERENCE: 0020-4426P
; CURRENT APPLICATION NUMBER: US/09/077,940A
; CURRENT FILING DATE: 1998-06-05
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 3524
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: (1)..(38)
; OTHER INFORMATION:
; NAME/KEY: 3'UTR
; LOCATION: (2706)..(3524)
; OTHER INFORMATION:
; NAME/KEY: CDS
; LOCATION: (39)..(2702)
; OTHER INFORMATION:
US-09-077-940A-3
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Query Match          4.0%; Score 126; DB 4; Length 3524;
Best Local Similarity 55.3%; Pred. No. 5.1e-24;
Matches 315; Conservative 0; Mismatches 240; Indels 15; Gaps 3;
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Qy      450 AAGAAGAAGAGCAATGAGACACAGTGTTCAACTTCATCCGTGTCCTGGTTTCTTACAAT 509
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Db      390 ATGAAGGGCAAACAGGAGGGCGAGTGTCGAAACTTCGTAAAGGTGCTGCTCCTTCGGGAC 449

Qy      510 GTCACCCATCTCTACACCTGCGGCACCTTCGCCTTCAGCCCTGCTTGACCTTCATTGAA 569
          |   |   |   |   |   |   |   |   |   |   |   |   |   |
Db      450 GAGTCCACGCTCTTTGTGTGCGGTTCCAACGCCTTCAACCCGGTGTGCGCCAACACTACAGC 509

Qy      570 CTTCAAGATTCCTACCTGTTGCCCATCTCGGAGGACAAGGTCATGGAGGGAAAAGGCCAA 629
          |   |   |   |   |   |   |   |   |   |   |   |   |   |
Db      510 ATAGA-----CACCTGCAGCCCGTCGGAGACAA-----CATCAGCGGTATGGCCCGC 557

Qy      630 AGCCCCTTTGACCCCGCTCACAAGCATAACGGCTGTCTTGGTGGATGGGATGCTCTATTCT 689
          |   |   |   |   |   |   |   |   |   |   |   |   |   |
Db      558 TGCCCGTACGACCCCAAGCACGCCAATGTTGCCCTCTTCTCTGACGGGATGCTCTTCACA 617

Qy      690 GGTACTATGAACAACTTCCTGGGCAGTGAGCCCATCCTGATGCGCACACTGGGATCCAG 749
          |   |   |   |   |   |   |   |   |   |   |   |   |   |
Db      618 GCTACTGTTACCGACTTCCTAGCCATTGATGCTGTCATCTACCGCAGCCTCGGGGACAGG 677

Qy      750 CCTGTCTCAAGACCGACAACCTTCCTCCGCTGGCTGCATCATGACGCCTCCTTTGTGGCA 809
          |   |   |   |   |   |   |   |   |   |   |   |   |   |
Db      678 CCCACCTGCGCACCGTGAAACATGACTCCAAGTGGTTCAAAGAGCCTTACTTTGTCCAT 737

Qy      810 GCCATCCCTTCGACCCAGGTCGTCTACTTCTTCTTCGAGGAGACAGCCAGCGAGTTTGAC 869
          |   |   |   |   |   |   |   |   |   |   |   |   |   |
Db      738 GCGGTGGAGTGGGGCAGCCATGTCTACTTCTTCTTCGAGGAGATTGCGATGGAGTTTAAC 797

Qy      870 TTCTTTGAGAGGCTCCACACATCGCGGGTGGCTAGAGTCTGCAAGAATGACGTGGGCGGC 929
          |   |   |   |   |   |   |   |   |   |   |   |   |   |
Db      798 TACCTGGAGAAGGTGGTGGTGTCCCGCGTGGCCCGAGTGTGCAAGAACGACGTGGGAGGC 857
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Qy      930 GAAAAGC---TGCTGCAGAAGAAGTGGACCACCTTCCTGAAGGCCAGCTGCTCTGCACC 986
          |   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      858 TCCCCCGCGTGTCTGGAGAAGCAGTGGACGTCTTCCTGAAGGCGGGCTCAACTGCTCT 917

Qy      987 CAGCCGGGGCAGCTGCCCTTCAACGTCATC 1016
          || || |   | ||| || ||| |
Db      918 GTACCCGGAGACTCCCATTTCTACTTCAAC 947

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RESULT 8

US-09-077-940A-1

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; Sequence 1, Application US/09077940A
; Patent No. 6576441
; GENERAL INFORMATION:
; APPLICANT: KIMURA, Toru et al.
; TITLE OF INVENTION: NOVEL SEMAPHORIN Z AND GENE ENCODING THE SAME
; FILE REFERENCE: 0020-4426P
; CURRENT APPLICATION NUMBER: US/09/077,940A
; CURRENT FILING DATE: 1998-06-05
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 3692
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: (1)..(18)
; OTHER INFORMATION:
; NAME/KEY: CDS
; LOCATION: (19)..(2682)
; OTHER INFORMATION:
; NAME/KEY: 3'UTR
; LOCATION: (2683)..(3653)
; OTHER INFORMATION:
; NAME/KEY: polyA_site
; LOCATION: (3654)..(3692)
; OTHER INFORMATION:
US-09-077-940A-1

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Query Match          4.0%; Score 125.4; DB 4; Length 3692;
Best Local Similarity 58.5%; Pred. No. 7.7e-24;
Matches 238; Conservative 0; Mismatches 166; Indels 3; Gaps 1;

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Qy      611 CATGGAGGGAAAAGGCCAAAGCCCCCTTTGACCCCGCTCACAAGCATACGGCTGTCTTGGT 670
          |||   || | | ||   ||||| ||||| ||   ||   ||   |||
Db      522 CATCAGTGGTATGGCCCGCTGCCCCACGACCCCAAGCATGCCAATGTCGCCCTCTTCTC 581

Qy      671 GGATGGGATGCTCTATTCTGGTACTATGAACAACTTCCTGGGCAGTGAGCCCATCCTGAT 730
          ||||| ||||| || | || | | ||||| || || || | | |
Db      582 AGATGGGATGCTCTTCACAGCCACAGTAACTGACTTCCTAGCCATCGACGCTGTTATCTA 641

Qy      731 GCGCACACTGGGATCCCAGCCTGTCCTCAAGACCGACAACCTTCCTCCGCTGGCTGCATCA 790
          || | || || || || || || || || || || || || || ||
Db      642 CCGTAGCCTTGGGGACCGGCCACACTGCGCACAGTAAAGCATGACTCCAAGTGGTTTAA 701

Qy      791 TGACGCCTCCTTTGTGGCAGCCATCCCTTCGACCCAGGTCGTCTACTTCTTCTTCGAGGA 850

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      || | | ||||| || | | ||||| ||||| |||
Db      702 AGAGCCATACTTTGTGCATGCGGTGGAGTGGGGAAGCCACGTCTACTTCTTCTCCGGA 761
Qy      851 GACAGCCAGCGAGTTTGACTTCTTTGAGAGGCTCCACACATCGCGGGTGGCTAGAGTCTG 910
      || |||| ||||| || | | | | || || |||| | || |
Db      762 GATCGCCATGGAGTTTAACTATCTGGAAGGTGGTGGTGTCCCGTGTGGCCCGTGTATG 821
Qy      911 CAAGAATGACGTGGGCGG---CGAAAAGCTGCTGCAGAAGAAGTGGACCACCTTCCTGAA 967
      ||||| ||||| || | | |||| ||||| ||||| |||||
Db      822 CAAGAATGATGTGGGCGGCTCCCCACGGGTGCTGGAGAAGCAGTGGACTTCCTTCCTGAA 881
Qy      968 GGCCCAGCTGCTCTGCACCCAGCCGGGGCAGCTGCCCTTCAACGTCA 1014
      |||| ||| |||| || ||| ||| | | |||| || |||
Db      882 GGCCCGGCTCAACTGCTCCGTGCCTGGGGACTCACACTTCTACTTCA 928

```

RESULT 9

US-09-854-845-15

; Sequence 15, Application US/09854845

; Patent No. 6750054

; GENERAL INFORMATION:

; APPLICANT: Walke, D. Wade

; APPLICANT: Wang, Xiaoming

; APPLICANT: Scoville, John

; APPLICANT: Turner, C. Alexander Jr.

; TITLE OF INVENTION: No. 6750054el Human Semaphorin Homologs and Polynucleotides Encoding the Same

; FILE REFERENCE: LEX-0177-USA

; CURRENT APPLICATION NUMBER: US/09/854,845

; CURRENT FILING DATE: 2001-05-14

; PRIOR APPLICATION NUMBER: US 60/205,274

; PRIOR FILING DATE: 2000-05-18

; PRIOR APPLICATION NUMBER: US 60/208,893

; PRIOR FILING DATE: 2000-06-02

; NUMBER OF SEQ ID NOS: 50

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 15

; LENGTH: 2820

; TYPE: DNA

; ORGANISM: homo sapiens

US-09-854-845-15

Query Match 3.9%; Score 121.4; DB 4; Length 2820;

Best Local Similarity 49.5%; Pred. No. 8.5e-23;

Matches 568; Conservative 1; Mismatches 527; Indels 51; Gaps 8;

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Qy      607 AGGTCATGGAGGGAAAAGGCCAAAGCCCCTTTGACCCCGCTCACAAGCATACGGCTG--- 663
      || || | || | || ||||| ||||| |||| | || |||
Db      71 AGAAGATCAATGGTGTGGCCCGCTGCCCCATATGACCCACGCCACAACCTCCACAGCTGTCA 130
Qy      664 TCTTGGTGGATGGGATGCTCTATTCTGGTACTATGAACAACTTCCTGGGCAGTGAGCCCA 723
      ||| | ||| ||||| || | || | | |||| || | || ||
Db      131 TCTCCTCCCAGGGGAGCTCTATGCAGCCACGGTCATCGACTTCTCAGGTCGGGACCCCTG 190
Qy      724 TCCTGATGCGCACACTGGGATCCCAGCCTGTCCTCAAGACCGACAACCTTCCTCCGCTGGC 783
      | | |||| |||| | || || | || | | | | | |
Db      191 CCATCTACCGCAGCCTGGGCAGTGGGCCACCGCTTCGCACTGCCCAATATAACTCCAAGT 250

```

Qy 784 TGCATCATGACGCCTCCTTTGTGGCAGCCATCCCTTCGACCCAGGTCGTCTACTTCTTCT 843
 || | |||| | ||| ||||| || | | | |||||

Db 251 GGCTTAATGAGCCAAACTTCGTGGCAGCCTATGATATTGGGCTGTTTGCATACTTCTTCC 310

Qy 844 TCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAGAGGCTCCACACATCGCGGGTGGCTA 903
 | |||| | || | || | | | | || |||||

Db 311 TGCGGGAGAACGCAGTGGAG---CACGACTGTGGACGCACCGTGTACTCTCGCGTGGCCC 367

Qy 904 GAGTCTGCAAGAATGACGTGGGCGGCGAAAAGCTGCTGCAGAAGAAGTGACCACCTTCC 963
 | || ||||| ||||| || | ||||| || | | ||||| |||

Db 368 GCGTGTGCAAGAATGACGTGGGGGGCCGATTCTTGCTGGAGGACACATGGACCACATTCA 427

Qy 964 TGAAGGCCAGCTGCTCTGCACCCAGCCGGGGCAGCTGCCCTTCAACGTATCCGCCACG 1023
 ||||| ||| ||| ||| ||| || | ||||| || | |||

Db 428 TGAAGGCCCGGCTCAACTGCTCCCGCCGGGCGAGTCCCCTTCTACTATA-----ACG 481

Qy 1024 CGGTCCTGCTCCCCGCCGATTCTCCACAGCTCCCCACATCTACGCAGTCTTACCTCCC 1083
 | | | | | || | | | || | ||||| | ||| ||||| ||

Db 482 AGCTGCAGAGTGCCCTTCCACTTGCCRGAGCAGGACCTCATCTATGGAGTTTTCACAACTA 541

Qy 1084 AGTGGCAGGTTGGCGGGACCAGGAGCTCTGCGGTTTGTGCCTTCTCTCTCTTGGACATTG 1143
 | | | | | : | ||||| || | ||||| || | | |

Db 542 A-----CGTAAACAGCATYGCGGCTTCTGCTGTCTGCGCCTTCAACCTCAGTGCTATCT 595

Qy 1144 AACGTGTCTTTAAGGGGAAATACAAAGAGTTGAACAAAGAACTTCACGCTGGACTACTT 1203
 | | | || || || || | | | | | | | || | |

Db 596 CCCAGGCTTTCATGGCCATTTCGCTACCAGGAGAACCCAGGGCTGCCTGGCTCCCCA 655

Qy 1204 ATAGGGGCCCTGAGACCAACCCCCGCCAGGCAGTTGCTCAGTGGGCCCCCTCCTCTGATA 1263
 ||| |||| || | |||| | | | | || |||

Db 656 TAGCCAACCCCATCCCCAATTTCAGTGTGGCACCCCTGCCTGAGACCGGTCCCAACGAGA 715

Qy 1264 AG-----GCCCTGACCTTCATGAAGGACCATTTCCTGATGGATGAGCAAGTGG 1311
 | |||| | | || | ||||| || | |||

Db 716 ACCTGACGGAGCGCAGCCTGCAGGACGCGCAGCGCCTCTTCCTGATGAGCGAGGCCGTGC 775

Qy 1312 TGGGG-----ACGCCCCGCTGGTGAAATCTGGCGTGGAGTATACACGGCTTGCA 1362
 | | |||| | | |||| | ||| || | |

Db 776 AGCCGGTGACACCCGAGCCCTGTGTCACCCAGGACAGCGTGCCTTCTCACACCTCGTGG 835

Qy 1363 TGGAGACAGCCCAGGGCCTTGATGGGCACAGCCAT-----CTTGTCTATGTACCTGG 1413
 |||| | |||| || | |||| || || | ||

Db 836 TGGACCTGGTGCAGGCTAAAGACACGCTCTACCATGTACTCTACATTGGCACCGAGTCGG 895

Qy 1414 GAACCACCACAGGGTCGCTCCACAAGGCTGTGGTAAGTGGGGACAGCAGTGCTCATCTGG 1473
 | |||| | |||| || || | || || | | ||

Db 896 GCACCATCCTGAAGGCGCTGTCCACGGCGAGCCGACGCTCCACGGCTGCTACCTGGAGG 955

Qy 1474 TGGAAGAGATTTCAGCTGTTCCCTGACCCTGAACCTGTTTCGCAACCTGCAGCTGGCCCCCA 1533
 | | | | | | || || | ||||| || | |||

Db 956 AGCTGCACGTGCTGCCCCCGGGCGCCGCGAGCCCTGCGCAGCTGCGCATCCTGCACA 1015

Qy 1534 CCCAGGGTGCAGTGTTTGTAGGCTTCTCAGGAGGTGTCTGGAGGGTGCCCCGAGCCAACT 1593
 | | || | || || | || || || | ||||| || | |

Db 1016 GCGCCCGCGCGCTCTTCGTGGGGCTGAGAGACGGCGTCTGCGGGTCCCCTGGAGAGGT 1075

```

Qy      1594 GTAGTGTCTATGAGAGCTGTGTGGACTGTGTCCCTTGCCCCGGGACCCCCACTGTGCCTGGG 1653
          |   | |||   |||   | ||  ||  |   ||||| ||||| ||||| |||||
Db      1076 GCGCCGCCTACCGCAGCCAGGGGGCATGCCTGGGGGCCCGGGACCCGTACTGTGGCTGGG 1135

Qy      1654 ACCCTGAGTCCCGAACCTGTTGC---CTCCTGTCTGCCCCAACCTGAACCTCTGGAAGC 1710
          ||   ||   | |   ||  ||   |||  |   | ||||| ||| | ||||| |
Db      1136 ACGGGAAGCAGCAACGTTGCAGCACACTCGAGGACAGCTCCAACATGAGCCTCTGGACCC 1195

Qy      1711 AGGACAT 1717
          || ||||
Db      1196 AGAACAT 1202

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RESULT 10

US-09-854-845-13

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; Sequence 13, Application US/09854845
; Patent No. 6750054
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Wang, Xiaoming
; APPLICANT: Scoville, John
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: No. 6750054el Human Semaphorin Homologs and
Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0177-USA
; CURRENT APPLICATION NUMBER: US/09/854,845
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: US 60/205,274
; PRIOR FILING DATE: 2000-05-18
; PRIOR APPLICATION NUMBER: US 60/208,893
; PRIOR FILING DATE: 2000-06-02
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 2865
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-854-845-13

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Query Match          3.9%; Score 121.4; DB 4; Length 2865;
Best Local Similarity 49.5%; Pred. No. 8.6e-23;
Matches 568; Conservative 1; Mismatches 527; Indels 51; Gaps 8;

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Qy      607 AGGTCATGGAGGGAAAAGGCCAAAGCCCTTTGACCCCGCTCACAAGCATACGGCTG--- 663
          ||   ||   | ||   | ||   ||||| |||||   ||||   || ||||
Db      71  AGAAGATCAATGGTGTGGCCCGCTGCCCCATGACCCACGCCACAACCTCCACAGCTGTCA 130

Qy      664 TCTTGGTGGATGGGATGCTCTATTTCTGGTACTATGAACAACCTCCTGGGCAGTGAGCCCA 723
          |||   | |||  ||||| | |  ||  | | | ||||   ||  | || ||
Db      131 TCTCCTCCCAGGGGAGCTCTATGCAGCCACGGTCATCGACTTCTCAGGTCGGGACCCTG 190

Qy      724 TCCTGATGCGCACACTGGGATCCCAGCCTGTCTCAAGACCGACAACCTCCTCCGCTGGC 783
          | |   ||||  |||||   |||  ||   || | | | | | | | | |
Db      191 CCATCTACCGCAGCCTGGGCAGTGGGCCACCGCTTCGCACCTGCCCAATATAACTCCAAGT 250

Qy      784 TGCATCATGACGCCTCCTTTGTGGCAGCCATCCCTTCGACCCAGGTCGTCTACTTCTTCT 843
          || | ||||  |   |||  ||||| |||   |   | | | | ||||| |||

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Db		251 GGCTTAATGAGCCAAACTTCGTGGCAGCCTATGATAATTGGGCTGTTTGACATACTTCTTCC	310
Qy	844 TCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAGAGGCTCCACACATCGCGGGTGGCTA	903	
Db	311 TGCGGGAGAACGCAGTGGAG---CACGACTGTGGACGCACC GTGACTCTCGCGTGGCCC	367	
Qy	904 GAGTCTGCAAGAATGACGTGGGCGGCCAAAAGCTGCTGCAGAAGAAGTGGACCACCTTCC	963	
Db	368 GCGTGTGCAAGAATGACGTGGGGGGCCGATT CCTGCTGGAGGACACATGGACCACATTCA	427	
Qy	964 TGAAGGCC CAGCTGCTCTGCACCCAGCCGGGGCAGCTGCCCTTCAAACGTCATCCGCCACG	1023	
Db	428 TGAAGGCC CGGCTCAACTGCTCCCCGCCCGGCGAGGTCCCCTTCTACTATA-----ACG	481	
Qy	1024 CGGTCCTGCTCCCCGCCGATTCTCC ACAGCTCCCCACATCTACGCAGTCTTACCTCCC	1083	
Db	482 AGCTGCAGAGTGCTTCCA CTGCCR GAGCAGGACCTCATCTATGGAGTTTTACAACCA	541	
Qy	1084 AGTGGCAGGTTGGCGGG ACCAGGAGCTCTGCGGTTTGTGCCTTCTCTCTTGGACATTG	1143	:
Db	542 A-----CGTAAACAGCATYGGGCTTCTGCTGTCTGCGCCTTCAAACCTCAGTGCTATCT	595	
Qy	1144 AACGTGTCTTTAAGGGG AAAATAC AAAGAGTTGAACAAAGAA ACTTCACGCTGGACTACTT	1203	
Db	596 CCCAGGCTTTCA ATGGCC ATTTCGCTACCAGGAGAACCCAGGGCTGCCTGGCTCCCCA	655	
Qy	1204 ATAGGGG CCCTGAGACCAACCCCGGCCAGGCAGTTGCTCAGTGGGCCCCCTCCTCTGATA	1263	
Db	656 TAGCCAACCC CATCCCCAATTTCCAGTGTGGCACCCTGCCTGAGACCGGTCCCAACGAGA	715	
Qy	1264 AG-----GCCCTGACCTTCATGAAGGACCATTTCCTGATGGATGAGCAAGTGG	1311	
Db	716 ACCTGACGGAGCGCAGCCTGCAGGACGCGCAGCGCTCTTCTGATGAGCGAGGCCGTGC	775	
Qy	1312 TGGGG-----ACGCCCCCTGCTGGTGAAATCTGGCGTGAGTATACACGGCTTG CAG	1362	
Db	776 AGCCGGTGACACCCGAGCCCTGTGTCA CCCAGGACAGCGTGCGCTTCTCACACCTCGTGG	835	
Qy	1363 TGGAGACAGCC CAGGGCCTTGATGGGCACAGCCAT-----CTTGTCATGTACCTGG	1413	
Db	836 TGGACCTGGTG CAGGCTAAAGACACGCTCTACCATGTACTCTACATTGGCACCAGTTCGG	895	
Qy	1414 GAACCACCACAGGGT CGCTCCACAAGGCTGTGGTAAGTGGGGACAGCAGTGCTCATCTGG	1473	
Db	896 GCACCATCCTGAAGGCGCTGTCCACGGCGAGCCG CAGCCTCCACGGCTGCTACCTGGAGG	955	
Qy	1474 TGGAAGAGATT CAGCTGTTCCTGACCCTGAACCTGTT CGAACCTGCAGCTGGCCCCCA	1533	
Db	956 AGCTGCACGTGCTGCCCCCGGGCGCCG CAGCCCCCTGCGCAGCCTGCGCATCTGCACA	1015	
Qy	1534 CCCAGGGTG CAGTGTTTGTAGGCTTCTCAGGAGGTGTCTGGAGGGTGCCCCGAGCCAACT	1593	
Db	1016 GCGCCCGCGCGCTCTTCGTGGGGCTGAGAGACGGCG TCCTGCGGGTCCCACTGGAGAGGT	1075	
Qy	1594 GTAGTGTCTATGAGAGCTGTGTGGACTGTGTCCTTG CCGGGACCCCCCCACTGTGCCTGGG	1653	
Db	1076 GCGCCGCTTACCGCAGCCAGGGGGCATGCCTGGGGG CCGGGACCCGTACTGTGGCTGGG	1135	

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Qy      1654 ACCCTGAGTCCCGAACCTGTTGC---CTCCTGTCTGCCCCAACCTGAACTCCTGGAAGC 1710
      ||      ||      | |      ||      ||      |||      |      | ||||| |||      | |||||      |
Db      1136 ACGGGAAGCAGCAACGTTGCAGCACACTCGAGGACAGCTCCAACATGAGCCTCTGGACCC 1195

Qy      1711 AGGACAT 1717
      || ||||
Db      1196 AGAACAT 1202

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RESULT 11

US-09-854-845-5

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; Sequence 5, Application US/09854845
; Patent No. 6750054
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Wang, Xiaoming
; APPLICANT: Scoville, John
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: No. 6750054el Human Semaphorin Homologs and
Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0177-USA
; CURRENT APPLICATION NUMBER: US/09/854,845
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: US 60/205,274
; PRIOR FILING DATE: 2000-05-18
; PRIOR APPLICATION NUMBER: US 60/208,893
; PRIOR FILING DATE: 2000-06-02
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 3105
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-854-845-5

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Query Match          3.9%; Score 121.4; DB 4; Length 3105;
Best Local Similarity 49.5%; Pred. No. 9e-23;
Matches 568; Conservative 1; Mismatches 527; Indels 51; Gaps 8;

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Qy      607 AGGTCATGGAGGGAAAAGGCCAAAGCCCCTTTGACCCCGCTCACAAGCATACGGCTG--- 663
      ||      ||      | ||      | ||      ||||| |||||      ||||      || ||||
Db      356 AGAAGATCAATGGTGTGGCCCGCTGCCCTATGACCCACGCCACAACCTCCACAGCTGTCA 415

Qy      664 TCTTGGTGGATGGGATGCTCTATTCTGGTACTATGAACAACCTTCTGCGGAGTGAGCCCA 723
      |||      | ||| ||||| || | || | | ||||      || | || ||
Db      416 TCTCCTCCCAGGGGGAGCTCTATGCAGCCACGGTCATCGACTTCTCAGGTCGGGACCCTG 475

Qy      724 TCCTGATGCGCACACTGGGATCCCAGCCTGTCTCAAGACCGACAACCTTCTCCGCTGGC 783
      | |      |||| ||||      |||      ||      || | | | | | | | |
Db      476 CCATCTACCGCAGCCTGGGAGTGGGCCACCGCTTCGCACTGCCCAATATAACTCCAAGT 535

Qy      784 TGCATCATGACGCCTCCTTTGTGGCAGCCATCCCTTCGACCCAGGTCGTCTACTTCTTCT 843
      || | |||| | ||| ||||| |||      |      | | | | ||||| |||
Db      536 GGCTTAATGAGCCAAACTTCGTGGCAGCCTATGATATTGGGCTGTTTGCATACTTCTTCC 595

Qy      844 TCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAGAGGCTCCACACATCGCGGGTGGCTA 903

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Db	596	TGCGGGGAGAACGCAGTGGAG---CACGACTGTGGACGCACCGTGTACTCTCGCGTGGCCC	652
Qy	904	GAGTCTGCAAGAATGACGTGGGCGGCGAAAAGCTGCTGCAGAAGAAGTGGACCACCTTCC	963
Db	653	GCGTGTGCAAGAATGACGTGGGGGGCCGATTCTGCTGGAGGACACATGGACCACATTCA	712
Qy	964	TGAAGGCCCAGCTGCTCTGCACCCAGCCGGGGCAGCTGCCCTTCAACGTCATCCGCCACG	1023
Db	713	TGAAGGCCCAGCTCAACTGCTCCCGCCGGGCGAGGTCCCTTCTACTATA-----ACG	766
Qy	1024	CGGTCTGCTCCCCGCCGATTCTCCACAGCTCCCCACATCTACGCAGTCTTCACCTCCC	1083
Db	767	AGCTGCAGAGTGCCTTCCACTTGCCRGAGCAGGACCTCATCTATGGAGTTTTCACAACCA	826
Qy	1084	AGTGGCAGGTTGGCGGGACCAGGAGCTCTGCGGTTTGTGCCTTCTCTCTTGGACATTG	1143
Db	827	A-----CGTAAACAGCATYGCGGCTTCTGCTGTCTGCGCCTTCAACCTCAGTGCTATCT	880
Qy	1144	AACGTGTCTTTAAGGGGAAATACAAAGAGTTGAACAAAGAACTTCACGCTGGACTACTT	1203
Db	881	CCCAGGCTTTCAATGGCCCATTTTCGCTACCAGGAGAACCCAGGGCTGCCTGGCTCCCCA	940
Qy	1204	ATAGGGGCCCTGAGACCAACCCCCGGCCAGGCAGTTGCTCAGTGGGCCCCCTCCTCTGATA	1263
Db	941	TAGCCAACCCCATCCCCAATTTCCAGTGTGGCACCTGCCTGAGACCGGTCCCAACGAGA	1000
Qy	1264	AG-----GCCCTGACCTTCATGAAGGACCATTTCCCTGATGGATGAGCAAGTGG	1311
Db	1001	ACCTGACGGAGCGCAGCCTGCAGGACGCGCAGCGCCTCTTCCTGATGAGCGAGGCCGTGC	1060
Qy	1312	TGGGG-----ACGCCCCGTGCTGGTGAATCTGGCGTGGAGTATACACGGCTTGCAG	1362
Db	1061	AGCCGGTGACACCCGAGCCCTGTGTACCCAGGACAGCGTGCGCTTCTCACACCTCGTGG	1120
Qy	1363	TGGAGACAGCCCAGGGCCTTGATGGGCACAGCCAT-----CTTGTCATGTACCTGG	1413
Db	1121	TGGACCTGGTGCAGGCTAAAGACACGCTCTACCATGTACTCTACATTGGGCACCGAGTCGG	1180
Qy	1414	GAACCACCACAGGGTCGCTCCACAAGGCTGTGGTAAGTGGGGACAGCAGTGCTCATCTGG	1473
Db	1181	GCACCATCCTGAAGGCGCTGTCCACGGCAGCCGAGCCTCCACGGCTGCTACCTGGAGG	1240
Qy	1474	TGGAAGAGATTGAGCTGTTCCCTGACCCTGAACCTGTTTCGCAACCTGCAGCTGGCCCCCA	1533
Db	1241	AGCTGCACGTGCTGCCCCCGGGCGCCGCGAGCCCCCTGCGCAGCCTGCGCATCCTGCACA	1300
Qy	1534	CCCAGGGTGCAGTGTTTGTAGGCTTCTCAGGAGGTGTCTGGAGGGTGGCCCCGAGCCAACT	1593
Db	1301	GCGCCCGCGCGCTCTTCGTGGGGCTGAGAGACGGCGTCCCTGCGGGTCCCACTGGAGAGGT	1360
Qy	1594	GTAGTGTCTATGAGAGCTGTGTGGACTGTGTCTTGTCCCTTGTCCCGGGACCCCCACTGTGCCCTGGG	1653
Db	1361	GCGCCGCTTACCGCAGCCAGGGGGCATGCCTGGGGGCCCGGGACCCGTACTGTGGCTGGG	1420
Qy	1654	ACCCTGAGTCCCGAACCTGTTGC---CTCCTGTCTGCCCCAACCTGAACCTCTGGAAGC	1710


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Db      1421  ACGGGAAGCAGCAACGTTGCAGCACACTCGAGGACAGCTCCAACATGAGCCTCTGGACCC 1480
Qy      1711  AGGACAT 1717
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Db      1481  AGAACAT 1487

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RESULT 12

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US-09-854-845-1
; Sequence 1, Application US/09854845
; Patent No. 6750054
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Wang, Xiaoming
; APPLICANT: Scoville, John
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: No. 6750054e1 Human Semaphorin Homologs and
Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0177-USA
; CURRENT APPLICATION NUMBER: US/09/854,845
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: US 60/205,274
; PRIOR FILING DATE: 2000-05-18
; PRIOR APPLICATION NUMBER: US 60/208,893
; PRIOR FILING DATE: 2000-06-02
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3150
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-854-845-1

```

Query Match 3.9%; Score 121.4; DB 4; Length 3150;
Best Local Similarity 49.5%; Pred. No. 9e-23;
Matches 568; Conservative 1; Mismatches 527; Indels 51; Gaps 8;

Qy	607	AGGTCATGGAGGGAAAAAGGCCAAAGCCCCTTTTGACCCCGCTCACAAGCATACGGCTG---	663
Db	356	AGAAGATCAATGGTGTGGCCCGCTGCCCCTATGACCACGCCACAACCTCCACAGCTGTCA	415
Qy	664	TCTTGGTGGATGGGATGCTCTATTCTGGTACTATGAACAACTTCCTGGGCAGTGAGCCCA	723
Db	416	TCTCCTCCAGGGGGAGCTCTATGCAGCCACGGTCATCGACTTCTCAGGTCGGGACCCTG	475
Qy	724	TCCTGATGCGCACACTGGGATCCCAGCCTGTCCTCAAGACCGACAACCTTCCTCCGCTGGC	783
Db	476	CCATCTACCGCAGCCTGGGCAGTGGGCCACCGCTTCGCACTGCCAATAAATACTCCAAGT	535
Qy	784	TGCATCATGACGCCTCCTTTGTGGCAGCCATCCCTTCGACCCAGGTCGTCTACTTCTTCT	843
Db	536	GGCTTAATGAGCCAAACTTCGTGGCAGCCTATGATATTGGGCTGTTTGCATACTTCTTCC	595
Qy	844	TCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAGAGGCTCCACACATCGCGGGTGGCTA	903
Db	596	TGCGGGGAGAACGCAGTGGAG---CACGACTGTGGACGCACCGTGTACTCTCGCGTGGCCC	652

Qy	904	GAGTCTGCAAGAATGACGTGGGCGGGCGAAAAGCTGCTGCAGAAGAAGTGGACCACCTTCC	963
Db	653	GCCTGTGCAAGAATGACGTGGGCGGGCGGATTCCTGCTGGAGGACACATGGACCACATTCA	712
Qy	964	TGAAGGCCCAGCTGCTCTGCACCCAGCCGGGGCAGCTGCCCTTCAACGTCATCCGCCACG	1023
Db	713	TGAAGGCCCAGCTCAACTGCTCCCGCCGGGCGAGGTCCCTTCTACTATA-----ACG	766
Qy	1024	CGGTCCCTGCTCCCCGCCGATTCCTCCACAGCTCCCCACATCTACGCAGTCTTCACCTCCC	1083
Db	767	AGCTGCAGAGTGCCTTCCACTTGCCRGAGCAGGACCTCATCTATGGAGTTTTTACAACCA	826
Qy	1084	AGTGGCAGGTTGGCGGGACCAGGAGCTCTGCGGTTTGTGCCTTCTCTCTCTTGGACATTG	1143
Db	827	A-----CGTAAACAGCATYGC GGCTTCTGCTGTCTGCGCCTTCAACCTCAGTGCTATCT	880
Qy	1144	AACGTGTCTTTTAAGGGGAAATACAAAGAGTTGAACAAAGAACTTCACGCTGGACTACTT	1203
Db	881	CCCAGGCTTTCAATGGCCCATTTTCGCTACCAGGAGAACCCAGGGCTGCCTGGCTCCCCA	940
Qy	1204	ATAGGGGGCCCTGAGACCAACCCCCGGCCAGGCAGTTGCTCAGTGGGCCCCCTCCTCTGATA	1263
Db	941	TAGCCAACCCCATCCCCAATTTCCAGTGTGGCACCCCTGCCTGAGACCGGTCCCAACGAGA	1000
Qy	1264	AG-----GCCCTGACCTTCATGAAGGACCATTTCTGATGGATGAGCAAGTGG	1311
Db	1001	ACCTGACGGAGCGCAGCCTGCAGGACGCGCAGCGCCTCTTCTGATGAGCGAGGCCGTGC	1060
Qy	1312	TGGGG-----ACGCCCCCTGCTGGTGAAATCTGGCGTGGAGTATACACGGCTTGCAG	1362
Db	1061	AGCCGGTGACACCCGAGCCCTGTGTCAACCCAGGACAGCGTGCCTTCTCACACCTCGTGG	1120
Qy	1363	TGGAGACAGCCAGGGCCTTGATGGGCACAGCCAT-----CTTGTCTATGTACCTGG	1413
Db	1121	TGGACCTGGTGCAGGCTAAAGACACGCTCTACCATGTACTCTACATTGGCACCGAGTCGG	1180
Qy	1414	GAACCACCACAGGGTCGCTCCACAAGGCTGTGGTAAGTGGGGACAGCAGTGCTCATCTGG	1473
Db	1181	GCACCATCCTGAAGGCGCTGTCCACGGCGAGCCGCAGCCTCCACGGCTGCTACCTGGAGG	1240
Qy	1474	TGGAAGAGATTAGCTGTTCCCTGACCCCTGAACCTGTTTCGCAACCTGCAGCTGGCCCCCA	1533
Db	1241	AGCTGCACGTGCTGCCCCCGGGCGCCGCGAGCCCCCTGCGCAGCCTGCGCATCCTGCACA	1300
Qy	1534	CCCAGGGTGCAGTGTTTTGTAGGCTTCTCAGGAGGTGTCTGGAGGGTGGCCCCGAGCCAACT	1593
Db	1301	GCGCCCGCGCGCTCTTCGTGGGGCTGAGAGACGGCGTCTGCGGGTCCCCTGGAGAGGT	1360
Qy	1594	GTAGTGTCTATGAGAGCTGTGTGGACTGTGTCTTGGCCGGGACCCCCACTGTGCCTGGG	1653
Db	1361	GCGCCGCCTACCGCAGCCAGGGGGCATGCCTGGGGGCCCCGGGACCCGTACTGTGGCTGGG	1420
Qy	1654	ACCCTGAGTCCCGAACCTGTTGC---CTCCTGTCTGCCCCCAACCTGAACTCCTGGAAGC	1710
Db	1421	ACGGGAAGCAGCAACGTTGCAGCACACTCGAGGACAGCTCCAACATGAGCCTCTGGACCC	1480
Qy	1711	AGGACAT	1717

Db 1481 AGAACAT 1487

RESULT 13

US-09-854-845-7

; Sequence 7, Application US/09854845

; Patent No. 6750054

; GENERAL INFORMATION:

; APPLICANT: Walke, D. Wade

; APPLICANT: Wang, Xiaoming

; APPLICANT: Scoville, John

; APPLICANT: Turner, C. Alexander Jr.

; TITLE OF INVENTION: No. 6750054el Human Semaphorin Homologs and Polynucleotides Encoding the Same

; FILE REFERENCE: LEX-0177-USA

; CURRENT APPLICATION NUMBER: US/09/854,845

; CURRENT FILING DATE: 2001-05-14

; PRIOR APPLICATION NUMBER: US 60/205,274

; PRIOR FILING DATE: 2000-05-18

; PRIOR APPLICATION NUMBER: US 60/208,893

; PRIOR FILING DATE: 2000-06-02

; NUMBER OF SEQ ID NOS: 50

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 7

; LENGTH: 3237

; TYPE: DNA

; ORGANISM: homo sapiens

US-09-854-845-7

Query Match 3.9%; Score 121.4; DB 4; Length 3237;
Best Local Similarity 49.5%; Pred. No. 9.2e-23;
Matches 568; Conservative 1; Mismatches 527; Indels 51; Gaps 8;

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Qy      607 AGGTCATGGAGGGAAAAGGCCAAAGCCCCTTTGACCCCGCTCACAAGCATACGGCTG--- 663
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Db      488 AGAAGATCAATGGTGTGGCCCGCTGCCCTATGACCCACGCCACAACCTCCACAGCTGTCA 547

Qy      664 TCTTGGTGGATGGGATGCTCTATTCTGGTACTATGAACAACTTCCTGGGCAGTGAGCCCA 723
          |||  | |||  ||||| | | ||  | | | ||||  ||  | || |
Db      548 TCTCCTCCCAGGGGAGCTCTATGACGCCACGGTCATCGACTTCTCAGGTCGGGACCCTG 607

Qy      724 TCCTGATGCGCACACTGGGATCCCAGCCTGTCCTCAAGACCGACAACCTTCCTCCGCTGGC 783
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Db      608 CCATCTACCGCAGCCTGGGCAGTGGGCCACCGCTTCGCACTGCCCAATATAACTCCAAGT 667

Qy      784 TGCATCATGACGCCTCCTTTGTGGCAGCCATCCCTTCGACCCAGGTCGTCTACTTCTTCT 843
          || | ||||  |  |||  ||||| |||  |  | | | | |||||
Db      668 GGCTTAATGAGCCAAACTTCGTGGCAGCCTATGATATTGGGCTGTTTGCATACTTCTTCC 727

Qy      844 TCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAGAGGCTCCACACATCGCGGGTGGCTA 903
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Db      728 TGCGGGGAGAACGCAGTGGAG---CACGACTGTGGACGCACCGTGTACTCTCGCGTGGCCC 784

Qy      904 GAGTCTGCAAGAATGACGTGGGCGGCGAAAAGCTGCTGCAGAAGAAGTGGACCACCTTCC 963
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Db      785 GCGTGTGCAAGAATGACGTGGGGGGCCGATTCCTGCTGGAGGACACATGGACCACATTCA 844
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Qy	964	TGAAGGCCACAGCTGCTCTGCACTCCAGCCGGGGCGAGCTGCCCTTCAACCTCATCCGCCACG	1023
Db	845	TGAAGGCCCGGCTCAACTGCTCCCGCCCGGGCGAGGTCCCCTTCTACTATA-----ACG	898
Qy	1024	CGGTCCTGCTCCCCGCCGATTCTCCCACAGCTCCCCACATCTACGCAGTCTTCACCTCCC	1083
Db	899	AGCTGCAGAGTGCCTTCCACTTGCCRAGACAGGACCTCATCTATGGAGTTTTCACAACCA	958
Qy	1084	AGTGGCAGGTTGGCGGGACCAGGAGCTCTGCGGTTTGTGCCTTCTCTCTCTTGGACATTG	1143
Db	959	A-----CGTAAACAGCATYGCGGCTTCTGCTGTCTGCGCCTTCAACCTCAGTGCTATCT	1012
Qy	1144	AACGTGTCTTTAAGGGGAAATACAAAGAGTTGAACAAAGAAACTTCACGCTGGACTACTT	1203
Db	1013	CCCAGGCTTTCAATGGCCCATTTTCGCTACCAGGAGAACCCAGGGCTGCCTGGCTCCCCA	1072
Qy	1204	ATAGGGGCCCTGAGACCAACCCCCGGCCAGGCAGTTGCTCAGTGGGCCCCCTCCTCTGATA	1263
Db	1073	TAGCCAACCCCATCCCCAATTTCCAGTGTGGCACCCCTGCCTGAGACCGGTCCCAACGAGA	1132
Qy	1264	AG-----GCCCTGACCTTCATGAAGGACCATTTCTGATGGATGAGCAAGTGG	1311
Db	1133	ACCTGACGGAGCGCAGCCTGCAGGACGCGCAGCGCCTCTTCTGATGAGCGAGGCCGTGC	1192
Qy	1312	TGGGG-----ACGCCCCCTGCTGGTGAAATCTGGCGTGGAGTATACACGGCTTGCAG	1362
Db	1193	AGCCGGTGACACCCGAGCCCTGTGTACCCAGGACAGCGTGCGCTTCTCACACCTCGTGG	1252
Qy	1363	TGGAGACAGCCCAGGGCCTTGATGGGACAGCCAT-----CTTGTCATGTACCTGG	1413
Db	1253	TGGACCTGGTGCAGGCTAAAGACACGCTCTACCATGTACTCTACATTGGCACCAGAGTCGG	1312
Qy	1414	GAACCACCACAGGGTCGCTCCACAAGGCTGTGGTAAGTGGGGACAGCAGTGCTCATCTGG	1473
Db	1313	GCACCATCCTGAAGGCGCTGTCCACGGCGAGCCGACGCTCCACGGCTGCTACCTGGAGG	1372
Qy	1474	TGGAAGAGATTTCAGCTGTTCCCTGACCCCTGAACCTGTTGCAACCTGCAGCTGGCCCCCA	1533
Db	1373	AGCTGCACGTGCTGCCCCCGGGCGCCGAGCCCTGCGCAGCCTGCGCATCTGCACA	1432
Qy	1534	CCCAGGGTGCAGTGTTTGTAGGCTTCTCAGGAGGTGTCTGGAGGGTGCCCCGAGCCAACT	1593
Db	1433	GCGCCCGCGCGCTCTTCGTGGGGCTGAGAGACGGCGTCTGCGGGTCCCCTGGAGAGGT	1492
Qy	1594	GTAGTGTCTATGAGAGCTGTGTGGACTGTGTCCTTGCCCGGGACCCCCACTGTGCCTGGG	1653
Db	1493	GCGCCGCTACCGCAGCCAGGGGGCATGCCTGGGGGGCCCGGGACCCGTACTGTGGCTGGG	1552
Qy	1654	ACCCTGAGTCCCGAACCTGTTGC---CTCCTGTCTGCCCCAACCTGAACTCCTGGAAGC	1710
Db	1553	ACGGGAAGCAGCAACGTTGCAGCACACTCGAGGACAGCTCCAACATGAGCCTCTGGACCC	1612
Qy	1711	AGGACAT	1717
Db	1613	AGAACAT	1619

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 Db 899 AGCTGCAGAGTGCCCTTCCACTTGCCRGAGCAGGACCTCATCTATGGAGTTTTCACAACCA 958
 Qy 1084 AGTGGCAGGTTGGCGGGACCAGGAGCTCTGCGGTTTGTGCCTTCTCTCTCTGGACATTG 1143
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 Db 959 A-----CGTAAACAGCATYGC GGCTTCTGCTGTCTGCGCCTTCAACCTCAGTGCTATCT 1012
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 Db 1013 CCCAGGCTTTCAATGGCCCATTTTCGCTACCAGGAGAACCCAGGGCTGCCTGGCTCCCCA 1072
 Qy 1204 ATAGGGGGCCCTGAGACCAACCCCCGGCCAGGCAGTTGCTCAGTGGGCCCCCTCCTCTGATA 1263
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 Db 1073 TAGCCAACCCCATCCCCAATTTCCAGTGTGGCACCCCTGCCTGAGACCGGTCCCAACGAGA 1132
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 Db 1133 ACCTGACGGAGCGCAGCCTGCAGGACGCGCAGCGCCTCTTCCTGATGAGCGAGGCCGTGC 1192
 Qy 1312 TGGGG-----ACGCCCCTGCTGGTGAAATCTGGCGTGGAGTATACACGGCTTGCAG 1362
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 Qy 1363 TGGAGACAGCCAGGGCCTTGATGGGCACAGCCAT-----CTTGTCTATGTACCTGG 1413
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 Db 1253 TGGACCTGGTGCAGGCTAAAGACACGCTCTACCATGTACTCTACATTGGCACCGAGTCGG 1312
 Qy 1414 GAACCACCACAGGGTCGCTCCACAAGGCTGTGGTAAGTGGGGACAGCAGTGCTCATCTGG 1473
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 Db 1613 AGAACAT 1619

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; Sequence 11, Application US/09854845
; Patent No. 6750054
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Wang, Xiaoming
; APPLICANT: Scoville, John
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: No. 6750054el Human Semaphorin Homologs and
Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0177-USA
; CURRENT APPLICATION NUMBER: US/09/854,845
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: US 60/205,274
; PRIOR FILING DATE: 2000-05-18
; PRIOR APPLICATION NUMBER: US 60/208,893
; PRIOR FILING DATE: 2000-06-02
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 3411
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-854-845-11
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Query Match          3.9%; Score 121.4; DB 4; Length 3411;
Best Local Similarity 49.5%; Pred. No. 9.4e-23;
Matches 568; Conservative 1; Mismatches 527; Indels 51; Gaps 8;
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Qy      607 AGGTCATGGAGGGAAAAGGCCAAAGCCCCTTTGACCCCGCTCACAAGCATACGGCTG--- 663
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Qy      664 TCTTGGTGGATGGGATGCTCTATTCTGGTACTATGAACAACTTCCTGGGCAGTGAGCCCA 723
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Db      722 TCTCCTCCCAGGGGAGCTCTATGCAGCCACGGTCATCGACTTCTCAGGTCGGGACCCCTG 781

Qy      724 TCCTGATGCGCACACTGGGATCCCAGCCTGTCCTCAAGACCGACAACCTTCCTCCGCTGGC 783
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Qy      784 TGCATCATGACGCCTCCTTTGTGGCAGCCATCCCTTCGACCCAGGTCGTCTACTTCTTCT 843
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Db	1073	AGCTGCAGAGTGCCCTTCCACTTGCCRGAGCAGGACCTCATCTATGGAGTTTTTCACAACCA	1132
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Db	1133	A-----CGTAAACAGCATYGC GGCTTCTGCTGTCTGCGCCTTCAACCTCAGTGCTATCT	1186
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Qy	1264	AG-----GCCCTGACCTTCATGAAGGACCATTTCCCTGATGGATGAGCAAGTGG	1311
Db	1307	ACCTGACGGAGCGCAGCCTGCAGGACGCGCAGCGCCTCTTCCTGATGAGCGAGGCCGTGC	1366
Qy	1312	TGGGG-----ACGCCCCTGCTGGTGAAATCTGGCGTGGAGTATACACGGCTTGCAG	1362
Db	1367	AGCCGGTGACACCCGAGCCCTGTGTCACCCAGGACAGCGTGCCTTCTCACACCTCGTGG	1426
Qy	1363	TGGAGACAGCCCAGGGCCTTGATGGGCACAGCCAT-----CTTGTCTATGTACCTGG	1413
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Qy	1414	GAACCACCACAGGGTCGCTCCACAAGGCTGTGGTAAGTGGGGACAGCAGTGCTCATCTGG	1473
Db	1487	GCACCATCCTGAAGGCGCTGTCCACGGCGAGCCGCAGCCTCCACGGCTGCTACCTGGAGG	1546
Qy	1474	TGGAAGAGATTTCAGCTGTTCCTGACCCCTGAACCTGTTTCGCAACCTGCAGCTGGCCCCCA	1533
Db	1547	AGCTGCACGTGCTGCCCCCGGGCGCCGCGAGCCCTGCGCAGCCTGCGCATCCTGCACA	1606
Qy	1534	CCCAGGGTGCAGTGTTTGTAGGCTTCTCAGGAGGTGTCTGGAGGGTGCCCCGAGCCAACT	1593
Db	1607	GCGCCCGCGCGCTCTTCGTGGGGCTGAGAGACGGCGTCTTGC GGTTCCCACTGGAGAGGT	1666
Qy	1594	GTAGTGTCTATGAGAGCTGTGTGGACTGTGTCCCTGCCCCGGGACCCCCACTGTGCCTGGG	1653
Db	1667	GCGCCGCTTACCGCAGCCAGGGGGCATGCCTGGGGGCCGGGACCCGTACTGTGGCTGGG	1726
Qy	1654	ACCCTGAGTCCCGAACCTGTTGC---CTCCTGTCTGCCCCCAACCTGAACTCCTGGAAGC	1710
Db	1727	ACGGGAAGCAGCAACGTTGCAGCACACTCGAGGACAGCTCCAACATGAGCCTCTGGACCC	1786
Qy	1711	AGGACAT	1717
Db	1787	AGAACAT	1793

Search completed: February 15, 2005, 17:08:49
Job time : 551 secs